

STIC-Biotech/ChemLib

174294

From: Duffy, Patricia  
Sent: Thursday, December 15, 2005 8:29 AM  
To: STIC-Biotech/ChemLib  
Subject: SPDI SEARCH

IN RE:10/063,549

PLEASE SEARCH SEQ ID NO:46 AND OLIGOMERS THEREOF.

Patricia A. Duffy, Ph.D.  
Art Unit 1645  
Remsen 3B05; Mailbox 3C18  
571-272-0855

RECEIVED  
DEC 15 2005  
STIC/BIOTECH DIV.  
(STIC)

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_



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GenCore version 5.1.6  
OM protein - protein search, using sw model  
Run on: December 16, 2005, 10:31:21 ; Search time 81 Seconds  
(without alignments)  
1817.184 Million cell updates/sec

Title: US-10-063-549-46  
Perfect score: 1772  
Sequence: 1 MAGSPCTCLTIYIMQLTGS.....PHSLTWDPFRLPAYENV1 335  
Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5  
2443163  
Total number of hits satisfying chosen parameters: 2443163  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :  
1: geneseqp1980s:\*  
A\_Geneseq\_21:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description
RESULT 1					
ID	AA66701	standard;	protein;	335	AA.
DE	Membrane-bound protein				PRO1138.
PN	WO9963088-A2.				
PD	09-DEC-1999.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1772;	DB 3;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 2					
ID	AA70431	standard;	protein;	335	AA.
DE	Human cell surface immunomodulator-1				(CSIMM-1).
PN	WO20011150-A1.				
PD	02-MAR-2000.				
PA	(INCYT-) INCYTE PHARM INC.				
Query Match	100.0%;	Score 1772;	DB 3;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 3					
ID	AA74609	standard;	protein;	335	AA.
DE	Human myocardin protein-7.				
PN	WO9967387-A2.				
PD	29-DEC-1999.				
PA	(MILL-) MILLENNITUM PHARM INC.				
Query Match	100.0%;	Score 1772;	DB 3;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 4					
ID	AAU29119	standard;	protein;	335	AA.
DE	Human PRO polypeptide sequence #96.				
PN	WO200168848-A2.				
PD	20-SEP-2001.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1772;	DB 4;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 5					
ID	AA87548	standard;	protein;	335	AA.
DE	Human PRO1138.				
PN	WO200116318-A2.				
PD	08-MAR-2001.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1772;	DB 4;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 6					
ID	AA847321	standard;	protein;	335	AA.

DE	APEX-1.				
PN	WO200146260-A2.				
PD	28-JUN-2001.				
PA	(BRIM ) BRISTOL-MYERS SQUIBB CO.				
Query Match	100.0%;	Score 1772;	DB 4;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 7					
ID	AA65224	standard;	protein;	335	AA.
DE	Human PRO1138 (UNQ576) protein sequence SEQ ID NO:253.				
PN	WO200073454-A1.				
PD	07-DEC-2000.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1772;	DB 4;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 8					
ID	ABG95873	standard;	protein;	335	AA.
DE	Human secreted/transmembrane protein PRO1138.				
PN	US2002119130-A1.				
PD	29-AUG-2002.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1772;	DB 5;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 9					
ID	ABU58495	standard;	protein;	335	AA.
DE	Human PRO polypeptide #96.				
PN	US2003027272-A1.				
PD	06-FEB-2003.				
Query Match	100.0%;	Score 1772;	DB 6;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 10					
ID	ABU88043	standard;	protein;	335	AA.
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003032127-A1.				
PD	13-FEB-2003.				
Query Match	100.0%;	Score 1772;	DB 6;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 11					
ID	ABU84358	standard;	protein;	335	AA.
DE	Human secreted/transmembrane protein (PRO) #96.				
PN	US2003032112-A1.				
PD	13-FEB-2003.				
Query Match	100.0%;	Score 1772;	DB 6;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 12					
ID	ABR66232	standard;	protein;	335	AA.
DE	Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN	US2003027278-A1.				
PD	06-FEB-2003.				
Query Match	100.0%;	Score 1772;	DB 6;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 13					
ID	ABR65622	standard;	protein;	335	AA.
DE	Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN	US2003036159-A1.				
PD	20-FEB-2003.				
Query Match	100.0%;	Score 1772;	DB 6;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 14					
ID	ABU9562	standard;	protein;	335	AA.
DE	Human secreted/transmembrane protein (PRO) #96.				
PN	US2003040070-A1.				
PD	27-FEB-2003.				
Query Match	100.0%;	Score 1772;	DB 6;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 15					
ID	ABU58039	standard;	protein;	335	AA.
DE	Human PRO polypeptide #71.				
PN	US2003027163-A1.				
PD	06-FEB-2003.				
Query Match	100.0%;	Score 1772;	DB 6;	Length 335;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;			
RESULT 16					
ID	ABU59117	standard;	protein;	335	AA.



DE Novel human secreted or transmembrane protein PRO1138.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 17  
ID AB082629 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 18  
ID AB082801 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 19  
ID AB089922 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 20  
ID ABR68171 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 21  
ID AB060548 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein. #100.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 22  
ID AB096224 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 23  
ID AB092655 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 24  
ID AB008732 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 25  
ID AB002784 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 26  
ID ABR74938 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 27  
ID ABR94700 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 28  
ID AB013930 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 29  
ID AB085673 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 30  
ID AB098833 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 31  
ID AB098048 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 32  
ID AB091754 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 33  
ID AB089447 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 34  
ID AB086288 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 35  
ID AB067501 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 36  
ID AB080529 standard; protein; 335 AA.



DE Human PRO protein #96.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 37  
ID ABU72515 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 38  
ID ABU90898 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 39  
ID ABO33957 standard; protein; 335 AA.  
DE Human secreted/cranmembrane protein PRO138.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 40  
ID ABR99447 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 41  
ID ABR98837 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 42  
ID ABO16360 standard; protein; 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 43  
ID ABR92260 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 44  
ID ABO18901 standard; protein; 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 45  
ID ABR78322 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 46  
ID ABU71974 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO138.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 47  
ID ABU85058 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 48  
ID ABO00197 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 49  
ID ABO11529 standard; protein; 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 50  
ID ABO02174 standard; protein; 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 51  
ID ABU88748 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 52  
ID ABU83443 standard; protein; 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 53  
ID ABO06244 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 54  
ID ABR59280 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 55  
ID ABO09342 standard; protein; 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 56  
ID ABO19206 standard; protein; 335 AA.



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DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 57
ID ABO11224 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 58
ID ABR66842 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 59
ID ABO16055 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 60
ID ABO13761 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 61
ID ABU71528 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138.
PN US2003013855-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 62
ID ABU65664 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, SEQ ID 192.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 63
ID ABO07512 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 64
ID ABO03699 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 65
ID ABR67147 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 66
ID ABO15750 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 67
ID ABU56031 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, PRO1138.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 68
ID ABU72309 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 69
ID ABU65359 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 70
ID ABU95304 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 71
ID ABU71207 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 72
ID ABO07817 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 73
ID ABR70058 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 74
ID ABR69391 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 75
ID ABO01532 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 76
ID ABU81334 standard; protein; 335 AA.
```



DE Human PRO polypeptide #96.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 77  
ID ABR60131 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 78  
ID ABU90982 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 79  
ID ABR67866 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 80  
ID ABR65254 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 81  
ID ABR68476 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 82  
ID ABR71888 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 83  
ID ABUS9264 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein; #100.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 84  
ID ABUS368 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US200302295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 85  
ID ABUS9058 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US200302297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 86  
ID ABUS3138 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 87  
ID ABUS9494 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 88  
ID ABUS90542 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 89  
ID ABUS4053 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 90  
ID ABUS3704 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 91  
ID ABO25961 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 92  
ID ABR64949 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 93  
ID ABO27303 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO138.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 94  
ID ABR68781 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 95  
ID ABO06597 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 96  
ID ABR99142 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.



PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 97  
ID ABU57026 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 98  
ID ABU85978 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 99  
ID ABU82265 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 100  
ID ABU87276 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 101  
ID ABU83748 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 102  
ID ABO08122 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 103  
ID ABU92498 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 104  
ID ABU81833 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 105  
ID ABU65997 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 106  
ID ABU81168 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138.  
PN US2003027212-A1.  
PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 107  
ID ABR59826 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 108  
ID ABU94014 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 109  
ID ABU99867 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 110  
ID ABR6537 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 111  
ID ABR90955 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 112  
ID ABO53283 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO138.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 113  
ID ABU58970 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein #100.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 114  
ID ABU94382 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 115  
ID ABU79264 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 116  
ID ABU86593 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032129-A1.



PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 117  
ID AB086898 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 118  
ID AB094687 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 119  
ID AB004614 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 120  
ID ABR70363 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 121  
ID AB092348 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 122  
ID AB098528 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 123  
ID ABR65927 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GRTN) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 124  
ID ABR64644 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 125  
ID AB059413 standard; protein; 335 AA.  
DE Novel human secreted or transmembrane protein PRO1054.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 126  
ID AB079569 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 127  
ID AB092960 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 128  
ID AB095919 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 129  
ID AB091139 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 130  
ID AB090332 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 131  
ID AB009647 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 132  
ID ABR58417 standard; protein; 335 AA.  
DE Human NOV27a.  
PN WO2003029423-A2.  
PD 10-APR-2003.  
PA (CORA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 133  
ID AB010919 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 134  
ID ABR07973 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 135  
ID AB019825 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GRTN) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;  
RESULT 136  
ID AB087581 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-162; Length 335;



RESULT 137  
ID ABU91449 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 138  
ID ABU89290 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 139  
ID ABU84663 standard; protein; 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 140  
ID ABU869753 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 141  
ID ABU80130 standard; protein; 335 AA.  
DE Human PRO protein #96.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 142  
ID ABU82497 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 143  
ID ABU92179 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 144  
ID ABU93399 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 145  
ID ABO09952 standard; protein; 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 146  
ID ABO09037 standard; protein; 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 147

ID ABU96461 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 148  
ID ABU10885 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 149  
ID ABU10605 standard; protein; 335 AA.  
DE Human secreted/cranmembrane protein #96.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 150  
ID ABU81637 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 151  
ID ABU72131 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 152  
ID ABU95614 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 153  
ID ABU96823 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 154  
ID ABR70668 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 155  
ID ABO05019 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
Pred. No. 1.1e-162;  
RESULT 156  
ID ABO08427 standard; protein; 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003044922-A1.



PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 157  
ID ABU8576 standard; protein; 335 AA.  
DE Human secreted and transmembrane polypeptide PRO1138.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 158  
ID ABO34090 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 159  
ID ABO05634 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 160  
ID ABR74023 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 161  
ID ABR95615 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 162  
ID ABR80912 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 163  
ID ABR81217 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 164  
ID ABR00913 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 165  
ID ABR88515 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 166  
ID ABR77336 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 167  
ID ABO28820 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 168  
ID ABO31565 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 169  
ID ABR07982 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 170  
ID ABO40462 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 171  
ID ABO35887 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 172  
ID ABO44026 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 173  
ID ADA77944 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 174  
ID ABR24621 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 175  
ID ABO03089 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.







ID AEM1642 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 195  
ID AEM02743 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 196  
ID AEM16039 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 197  
ID ABO27600 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 198  
ID AEM29091 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 199  
ID ABO07067 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 200  
ID AEM21161 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 201  
ID ABO09507 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 202  
ID ABO41377 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 203  
ID ABO36192 standard; protein; 335 AA.

DE Human PRO polypeptide #96.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 204  
ID ABO43721 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 205  
ID AEM76421 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 206  
ID AEM76117 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 207  
ID AEM25736 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 208  
ID AEM26041 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 209  
ID ADA21450 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO1138.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 210  
ID ABO03394 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 211  
ID ABO02479 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 212  
ID ABO44261 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO 1138.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 213



ID ABR90650 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 214  
ID ABR73718 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 215  
ID ABO16970 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 216  
ID ABR94395 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 217  
ID ABR75902 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 218  
ID ABR71278 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 219  
ID ABR93175 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 220  
ID ABR93480 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 221  
ID ADA10237 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, PRO1138.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 222  
ID ABR87905 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 223  
ID ABO27905 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 224  
ID ABO30040 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 225  
ID ABO33249 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 226  
ID ABW04937 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 227  
ID ABW08897 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 228  
ID ABO36497 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 229  
ID ABO35582 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 230  
ID ABO39547 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 231  
ID ABW10422 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 232  
ID ABR87905 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.



Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 232  
ID ABM11947 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 233  
ID ABO52093 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 234  
ID ABO52398 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 235  
ID ADA19908 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 236  
ID ABO23716 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 237  
ID ADB17291 standard; protein; 335 AA.  
DE Human transmembrane PRO polypeptide (SegID 46).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 238  
ID ADA17781 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 239  
ID ABR97202 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 240  
ID ABR86990 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 241  
ID ABM11032 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 242  
ID ABM28176 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 243  
ID ABO32175 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 244  
ID ABM15302 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 245  
ID ABM06457 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 246  
ID ABM04268 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 247  
ID ABM22381 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 248  
ID ABM07677 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 249  
ID ABO40767 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 250  
ID ABM35414 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.



PN US2003073179-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 251  
ID ABM33177 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 252  
ID ABO52703 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 253  
ID ABO50263 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 254  
ID ABU9257 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 255  
ID ABO04309 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 256  
ID ABO05939 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 257  
ID ABM18479 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 258  
ID ADA27889 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 259  
ID ABR97507 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 260

ID ABR80607 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 261  
ID ABM01218 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 262  
ID ABR8820 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 263  
ID ABM13472 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 264  
ID ABM20856 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 265  
ID ABO41987 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003048745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 266  
ID ABO42597 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 267  
ID ABM10117 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 268  
ID ABO38632 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 269  
ID ABM32872 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.



PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 270  
ID ABM22686 standard; protein, 335 AA.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 271  
ID ABM74897 standard; protein, 335 AA.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 272  
ID ADA79736 standard; protein, 335 AA.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 273  
ID ABR96287 standard; protein, 335 AA.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 274  
ID ABM02438 standard; protein, 335 AA.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 275  
ID ABR86380 standard; protein, 335 AA.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 276  
ID ABR86685 standard; protein, 335 AA.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 277  
ID ABM16649 standard; protein, 335 AA.  
PN US2003064448-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 278  
ID ABM29701 standard; protein, 335 AA.  
PN US2003064456-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 279  
ID ABO29125 standard; protein, 335 AA.  
PN US2003068693-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 280  
ID ABM23906 standard; protein, 335 AA.  
PN US2003068735-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 281  
ID ABM23296 standard; protein, 335 AA.  
PN US2003068753-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 282  
ID ABM22076 standard; protein, 335 AA.  
PN US2003068742-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 283  
ID ABO37717 standard; protein, 335 AA.  
PN US2003068756-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 284  
ID ABM28481 standard; protein, 335 AA.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 285  
ID ABM28786 standard; protein, 335 AA.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 286  
ID ABM66430 standard; protein, 335 AA.  
PN US2003068737-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 287  
ID ABM75812 standard; protein, 335 AA.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 288  
ID ABM34092 standard; protein, 335 AA.  
PN US2003068753-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;



PN US2003096359-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 289  
ID ABM34397 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 290  
ID ABO20328 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 291  
ID ABO21243 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 292  
ID ABO22158 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 293  
ID ADA20080 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 294  
ID ABO34189 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO 1138.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 295  
ID ABR96592 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 296  
ID ADA94469 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 297  
ID ABR85770 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 298  
ID ABR9752 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 299  
ID ABM0608 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 300  
ID ABM0303 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 301  
ID ABO29735 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 302  
ID ABM23601 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 303  
ID ABM29396 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 304  
ID ABO38327 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 305  
ID ABO45627 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 306  
ID ABM20551 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 307  
ID ADA81463 standard; protein; 335 AA.



DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 308  
ID ABO16665 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 309  
ID ABO18291 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 310  
ID ABO22718 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 311  
ID ABO23023 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 312  
ID ABR92565 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 313  
ID ABR81522 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 314  
ID ABM77946 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 315  
ID ABR89735 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 316  
ID ABM26651 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 317  
ID ABM13777 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 318  
ID ABO28515 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 319  
ID ABO30345 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 320  
ID ABM07372 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 321  
ID ABM03963 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 322  
ID ABO37107 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 323  
ID ABO41682 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 324  
ID ABO35277 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 325  
ID ABM25126 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 326  
ID ABO47518 standard; protein; 335 AA.



DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 327  
ID ABO47823 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 328  
ID ABO48433 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 329  
ID ABO51483 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 330  
ID ABO51788 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 331  
ID ABO50568 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 332  
ID ABR79692 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 333  
ID ABR16954 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 334  
ID ABO17986 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 335  
ID ABO20938 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032132-A1.  
PD 13-FEB-2003.

Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 336  
ID ABR96897 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 337  
ID ADA38694 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 338  
ID ABR12252 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 339  
ID ABR16344 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 340  
ID ABR24211 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 341  
ID ABR14692 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 342  
ID ABR04573 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 343  
ID ABR06762 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 344  
ID ABR09202 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 345  
ID ABO39242 standard; protein; 335 AA.



[illegible]

Best Local Similarity	100.0%;	Pred. No.1.1e-162;	
RESULT 355			
ID ABO06902 standard; protein; 335 AA.			
DE Human secreted/transmembrane protein (PRO) #96.			
PN US2003040053-A1.			
PD 27-FEB-2003.			
Query Match	100.0%;	Score 1772; DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No.1.1e-162;	
RESULT 356			
ID ABR44855 standard; protein; 335 AA.			
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.			
PN US2003040057-A1.			
PD 27-FEB-2003.			
Query Match	100.0%;	Score 1772; DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No.1.1e-162;	
RESULT 357			
ID ABR73413 standard; protein; 335 AA.			
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.			
PN US2003054467-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772; DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No.1.1e-162;	
RESULT 358			
ID ABR76507 standard; protein; 335 AA.			
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.			
PN US2003044932-A1.			
PD 06-MAR-2003.			
Query Match	100.0%;	Score 1772; DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No.1.1e-162;	
RESULT 359			
ID ABR73108 standard; protein; 335 AA.			
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.			
PN US2003027270-A1.			
PD 06-FEB-2003.			
Query Match	100.0%;	Score 1772; DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No.1.1e-162;	
RESULT 360			
ID ABM18174 standard; protein; 335 AA.			
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.			
PN US2003054469-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772; DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No.1.1e-162;	
RESULT 361			
ID ABO20633 standard; protein; 335 AA.			
DE Human secreted/transmembrane protein (PRO) #96.			
PN US2003032126-A1.			
PD 13-FEB-2003.			
Query Match	100.0%;	Score 1772; DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No.1.1e-162;	
RESULT 362			
ID ABO25376 standard; protein; 335 AA.			
DE Human PRO polypeptide #96.			
PN US2003054463-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772; DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No.1.1e-162;	
RESULT 363			
ID ABO25681 standard; protein; 335 AA.			
DE Human PRO polypeptide #96.			
PN US2003054466-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772; DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No.1.1e-162;	
RESULT 364			
ID ABR94090 standard; protein; 335 AA.			
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.			
PN US2003059879-A1.			
PD 27-MAR-2003.			



PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 365  
ID ADA92815 standard; protein, 335 AA.  
DE Human secreted/cranmembrane protein PRO1138.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 366  
ID ABR79997 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 367  
ID ABM11337 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064469-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 368  
ID ABO32944 standard; protein, 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003064453-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 369  
ID ABO30650 standard; protein, 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003064466-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 370  
ID ABO30955 standard; protein, 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003064468-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 371  
ID ABM27261 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068760-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 372  
ID ABM30006 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068769-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 373  
ID ABM05542 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 374  
ID ABM15607 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068698-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 375  
ID ABM08592 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068759-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 376  
ID ABO42292 standard; protein, 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 377  
ID ABO38022 standard; protein, 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003068765-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 378  
ID ABO45932 standard; protein, 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 379  
ID ABM66735 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068688-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 380  
ID ADB20304 standard; protein, 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 381  
ID ABM19636 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 382  
ID ABO49348 standard; protein, 335 AA.  
DE Human secreted/cranmembrane protein (PRO) #96.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 383  
ID ABO49653 standard; protein, 335 AA.



DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 384  
ID ADA78556 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 385  
ID ABR88210 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 386  
ID ADA00377 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO 138.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 387  
ID ABM26956 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 388  
ID ABM03353 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 389  
ID ABO39852 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 390  
ID ABO49958 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 391  
ID ABO50873 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 392  
ID ABO05329 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 393  
ID ABR74633 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 394  
ID ABR77112 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 395  
ID ABM17869 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 396  
ID ABR95920 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 397  
ID ABO21853 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 398  
ID ABO20023 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 399  
ID ABO24326 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 400  
ID ABR86075 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 401  
ID ABM10727 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 402  
ID ABM76726 standard; protein; 335 AA.



DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 403  
ID ABR89430 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 404  
ID ABR12557 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 405  
ID ABR05847 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 406  
ID ABO34972 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 407  
ID ABR03048 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 408  
ID ABR19026 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 409  
ID ABR19331 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 410  
ID ABO46542 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 411  
ID ABO49043 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 412  
ID ABR69086 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 413  
ID ABR89125 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 414  
ID ABR72498 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 415  
ID ABR74328 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 416  
ID ABR18596 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 417  
ID ABR80302 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 418  
ID ABR01523 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 419  
ID ABR02133 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 420  
ID ABR87295 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 421



ID ABM12862 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 422  
ID ABM30616 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 423  
ID ABM24516 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 424  
ID ABM09430 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 425  
ID ABM031260 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 426  
ID ABM14387 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 427  
ID ABM09812 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 428  
ID ABO38937 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 429  
ID ABM34702 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US200304538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 430  
ID ABO51178 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 431  
ID ABO04004 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 432  
ID ABO10474 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 433  
ID ABO53176 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 434  
ID ABR7717 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 435  
ID ABR78927 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 436  
ID ABO24021 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 437  
ID ABR93785 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 438  
ID ABO01828 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 439  
ID ABR78251 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 440



ID ABR90040 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 441  
ID AD2376 standard; protein, 335 AA.  
DE Human secreted/transmembrane polypeptide PRO1138.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 442  
ID ABM27566 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 443  
ID ABM13167 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 444  
ID ABO31670 standard; protein, 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 445  
ID ABM14082 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 446  
ID ABR08287 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 447  
ID ABO40157 standard; protein, 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 448  
ID ABM74592 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 449  
ID ABM33787 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003096358-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 450  
ID ABM20246 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 451  
ID ABO48738 standard; protein, 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 452  
ID ABO25446 standard; protein, 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 453  
ID ABR72803 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 454  
ID ABO15445 standard; protein, 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 455  
ID ABR85160 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 456  
ID ABO15140 standard; protein, 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 457  
ID ABO17275 standard; protein, 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 458  
ID ABM17564 standard; protein, 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 459  
ID ADA06542 standard; protein, 335 AA.  
DE Human secreted/transmembrane PRO polypeptide #71.  
PN US2003049638-A1.



PD 13-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 460  
ID ADA39235 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 461  
ID AB885465 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 462  
ID ABW77031 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 463  
ID ABO28210 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 464  
ID ABM22991 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 465  
ID ABM30311 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 466  
ID ABM21771 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 467  
ID ABM21466 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 468  
ID ABM14997 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 469  
ID ABO41072 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 470  
ID ABO36802 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 471  
ID ABO37412 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 472  
ID ABW75202 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 473  
ID ABM33482 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 474  
ID ABO46237 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 475  
ID ADA82627 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 476  
ID ADB85619 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 477  
ID ADB96261 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 478



ID AEM31836 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068680-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 479  
ID AEM31226 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 480  
ID ADB85935 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 481  
ID AEM32141 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 482  
ID AEM32446 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 483  
ID ADB68298 standard; protein; 335 AA.  
DE Human PRO1138 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 484  
ID ADB68105 standard; protein; 335 AA.  
DE Human PRO1138 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 485  
ID AEM31531 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 486  
ID AEM30921 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 487  
ID ADB90922 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.

PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 488  
ID ADC57733 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 489  
ID ADC55097 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 490  
ID ADC11964 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 491  
ID ADC07002 standard; protein; 335 AA.  
DE Human PRO1138 protein.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 492  
ID ADC56386 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 493  
ID ADC17181 standard; protein; 335 AA.  
DE Mammalian PRO polypeptide (SeqID 46).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 494  
ID ADC07441 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003066447-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 495  
ID ADC11431 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 496  
ID ADC114879 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 1.1e-162;  
RESULT 497  
ID ADC52374 standard; protein; 335 AA.



DE Novel human secreted and transmembrane protein PRO1138.  
PN US200313882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 498  
ID ADCl453 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 499  
ID AD008085 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 500  
ID ADc81910 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 501  
ID AD007552 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US200219329-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 502  
ID ADc82443 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 503  
ID AD005665 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 504  
ID AD008623 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 505  
ID AD006872 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 506  
ID ADc89503 standard; protein; 335 AA.  
DE Human natural killer cell surface receptor CSL.  
PN US2003113332-A1.  
PD 19-JUN-2003.  
PA (UNVT-) UNIV NORTH TEXAS HEALTH SCI CENT.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 507  
ID ADc83119 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 508  
ID AD67525 standard; protein; 335 AA.  
DE Human ly1728P protein SEQ ID NO:2.  
PN WO2003062401-A2.  
PD 31-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 509  
ID AD55226 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 510  
ID ADJ36050 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 511  
ID AD56184 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 512  
ID AD54622 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 513  
ID AD526776 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 514  
ID AD526243 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 515  
ID ADP67180 standard; protein; 335 AA.  
DE Human PRO1138 amino acid sequence SEQ ID NO:253.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 516  
ID ADG01051 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.



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Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 517
ID ADG08604 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 518
ID ADG02660 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 519
ID ADG01367 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 520
ID ADF95542 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 521
ID ADF95425 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 522
ID ADG12357 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 523
ID ADH24078 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 524
ID ADH34104 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 525
ID ADH29337 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 526
ID ADH23908 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 527
ID ADH09017 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 528
ID ADG85112 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 529
ID ADH24588 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 530
ID ADH37444 standard; protein; 335 AA.
DE Human secreted and transmembrane protein PRO138 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 531
ID ADH02033 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 532
ID ADH37614 standard; protein; 335 AA.
DE Human secreted and transmembrane protein PRO138 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 533
ID ADG85652 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 534
ID ADH24248 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match                               100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 535
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ID ADH38542 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 536  
ID ADH83663 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 537  
ID ADH29471 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 538  
ID ADH27587 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 539  
ID ADH37784 standard; protein; 335 AA.  
DE Human secreted and transmembrane protein PRO1138 cDNA.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 540  
ID ADH37961 standard; protein; 335 AA.  
DE Human secreted and transmembrane protein PRO138 cDNA.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 541  
ID ADH57381 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 542  
ID ADH53523 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 543  
ID ADH53693 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 544  
ID ADH52029 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 545  
ID ADH49884 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 546  
ID ADI25394 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 547  
ID ADH90187 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 548  
ID ADI25564 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 549  
ID ADH97738 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 550  
ID ADI35434 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 551  
ID ADI03586 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 552  
ID ADI11943 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 553  
ID ADH90017 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181697-A1.



[illegible]

Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 563				
ID	AD104811 standard;	protein; 335 AA.		
ID	Novel human secreted and transmembrane protein PRO1138.			
PN	US2003181657-A1.			
PD	25-SEP-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 564				
ID	ADH78265 standard;	protein; 335 AA.		
DE	Human PRO polypeptide #23.			
PN	US2003181668-A1.			
PD	25-SEP-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 565				
ID	AD119609 standard;	protein; 335 AA.		
DE	Novel human secreted and transmembrane protein PRO1138.			
PN	US2003181676-A1.			
PD	25-SEP-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 566				
ID	ADH90357 standard;	protein; 335 AA.		
DE	Novel human secreted and transmembrane protein PRO1138.			
PN	US2003181699-A1.			
PD	25-SEP-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 567				
ID	AD103076 standard;	protein; 335 AA.		
DE	Novel human secreted and transmembrane protein PRO1138.			
PN	US2003181653-A1.			
PD	25-SEP-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 568				
ID	ADH77925 standard;	protein; 335 AA.		
DE	Human PRO polypeptide #23.			
PN	US2003181666-A1.			
PD	25-SEP-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 569				
ID	ADH97908 standard;	protein; 335 AA.		
DE	Novel human secreted and transmembrane protein PRO1138.			
PN	US2003181674-A1.			
PD	25-SEP-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 570				
ID	AD101293 standard;	protein; 335 AA.		
DE	Novel human secreted and transmembrane protein PRO1138.			
PN	US2003190669-A1.			
PD	09-OCT-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 571				
ID	AD101988 standard;	protein; 335 AA.		
DE	Novel human secreted and transmembrane protein PRO1138.			
PN	US2003181652-A1.			
PD	25-SEP-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 572				
ID	AD101988 standard;	protein; 335 AA.		
DE	Novel human secreted and transmembrane protein PRO1138.			
PN	US2003181652-A1.			
PD	25-SEP-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 573				
ID	AD101988 standard;	protein; 335 AA.		
DE	Novel human secreted and transmembrane protein PRO1138.			
PN	US2003181652-A1.			
PD	25-SEP-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 574				
ID	AD101988 standard;	protein; 335 AA.		
DE	Novel human secreted and transmembrane protein PRO1138.			
PN	US2003181652-A1.			
PD	25-SEP-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1772;	DB 7;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1.1e-162;		
RESULT 575				
ID	AD101988 standard;	protein; 335 AA.		
DE	Novel human secreted and transmembrane protein PRO1138.			



Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 572  
ID AD103246 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 573  
ID AD111433 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 574  
ID AD102335 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 575  
ID AD111773 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 576  
ID AD105410 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 577  
ID ADH79482 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 578  
ID AD119439 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 579  
ID AD105240 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 580  
ID ADH79652 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 581  
ID AD101478 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 582  
ID AD101648 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 583  
ID AD101818 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 584  
ID ADH79822 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 585  
ID AD104640 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 586  
ID AD102776 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 587  
ID ADH78095 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 588  
ID AD125734 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 589  
ID AD125904 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 590



ID ADK65416 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 591  
ID ADH98758 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 592  
ID ADH79999 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 593  
ID ADJ32798 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 594  
ID ADH06166 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 595  
ID ADJ93730 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 596  
ID ADC52184 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 597  
ID ADH74432 standard; protein; 335 AA.  
DE Human secreted and transmembrane protein (PRO) #96.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 598  
ID ADH74941 standard; protein; 335 AA.  
DE Human secreted and transmembrane protein (PRO) #96.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 599  
ID ADH35379 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003194760-A1.

PD 16-OCT-2003.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 600  
ID ADG11629 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 601  
ID ADP96154 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 602  
ID ADG04425 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 603  
ID ADG00585 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 604  
ID ADH06616 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 605  
ID ADH06446 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 606  
ID ADG68867 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 607  
ID ADH27757 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 608  
ID ADH25098 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 609  
ID ADH35379 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003194760-A1.



Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 609  
ID ADH33730 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 610  
ID ADG82841 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 611  
ID ADH02373 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 612  
ID ADH07980 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 613  
ID ADG69377 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 614  
ID ADH39198 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 615  
ID ADH26122 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 616  
ID ADG83938 standard; protein; 335 AA.  
DE Human PRO polypeptide #33.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 617  
ID ADH19499 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 618  
ID ADG85482 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 619  
ID ADH06276 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 620  
ID ADH30106 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 621  
ID ADH24418 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 622  
ID ADH33091 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 623  
ID ADG69547 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 624  
ID ADH07810 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 625  
ID ADG85822 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 626  
ID ADH39368 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 627



ID ADH33560 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH33900 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH0110 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADG69717 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH20992 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH02203 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADG69707 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH85992 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH24928 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH57211 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181642-A1.

PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH20032 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH02543 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADG69037 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH07640 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH86162 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH24758 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH25806 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH38372 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;  
Pred. No. 1.1e-162;  
ID ADH57211 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181642-A1.



PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 646  
ID ADH52199 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 647  
ID ADH49565 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 648  
ID ADH90527 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 649  
ID ADH11263 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 650  
ID ADH98928 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 651  
ID ADH102158 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 652  
ID ADH90697 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 653  
ID ADH54830 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 654  
ID ADH98572 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 655  
ID ADH98742 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 656  
ID ADH78901 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 657  
ID ADH99135 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 658  
ID ADH99305 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 659  
ID ADH98923 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 660  
ID ADH79071 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 661  
ID ADH00931 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 662  
ID ADH14452 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 663  
ID ADH64601 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.



Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 664  
ID ADM3197 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 665  
ID ADM36544 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 666  
ID ADM40349 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 667  
ID ADM80901 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 668  
ID ADN37957 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 669  
ID ADU87689 standard; protein; 335 AA.  
DE Human CSI (SLAMF7) protein.  
PN WO2004100898-A2.  
PD 25-NOV-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 670  
ID ADY19131 standard; protein; 335 AA.  
DE PRO polypeptide SEQ ID NO 4937.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 671  
ID ADY77741 standard; protein; 335 AA.  
DE Neoplastic disease detection protein PRO1138.  
PN US2005059102-A1.  
PD 17-MAR-2005.  
PA (EATO/) BATON D L.  
PA (FLIV/) FLIVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 1772; DB 9; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 672  
ID AEA38506 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, #139.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 673  
ID AAB32373 standard; protein; 336 AA.  
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:59.  
PN WO200047602-A1.  
PD 17-AUG-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 100.0%; Score 1772; DB 3; Length 336;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 674  
ID ADS98579 standard; protein; 340 AA.  
DE Protein factor discovery related human contig polypeptide, SEQ ID 843.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
PA (DRMA/) DRMAVAC R T.  
Query Match 100.0%; Score 1772; DB 8; Length 340;  
Best Local Similarity 100.0%; Pred. No. 1.1e-162;  
RESULT 675  
ID ADD18672 standard; protein; 335 AA.  
DE Human disease related protein SegID103.  
PN WO2003018621-A2.  
PD 06-MAR-2003.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 99.8%; Score 1769; DB 7; Length 335;  
Best Local Similarity 99.7%; Pred. No. 2.1e-162;  
RESULT 676  
ID ADI69599 standard; protein; 335 AA.  
DE Human heat mitochondrial protein as a therapeutic target SegID1405.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 99.8%; Score 1769; DB 7; Length 335;  
Best Local Similarity 99.7%; Pred. No. 2.1e-162;  
RESULT 677  
ID ABR58418 standard; protein; 348 AA.  
DE Human NOV27b.  
PN WO2003029423-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 99.1%; Score 1755.5; DB 6; Length 348;  
Best Local Similarity 96.3%; Pred. No. 4.5e-161;  
RESULT 678  
ID AAY44610 standard; protein; 312 AA.  
DE Mature human myocardium protein-7.  
PN WO9967387-A2.  
PD 29-DEC-1999.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 93.3%; Score 1653; DB 3; Length 312;  
Best Local Similarity 100.0%; Pred. No. 3.3e-151;  
RESULT 679  
ID ABB97473 standard; protein; 328 AA.  
DE Novel human protein SEQ ID NO: 741.  
PN WO200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 78.6%; Score 1392.5; DB 5; Length 328;  
Best Local Similarity 86.4%; Pred. No. 6.4e-126;  
RESULT 680  
ID ADS98765 standard; protein; 328 AA.  
DE Protein factor discovery related human contig polypeptide, SEQ ID 1029.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.



PA (DRMA/) DRMANAC R T.  
Query Match 78.6%; Score 1392.5; DB 8; Length 328;  
Best Local Similarity 86.4%; Pred. No. 6.4e-126;  
RESULT 681  
ID ADS97998 standard; protein: 296 AA.  
DE Protein factor discovery related isolated human polypeptide, SEQ ID 262.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NIVE-) NIVELO INC.  
PA (DRMA/) DRMANAC R T.  
Query Match 76.1%; Score 1349; DB 8; Length 296;  
Best Local Similarity 100.0%; Pred. No. 9.1e-122;  
RESULT 682  
ID ADN02731 standard; protein: 204 AA.  
DE Human receptor and membrane-associated protein #34.  
PN WO2004029218-A2.  
PD 08-APR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 56.3%; Score 997.5; DB 8; Length 204;  
Best Local Similarity 60.9%; Pred. No. 6.4e-88;  
RESULT 683  
ID ABG11697 standard; protein: 684 AA.  
DE Novel human diagnostic protein #11688.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 52.7%; Score 933.5; DB 4; Length 684;  
Best Local Similarity 64.9%; Pred. No. 6e-81;  
RESULT 684  
ID ABG12169 standard; protein: 684 AA.  
DE Novel human diagnostic protein #12160.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 52.7%; Score 933.5; DB 4; Length 684;  
Best Local Similarity 64.9%; Pred. No. 6e-81;  
RESULT 685  
ID ADS98714 standard; protein: 684 AA.  
DE Protein factor discovery related human contig polypeptide, SEQ ID 978.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NIVE-) NIVELO INC.  
PA (DRMA/) DRMANAC R T.  
Query Match 52.7%; Score 933.5; DB 8; Length 684;  
Best Local Similarity 64.9%; Pred. No. 6e-81;  
RESULT 686  
ID ADR20055 standard; protein: 165 AA.  
DE Human immune response associated protein (IRAP), seq id 15.  
PN WO2004048550-A2.  
PD 10-JUN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 36.9%; Score 653; DB 8; Length 165;  
Best Local Similarity 90.9%; Pred. No. 1.2e-54;  
RESULT 687  
ID AAY12645 standard; protein: 124 AA.  
DE Human 5' EST secreted protein SEQ ID NO: 310 from WO 9906553.  
PN WO9906553-A2.  
PD 11-FEB-1999.  
PA (GENST-) GENSET.  
Query Match 35.1%; Score 622; DB 2; Length 124;  
Best Local Similarity 97.6%; Pred. No. 8e-52;  
RESULT 688  
ID AAW67811 standard; protein: 110 AA.  
DE Human secreted protein encoded by gene 5 clone HASAV70.  
PN WO9842738-A1.  
PD 01-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 582; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 5e-48;  
RESULT 689  
ID AAB32405 standard; protein: 110 AA.  
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:91.  
PN WO20047602-A1.  
PD 17-AUG-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 582; DB 3; Length 110;  
Best Local Similarity 100.0%; Pred. No. 5e-48;  
RESULT 690  
ID ADA57321 standard; protein: 110 AA.  
DE Human secreted protein #32.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 582; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 5e-48;  
RESULT 691  
ID ADA6750 standard; protein: 110 AA.  
DE Human secreted protein #32.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 582; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 5e-48;  
RESULT 692  
ID ADA40601 standard; protein: 110 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 582; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 5e-48;  
RESULT 693  
ID ADA41198 standard; protein: 110 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 582; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 5e-48;  
RESULT 694  
ID AAG00391 standard; protein: 97 AA.  
DE Human secreted protein, SEQ ID NO: 4472.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GENST-) GENSET.  
Query Match 28.1%; Score 498; DB 3; Length 97;  
Best Local Similarity 100.0%; Pred. No. 5.9e-40;  
RESULT 695  
ID AAY11662 standard; protein: 98 AA.  
DE Human 5' EST secreted protein SEQ ID NO:314.  
PN WO9906439-A2.  
PD 11-FEB-1999.  
PA (GENST-) GENSET.  
Query Match 28.1%; Score 498; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 5.9e-40;  
RESULT 696  
ID AAM21122 standard; protein: 91 AA.  
DE Peptide #7556 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.2e-37;  
RESULT 697  
ID ABA43438 standard; peptide: 91 AA.  
DE Peptide #10944 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.2e-37;  
RESULT 698  
ID AAM37326 standard; protein: 91 AA.  
DE Peptide #11363 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.



PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.2e-37;  
RESULT 699  
ID AAB26408 standard; protein; 91 AA.  
DE Protein #8407 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.2e-37;  
RESULT 700  
ID AAM77190 standard; protein; 91 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37496.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.2e-37;  
RESULT 701  
ID AAM64367 standard; protein; 91 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36472.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.2e-37;  
RESULT 702  
ID ABG58815 standard; peptide; 91 AA.  
DE Human liver peptide, SEQ ID NO 37463.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.2e-37;  
RESULT 703  
ID AAG46203 standard; peptide; 91 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35868.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.2e-37;  
RESULT 704  
ID AAB32404 standard; protein; 90 AA.  
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:90.  
PN WO200047602-A1.  
PD 17-AUG-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 25.1%; Score 445; DB 3; Length 90;  
Best Local Similarity 100.0%; Pred. No. 7.2e-35;  
RESULT 705  
ID AAB47878 standard; protein; 328 AA.  
DE SCZ/CD84.  
PN WO200202054-A2.  
PD 10-JAN-2002.  
PA (RUTP-) UNIV RUTGERS STATE NEW JERSEY.  
Query Match 20.5%; Score 362.5; DB 5; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 706  
ID AAB26238 standard; protein; 328 AA.  
DE Human CD84 protein.  
PN BP1223218-A1.  
PD 17-JUL-2002.  
PA (MILT-) MILLENNIUM PHARM INC.  
Query Match 20.5%; Score 362.5; DB 5; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 707  
ID ADI82907 standard; protein; 328 AA.  
DE Human PRO24934, SEQ ID 109.  
PN WO2004024097-A2.  
PD 25-MAR-2004.  
PA (GERTH) GENENTECH INC.

Query Match 20.5%; Score 362.5; DB 8; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 708  
ID ADO05708 standard; protein; 328 AA.  
DE Human leukocyte differentiation antigen CD84.  
PN WO2004032867-A2.  
PD 22-APR-2004.  
PA (TOLR-) TOLERRX INC.  
Query Match 20.5%; Score 362.5; DB 8; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 709  
ID ADQ19067 standard; protein; 328 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1886.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 20.5%; Score 362.5; DB 8; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 710  
ID ADP23943 standard; protein; 328 AA.  
DE PRO polypeptide SEQ ID NO:1121.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GERTH) GENENTECH INC.  
Query Match 20.5%; Score 362.5; DB 8; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 711  
ID ADY16548 standard; protein; 328 AA.  
DE PRO polypeptide SEQ ID NO 2354.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GERTH) GENENTECH INC.  
Query Match 20.5%; Score 362.5; DB 9; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 712  
ID ADY16566 standard; protein; 328 AA.  
DE PRO polypeptide SEQ ID NO 1462.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GERTH) GENENTECH INC.  
Query Match 20.5%; Score 362.5; DB 9; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 713  
ID AAW74891 standard; protein; 329 AA.  
DE Human secreted protein encoded by gene 164 clone HSAMP26.  
PN WO9839448-A2.  
PD 11-SEP-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 20.5%; Score 362.5; DB 2; Length 329;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 714  
ID ABG95343 standard; protein; 329 AA.  
DE Human novel secreted protein #164.  
PN US6420526-B1.  
PD 16-JUL-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 20.5%; Score 362.5; DB 5; Length 329;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 715  
ID AB034537 standard; protein; 329 AA.  
DE Region of human secreted protein encoded by cDNA sequence #164.  
PN US2003049618-A1.  
PD 13-MAR-2003.  
PA (ROSE/) ROSEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOPE/) SOPERT D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NITJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.



PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN D R.  
PA (HUJI/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (FISC/) FISCHER C L.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAFI/) LAFLEUR D W.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (KYAW/) KYAW H.  
Query Match 20.5%; Score 362.5; DB 6; Length 329;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 716  
ID ADI23198 standard; protein; 329 AA.  
DE Novel human secreted protein seq id 483.  
PN US2003175858-A1.  
PD 18-SEP-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN D R.  
PA (HUJI/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (FISC/) FISCHER C L.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAFI/) LAFLEUR D W.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (KYAW/) KYAW H.  
Query Match 20.5%; Score 362.5; DB 7; Length 329;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 717  
ID ADH74200 standard; protein; 329 AA.  
DE Human secreted protein #164.  
PN US2003225248-A1.  
PD 04-DEC-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 20.5%; Score 362.5; DB 8; Length 329;  
Best Local Similarity 31.5%; Pred. No. 4.8e-26;  
RESULT 718  
ID AAU74424 standard; protein; 629 AA.  
DE Mouse protein sequence #3, related to isolation of genes within SLE-1B.  
PN WO000188200-A2.  
PD 22-NOV-2001.  
PA (TEKA) UNITV TEXAS SYSTEM.  
Query Match 19.4%; Score 343; DB 5; Length 629;  
Best Local Similarity 29.3%; Pred. No. 9.7e-24;  
RESULT 719  
ID AAE26250 standard; protein; 289 AA.  
DE Human CD2001 protein #2.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.8%; Score 333.5; DB 5; Length 289;  
Best Local Similarity 31.0%; Pred. No. 2.6e-23;

RESULT 720  
ID ABW01830 standard; protein; 289 AA.  
DE Human CD2001 protein #3.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.8%; Score 333.5; DB 7; Length 289;  
Best Local Similarity 31.0%; Pred. No. 2.6e-23;  
RESULT 721  
ID AAE12078 standard; protein; 289 AA.  
DE Dendritic cell (DC) DC1XR protein.  
PN WO200172773-A2.  
PD 04-OCT-2001.  
PA (NOVS) NOVARTIS AG.  
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
Query Match 18.7%; Score 330.5; DB 4; Length 289;  
Best Local Similarity 30.6%; Pred. No. 5e-23;  
RESULT 722  
ID AAE26243 standard; protein; 289 AA.  
DE Human CD2001 protein.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.7%; Score 330.5; DB 5; Length 289;  
Best Local Similarity 30.6%; Pred. No. 5e-23;  
RESULT 723  
ID AAE26253 standard; protein; 289 AA.  
DE Human CD2001 protein #5.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.7%; Score 330.5; DB 5; Length 289;  
Best Local Similarity 30.6%; Pred. No. 5e-23;  
RESULT 724  
ID ABP65110 standard; protein; 289 AA.  
DE Hypoxia-induced protein #36.  
PN WO200246465-A2.  
PD 13-JUN-2002.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 18.7%; Score 330.5; DB 5; Length 289;  
Best Local Similarity 30.6%; Pred. No. 5e-23;  
RESULT 725  
ID ABW01823 standard; protein; 289 AA.  
DE Human CD2001 protein #1.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.7%; Score 330.5; DB 7; Length 289;  
Best Local Similarity 30.6%; Pred. No. 5e-23;  
RESULT 726  
ID ABW01833 standard; protein; 289 AA.  
DE Human CD2001 protein #6.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.7%; Score 330.5; DB 7; Length 289;  
Best Local Similarity 30.6%; Pred. No. 5e-23;  
RESULT 727  
ID AAE26251 standard; protein; 289 AA.  
DE Human CD2001 protein #3.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.5%; Score 327.5; DB 5; Length 289;  
Best Local Similarity 30.3%; Pred. No. 9.9e-23;  
RESULT 728  
ID AAE26252 standard; protein; 289 AA.  
DE Human CD2001 protein #4.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.5%; Score 327.5; DB 5; Length 289;  
Best Local Similarity 30.3%; Pred. No. 9.9e-23;



RESULT 729  
ID ABW01831 standard; protein; 289 AA.  
DE Human CD2001 protein #4.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.5%; Score 327.5; DB 7; Length 289;  
Best Local Similarity 30.3%; Pred. No. 9.9e-23;  
RESULT 730  
ID ABW01832 standard; protein; 289 AA.  
DE Human CD2001 protein #5.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.5%; Score 327.5; DB 7; Length 289;  
Best Local Similarity 30.3%; Pred. No. 9.9e-23;  
RESULT 731  
ID AAE26244 standard; protein; 270 AA.  
DE Human CD2001 mature protein.  
PN EP123218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.5%; Score 327; DB 5; Length 270;  
Best Local Similarity 31.4%; Pred. No. 1e-22;  
RESULT 732  
ID ABW01824 standard; protein; 270 AA.  
DE Human CD2001 mature protein.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.5%; Score 327; DB 7; Length 270;  
Best Local Similarity 31.4%; Pred. No. 1e-22;  
RESULT 733  
ID ADS98002 standard; protein; 632 AA.  
DE Protein factor discovery related isolated human polypeptide, SEQ ID 266.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
(DRMA/) DRMANAC R T.  
Query Match 18.2%; Score 323; DB 8; Length 632;  
Best Local Similarity 30.3%; Pred. No. 8.5e-22;  
RESULT 734  
ID ADS97999 standard; protein; 655 AA.  
DE Protein factor discovery related isolated human polypeptide, SEQ ID 263.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
(DRMA/) DRMANAC R T.  
Query Match 18.2%; Score 323; DB 8; Length 655;  
Best Local Similarity 30.3%; Pred. No. 8.9e-22;  
RESULT 735  
ID ADS98003 standard; protein; 669 AA.  
DE Protein factor discovery related isolated human polypeptide, SEQ ID 267.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
(DRMA/) DRMANAC R T.  
Query Match 18.2%; Score 323; DB 8; Length 669;  
Best Local Similarity 30.3%; Pred. No. 9.2e-22;  
RESULT 736  
ID AAE26239 standard; protein; 331 AA.  
DE Human CD2000 protein #3.  
PN EP123218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.0%; Score 319.5; DB 5; Length 331;  
Best Local Similarity 29.9%; Pred. No. 7.2e-22;  
RESULT 737  
ID ABW01818 standard; protein; 331 AA.  
DE Human CD2000 protein #2.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 18.0%; Score 319.5; DB 7; Length 331;  
Best Local Similarity 29.9%; Pred. No. 7.2e-22;  
RESULT 738  
ID ADL57103 standard; protein; 615 AA.  
DE Human NOV5A protein SEQ ID NO:46.  
PN WO2004022723-A2.  
PD 18-MAR-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 17.9%; Score 318; DB 8; Length 615;  
Best Local Similarity 30.3%; Pred. No. 2.5e-21;  
RESULT 739  
ID AD063782 standard; protein; 654 AA.  
DE Human Ly-9 polypeptide.  
PN US2004109862-A1.  
PD 10-JUN-2004.  
PA (EMTA/) EMTAGE P C R.  
Query Match 17.9%; Score 318; DB 8; Length 654;  
Best Local Similarity 30.3%; Pred. No. 2.7e-21;  
RESULT 740  
ID AD078174 standard; protein; 654 AA.  
DE Human Ly-9 polypeptide.  
PN US2004109863-A1.  
PD 10-JUN-2004.  
PA (EMTA/) EMTAGE P.  
Query Match 17.9%; Score 318; DB 8; Length 654;  
Best Local Similarity 30.3%; Pred. No. 2.7e-21;  
RESULT 741  
ID ADK41513 standard; protein; 331 AA.  
DE Anti-cell surface antigen related protein #1.  
PN WO2003068935-A2.  
PD 21-AUG-2003.  
PA (NUVE-) NUVELO INC.  
Query Match 17.9%; Score 316.5; DB 7; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.4e-21;  
RESULT 742  
ID AAE26222 standard; protein; 309 AA.  
DE Human CD2000 mature protein.  
PN EP123218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.8%; Score 315.5; DB 5; Length 309;  
Best Local Similarity 29.6%; Pred. No. 1.6e-21;  
RESULT 743  
ID ABW01801 standard; protein; 309 AA.  
DE Human CD2000 mature protein.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.8%; Score 315.5; DB 7; Length 309;  
Best Local Similarity 29.6%; Pred. No. 1.6e-21;  
RESULT 744  
ID ABB90183 standard; protein; 331 AA.  
DE Human polypeptide SEQ ID NO 2559.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMANA GENOME SCI INC.  
Query Match 17.8%; Score 315.5; DB 5; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.8e-21;  
RESULT 745  
ID AAE26220 standard; protein; 331 AA.  
DE Human CD2000 protein.  
PN EP123218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.8%; Score 315.5; DB 5; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.8e-21;  
RESULT 746  
ID ABR39107 standard; protein; 331 AA.  
DE Human NTB-A protein SEQ ID NO:2.  
PN WO2003008449-A1.  
PD 30-JAN-2003.  
PA (INNA-) INNATE PHARMA.  
(DYGE-) UNIV GENOVA.



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Query Match 17.8%; Score 315.5; DB 6; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 747
ID AB003145 standard; protein; 331 AA.
DE Human Immunoglobulin (Ig) APEX4 protein.
PN WO20027173-A2.
PD 03-OCT-2002.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 17.8%; Score 315.5; DB 6; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 748
ID ADC52556 standard; protein; 331 AA.
DE human dendritic cell membrane protein #SEQ ID 9.
PN JP2003052374-A.
PD 25-FEB-2003.
PA (KIRI ) KIRIN BREWERY KK.
Query Match 17.8%; Score 315.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 749
ID ABW01799 standard; protein; 331 AA.
DE Human CD2000 protein #1.
PN US200318088-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.8%; Score 315.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 750
ID ADI37022 standard; protein; 331 AA.
DE Novel human secreted and transmembrane protein PRO 71240.
PN WO2004004649-A2.
PD 15-JAN-2004.
PA (GERTH ) GENENTECH INC.
Query Match 17.8%; Score 315.5; DB 8; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 751
ID ADO6345 standard; protein; 331 AA.
DE Novel human protein sequence #1318.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (RRAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 17.8%; Score 315.5; DB 8; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 752
ID ADY19430 standard; protein; 331 AA.
DE PRO polypeptide SEQ ID NO 5236.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GERTH ) GENENTECH INC.
Query Match 17.8%; Score 315.5; DB 9; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 753
ID AD213231 standard; protein; 331 AA.
DE Human cancer-associated protein #235.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR ) CHIRON CORP.
Query Match 17.8%; Score 315.5; DB 9; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 754
ID AEB98756 standard; protein; 331 AA.
DE Human dendritic cell membrane molecule, SEQ ID 2.
PN JP2005206478-A.
PD 04-AUG-2005.
PA (KIRI ) KIRIN BREWERY KK.
Query Match 17.8%; Score 315.5; DB 9; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 755
ID AAU09868 standard; protein; 346 AA.
DE Novel human secreted protein #9.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIX ) SMITHKLINE BEECHAM PLC.
Query Match 17.8%; Score 315.5; DB 5; Length 346;
Best Local Similarity 29.6%; Pred. No. 1.9e-21;
RESULT 756
ID AAE26241 standard; protein; 331 AA.
DE Human CD2000 protein #5.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.7%; Score 314.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 2.2e-21;
RESULT 757
ID ABW01820 standard; protein; 331 AA.
DE Human CD2000 protein #4.
PN US200318088-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.7%; Score 314.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 2.2e-21;
RESULT 758
ID AAE26240 standard; protein; 331 AA.
DE Human CD2000 protein #4.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.7%; Score 313.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 2.7e-21;
RESULT 759
ID ABW01819 standard; protein; 331 AA.
DE Human CD2000 protein #3.
PN US200318088-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.7%; Score 313.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 2.7e-21;
RESULT 760
ID AAU74425 standard; protein; 610 AA.
DE Human protein sequence #3, related to isolation of genes within SLE-IB.
PN WO200188200-A2.
PD 22-NOV-2001.
PA (TEXA ) UNIV TEXAS SYSTEM.
Query Match 17.6%; Score 312.5; DB 5; Length 610;
Best Local Similarity 25.7%; Pred. No. 8.4e-21;
RESULT 761
ID ADS98001 standard; protein; 641 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 265.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
Query Match 17.6%; Score 312.5; DB 8; Length 641;
Best Local Similarity 25.7%; Pred. No. 9e-21;
RESULT 762
ID AAE26242 standard; protein; 331 AA.
DE Human CD2000 protein #6.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.6%; Score 311.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 4.3e-21;
RESULT 763
ID ABW01821 standard; protein; 331 AA.
DE Human CD2000 protein #5.
PN US200318088-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.6%; Score 311.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 4.3e-21;
RESULT 764
ID AAG63166 standard; protein; 332 AA.
DE Amino acid sequence of a CD84-like polypeptide.
PN WO200155336-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
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Query Match 17.6%; Score 311; DB 4; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 765  
ID ADB96267 standard; protein; 332 AA.  
DE Human immunoglobulin superfamily protein IGSFP-5.  
PN W0200272794-A2.  
PD 19-SEP-2002.  
PA (INCYTE) INCYTE GENOMICS INC.  
Query Match 17.6%; Score 311; DB 5; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 766  
ID ADB34067 standard; protein; 332 AA.  
DE Human Pro peptide #38.  
PN W0200224868-A2.  
PD 28-MAR-2002.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 5; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 767  
ID ADBU03170 standard; protein; 332 AA.  
DE Human immunoglobulin (Ig) APEX4v1 protein.  
PN W0200277173-A2.  
PD 03-OCT-2002.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 17.6%; Score 311; DB 6; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 768  
ID ADA37159 standard; protein; 332 AA.  
DE Human PRO20080 protein SEQ ID NO.2.  
PN W02003055440-A2.  
PD 10-JUL-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 6; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 769  
ID ADA01344 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003068779-A1.  
PD 10-APR-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 6; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 770  
ID ADA43773 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003064474-A1.  
PD 03-APR-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 6; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 771  
ID ADA43541 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003073196-A1.  
PD 17-APR-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 6; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 772  
ID ADA01216 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003068782-A1.  
PD 10-APR-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 6; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 773  
ID ADA01100 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003068780-A1.  
PD 10-APR-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
Query Match 17.6%; Score 311; DB 7; Length 332;

Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 774  
ID ADA43657 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003073190-A1.  
PD 17-APR-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 775  
ID ADA06919 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003068781-A1.  
PD 10-APR-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 776  
ID ADA08407 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003068783-A1.  
PD 10-APR-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 777  
ID ADB99700 standard; protein; 332 AA.  
DE Human PRO polypeptide SEQ ID 76.  
PN US2003082728-A1.  
PD 01-MAY-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 778  
ID ADB86983 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003082726-A1.  
PD 01-MAY-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 779  
ID ADB66138 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003082729-A1.  
PD 01-MAY-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 780  
ID ADB99816 standard; protein; 332 AA.  
DE Human PRO polypeptide SEQ ID 76.  
PN US2003073192-A1.  
PD 17-APR-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 781  
ID ADB99471 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003082731-A1.  
PD 01-MAY-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 782  
ID ADB66022 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003082732-A1.  
PD 01-MAY-2003.  
PA (GENTH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
Query Match 17.6%; Score 311; DB 7; Length 332;



RESULT 783  
ID ADC23420 standard; protein; 332 AA.  
DE Human transmembrane PRO polypeptide (Segid 76).  
PN US2003073193-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 784  
ID ADC26113 standard; protein; 332 AA.  
DE Human PRO20080 protein.  
PN US2003073194-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 785  
ID AD804940 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003068778-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 786  
ID ADE11246 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003073191-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 787  
ID AD88177 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003082733-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 788  
ID AD955472 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003064473-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 789  
ID AD806402 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003073195-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 790  
ID ADE38177 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119120-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 791  
ID AD88293 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003073189-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 792  
ID AD95356 standard; protein; 332 AA.

ID AD990874 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003073188-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 793  
ID ADP9429 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003078401-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 794  
ID ADG06522 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003077742-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 795  
ID ADG05473 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003077741-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 796  
ID ADG82474 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003077744-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 797  
ID ADE51727 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003104560-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 798  
ID ADE51843 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003104561-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 799  
ID ADE37701 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003104564-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 800  
ID ADE37585 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003104565-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 801  
ID AD95356 standard; protein; 332 AA.



DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003138901-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 802  
ID ADE52379 standard; protein; 332 AA.  
DE Human PRO20080.  
PN US2003099661-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 803  
ID ADE38056 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003104566-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 804  
ID ADE76145 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003124665-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 805  
ID ADE39468 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119117-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 806  
ID ADE04472 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003096364-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 807  
ID ADE39869 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003138896-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 808  
ID ADE19734 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003138903-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 809  
ID ADE77312 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003124666-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 810  
ID ADE65420 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.

PN US2003119116-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 811  
ID ADE76029 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003124663-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 812  
ID ADE37940 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119119-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 813  
ID ADE64550 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119114-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 814  
ID ADE38885 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003096363-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 815  
ID ADE51959 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003104562-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 816  
ID ADE90990 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003138902-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 817  
ID ADE38769 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003108996-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 818  
ID ADE37469 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003104563-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 819  
ID ADE06286 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003138898-A1.



PD 24-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 820  
ID AD90145 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003138904-A1.  
PD 24-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 821  
ID AD38653 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119086-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 822  
ID AD39584 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119118-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 823  
ID AD89189 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003138897-A1.  
PD 24-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 824  
ID AD88956 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003138899-A1.  
PD 24-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 825  
ID AD819850 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003138900-A1.  
PD 24-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 826  
ID AD877428 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003124667-A1.  
PD 03-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 827  
ID AD865304 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 828  
ID AD839352 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 829  
ID AD38537 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 830  
ID AD81090 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 831  
ID AD810974 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 832  
ID AD831502 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 833  
ID AD838750 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 834  
ID AD829385 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 835  
ID AD823688 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 836  
ID AD827018 standard; protein; 332 AA.  
DE Human secreted/cranmembrane polypeptide PRO20080.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 837  
ID AD838286 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.



Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 838  
ID ADH26902 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003119134-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 839  
ID ADH38170 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 840  
ID ADH38866 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 841  
ID ADH23804 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 842  
ID ADH40179 standard; protein; 332 AA.  
DE Human PRO20080 protein.  
PN US2003119132-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 843  
ID ADH40064 standard; protein; 332 AA.  
DE Human PRO20080 protein.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 844  
ID ADH31386 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 845  
ID ADH29264 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 846  
ID ADH49479 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;

Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 847  
ID ADH51943 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 848  
ID ADH49798 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 849  
ID ADH52399 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 850  
ID ADH52515 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 851  
ID ADH58512 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119121-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 852  
ID ADH51827 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 853  
ID ADH58388 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 854  
ID ADH13585 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 855  
ID ADK00841 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003186373-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;



RESULT 856  
ID AD08582 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003186372-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 857  
ID ADS10567 standard; protein; 332 AA.  
DE Human therapeutic protein - SEQ ID 804.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.8e-21;  
RESULT 858  
ID ADY16550 standard; protein; 280 AA.  
DE PRO polypeptide SEQ ID NO 2356.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 17.4%; Score 308; DB 9; Length 280;  
Best Local Similarity 32.3%; Pred. No. 7.3e-21;  
RESULT 859  
ID AAE26249 standard; protein; 236 AA.  
DE Human CD2001 protein #1.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.0%; Score 301.5; DB 5; Length 236;  
Best Local Similarity 32.6%; Pred. No. 2.4e-20;  
RESULT 860  
ID AEW01829 standard; protein; 236 AA.  
DE Human CD2001 protein #2.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.0%; Score 301.5; DB 7; Length 236;  
Best Local Similarity 32.6%; Pred. No. 2.4e-20;  
RESULT 861  
ID AAE26246 standard; protein; 217 AA.  
DE Human CD2001 protein transmembrane domain.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.8%; Score 298; DB 5; Length 217;  
Best Local Similarity 33.8%; Pred. No. 4.7e-20;  
RESULT 862  
ID AEW01826 standard; protein; 217 AA.  
DE Human CD2001 protein extracellular domain.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.8%; Score 298; DB 7; Length 217;  
Best Local Similarity 33.8%; Pred. No. 4.7e-20;  
RESULT 863  
ID ABE96270 standard; protein; 551 AA.  
DE Human immunoglobulin superfamily protein IGSFP-8.  
PN WO2002272794-A2.  
PD 19-SEP-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 16.6%; Score 294.5; DB 5; Length 551;  
Best Local Similarity 30.4%; Pred. No. 4e-19;  
RESULT 864  
ID ADG98560 standard; protein; 565 AA.  
DE Human immune response associated protein IRAF-23 protein.  
PN WO2004020593-A2.  
PD 11-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 16.6%; Score 294.5; DB 8; Length 565;  
Best Local Similarity 30.4%; Pred. No. 4.2e-19;  
RESULT 865

ID ADS98832 standard; protein; 284 AA.  
DE Protein factor discovery related human contig polypeptide, SEQ ID 1096.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 16.5%; Score 291.5; DB 8; Length 284;  
Best Local Similarity 32.3%; Pred. No. 3e-19;  
RESULT 866  
ID AEA20174 standard; protein; 284 AA.  
DE Novel human polypeptide SEQ ID NO 868.  
PN WO2005049806-A2.  
PD 02-JUN-2005.  
PA (NUVE-) NUVELO INC.  
Query Match 16.5%; Score 291.5; DB 9; Length 284;  
Best Local Similarity 32.3%; Pred. No. 3e-19;  
RESULT 867  
ID ADL57243 standard; protein; 526 AA.  
DE Human NOV5c protein SEQ ID NO:188.  
PN WO2004022723-A2.  
PD 18-MAR-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.9%; Score 282.5; DB 8; Length 526;  
Best Local Similarity 31.5%; Pred. No. 5.5e-16;  
RESULT 868  
ID ADL57105 standard; protein; 526 AA.  
DE Human NOV5b protein SEQ ID NO:50.  
PN WO2004022723-A2.  
PD 18-MAR-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.9%; Score 282.5; DB 8; Length 526;  
Best Local Similarity 31.5%; Pred. No. 5.5e-16;  
RESULT 869  
ID ADR20041 standard; protein; 91 AA.  
DE Human immune response associated protein (IRAP), seq id 1.  
PN WO2004048550-A2.  
PD 10-JUN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 15.3%; Score 272; DB 8; Length 91;  
Best Local Similarity 100.0%; Pred. No. 4.4e-18;  
RESULT 870  
ID ADL13233 standard; protein; 271 AA.  
DE Human cancer-associated protein #236.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 15.1%; Score 267; DB 9; Length 271;  
Best Local Similarity 31.2%; Pred. No. 6.6e-17;  
RESULT 871  
ID ADL13235 standard; protein; 317 AA.  
DE Human cancer-associated protein #237.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 14.8%; Score 263; DB 9; Length 317;  
Best Local Similarity 31.0%; Pred. No. 2e-16;  
RESULT 872  
ID ABE98758 standard; protein; 445 AA.  
DE Dendritic cell membrane molecule-immunoglobulin (Ig) Fc fusion protein.  
PN JP2005206478-A.  
PD 04-AUG-2005.  
PA (KIRI ) KIRIN BREWERY KK.  
Query Match 14.3%; Score 254; DB 9; Length 445;  
Best Local Similarity 29.1%; Pred. No. 2.5e-15;  
RESULT 873  
ID AAU09867 standard; protein; 220 AA.  
DE Novel human secreted protein #8.  
PN WO200179454-A1.  
PD 25-OCT-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match 14.2%; Score 251; DB 5; Length 220;  
Best Local Similarity 35.4%; Pred. No. 1.7e-15;



RESULT 874  
ID ABB53269 standard; protein; 310 AA.  
DE Human polypeptide #9.  
PN WO200181363-A1.  
PD 01-NOV-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match 13.9%; Score 247; DB 5; Length 310;  
Best Local Similarity 26.7%; Pred. No. 7e-15;  
RESULT 875  
ID AAB26231 standard; protein; 195 AA.  
DE Human CD2000 protein #2.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.8%; Score 245; DB 5; Length 195;  
Best Local Similarity 35.1%; Pred. No. 5.5e-15;  
RESULT 876  
ID ABW01810 standard; protein; 195 AA.  
DE Human CD2000 protein extracellular domain #4.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.8%; Score 245; DB 7; Length 195;  
Best Local Similarity 35.1%; Pred. No. 5.5e-15;  
RESULT 877  
ID AAB26232 standard; protein; 203 AA.  
DE Human CD2000 protein transmembrane domain.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.8%; Score 245; DB 7; Length 203;  
Best Local Similarity 35.1%; Pred. No. 5.9e-15;  
RESULT 878  
ID ABW01811 standard; protein; 203 AA.  
DE Human CD2000 protein extracellular domain #5.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.8%; Score 245; DB 7; Length 203;  
Best Local Similarity 35.1%; Pred. No. 5.9e-15;  
RESULT 879  
ID AAB23943 standard; protein; 423 AA.  
DE Human PRO polypeptide SEQ ID NO 485.  
PN WO2005051988-A2.  
PD 09-JUN-2005.  
PA (SETH ) GENENTECH INC.  
Query Match 13.5%; Score 238.5; DB 9; Length 423;  
Best Local Similarity 32.1%; Pred. No. 7.3e-14;  
RESULT 880  
ID ABB53268 standard; protein; 229 AA.  
DE Human polypeptide #8.  
PN WO200181363-A1.  
PD 01-NOV-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match 13.3%; Score 236.5; DB 5; Length 229;  
Best Local Similarity 28.6%; Pred. No. 4.7e-14;  
RESULT 881  
ID AD21328 standard; protein; 331 AA.  
DE Murine cancer-associated protein #79.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 12.7%; Score 225.5; DB 9; Length 331;  
Best Local Similarity 26.0%; Pred. No. 9.3e-13;  
RESULT 882  
ID AAB47322 standard; protein; 351 AA.  
DE APEX-2.  
PN WO200146260-A2.  
PD 28-JUN-2001.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 12.7%; Score 225.5; DB 4; Length 351;

Best Local Similarity 26.0%; Pred. No. 1e-12;  
RESULT 883  
ID ABB89245 standard; protein; 168 AA.  
DE Human polypeptide SEQ ID NO 1621.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.4%; Score 219; DB 5; Length 168;  
Best Local Similarity 32.3%; Pred. No. 1.5e-12;  
RESULT 884  
ID ABU03171 standard; protein; 220 AA.  
DE Human immunoglobulin (Ig) APEX4sv1 protein.  
PN WO200272173-A2.  
PD 03-OCT-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 11.6%; Score 206; DB 6; Length 220;  
Best Local Similarity 28.3%; Pred. No. 4e-11;  
RESULT 885  
ID AAB26225 standard; protein; 159 AA.  
DE Human CD2000 protein #1.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.3%; Score 200.5; DB 5; Length 159;  
Best Local Similarity 35.2%; Pred. No. 8.5e-11;  
RESULT 886  
ID ABW01804 standard; protein; 159 AA.  
DE Human CD2000 protein cytoplasmic domain #1.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.3%; Score 200.5; DB 7; Length 159;  
Best Local Similarity 35.2%; Pred. No. 8.5e-11;  
RESULT 887  
ID ABB96266 standard; protein; 221 AA.  
DE Human immunoglobulin superfamily protein IGSPF-4.  
PN WO200272794-A2.  
PD 19-SEP-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 11.3%; Score 199.5; DB 5; Length 221;  
Best Local Similarity 28.3%; Pred. No. 1.7e-10;  
RESULT 888  
ID ABB85690 standard; protein; 275 AA.  
DE Mouse protein sequence MCP1591.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.8%; Score 190.5; DB 7; Length 275;  
Best Local Similarity 29.1%; Pred. No. 1.8e-09;  
RESULT 889  
ID AAR97632 standard; protein; 343 AA.  
DE Mouse SLAMF1 T-cell co-stimulatory protein.  
PN WO9617060-A1.  
PD 06-JUN-1996.  
PA (SCHE ) SCHERING CORP.  
Query Match 10.5%; Score 186; DB 2; Length 343;  
Best Local Similarity 24.3%; Pred. No. 6.7e-09;  
RESULT 890  
ID AAR97628 standard; protein; 335 AA.  
DE Human SLAMF1 T-cell co-stimulatory protein.  
PN WO9617060-A1.  
PD 06-JUN-1996.  
PA (SCHE ) SCHERING CORP.  
Query Match 10.3%; Score 182.5; DB 2; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.4e-08;  
RESULT 891  
ID AAB71853 standard; protein; 335 AA.  
DE Human SLAM protein.  
PN WO200111046-A1.  
PD 15-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.3%; Score 182.5; DB 4; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.4e-08;



RESULT 892  
ID AAU11927 standard; protein; 335 AA.  
DE Human protein sequence #1, related to isolation of genes within SLR-1B.  
PN WO200188200-A2.  
PD 22-NOV-2001.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 10.3%; Score 182.5; DB 5; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.4e-08;  
RESULT 893  
ID ABB90776 standard; protein; 335 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 285.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 10.3%; Score 182.5; DB 5; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.4e-08;  
RESULT 894  
ID ABU54483 standard; protein; 335 AA.  
DE Human normal endothelial marker NEM 23.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 10.3%; Score 182.5; DB 6; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.4e-08;  
RESULT 895  
ID ADL82887 standard; protein; 335 AA.  
DE Human PRO12612, SEQ ID 89.  
PN WO2004024097-A2.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 182.5; DB 8; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.4e-08;  
RESULT 896  
ID ADP54607 standard; protein; 335 AA.  
DE Human PRO protein sequence SEQ ID NO:583.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 182.5; DB 8; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.4e-08;  
RESULT 897  
ID ADY19726 standard; protein; 335 AA.  
DE PRO polypeptide SEQ ID NO 5532.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 182.5; DB 9; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.4e-08;  
RESULT 898  
ID ADY15680 standard; protein; 335 AA.  
DE PRO polypeptide SEQ ID NO 1486.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 182.5; DB 9; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.4e-08;  
RESULT 899  
ID AAG77978 standard; protein; 334 AA.  
DE Human signalling lymphocytic activation molecule (SLAM)/SCZ.  
PN WO200180717-A2.  
PD 01-NOV-2001.  
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
Query Match 10.2%; Score 181.5; DB 5; Length 334;  
Best Local Similarity 22.6%; Pred. No. 1.7e-08;  
RESULT 900  
ID AAR97631 standard; protein; 307 AA.  
DE Human SLAMF4 T-cell co-stimulatory protein.  
PN WO9617060-A1.  
PD 06-JUN-1996.  
PA (SCHE ) SCHERING CORP.  
Query Match 10.2%; Score 180; DB 2; Length 307;  
Best Local Similarity 22.6%; Pred. No. 2.2e-08;  
RESULT 901

ID AAY92181 standard; protein; 278 AA.  
DE Murine TANGO 195.  
PN WO200018800-A1.  
PD 06-APR-2000.  
PA (MILL-) MILENNIUM BIOTHERAPEUTICS INC.  
Query Match 10.1%; Score 179; DB 3; Length 278;  
Best Local Similarity 25.9%; Pred. No. 2.3e-08;  
RESULT 902  
ID ABG74266 standard; protein; 278 AA.  
DE Human transmembrane protein TANGO 195 form 2.  
PN US2002155526-A1.  
PD 24-OCT-2002.  
PA (BUSF/) BUSFIELD S J.  
Query Match 10.1%; Score 179; DB 6; Length 278;  
Best Local Similarity 25.9%; Pred. No. 2.3e-08;  
RESULT 903  
ID ABW01426 standard; protein; 278 AA.  
DE Murine TANGO 195 protein.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILENNIUM PHARM INC.  
Query Match 10.1%; Score 179; DB 7; Length 278;  
Best Local Similarity 25.9%; Pred. No. 2.3e-08;  
RESULT 904  
ID ABW01428 standard; protein; 258 AA.  
DE Murine TANGO 195 mature protein.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILENNIUM PHARM INC.  
Query Match 10.0%; Score 177.5; DB 7; Length 258;  
Best Local Similarity 27.0%; Pred. No. 2.9e-08;  
RESULT 905  
ID AAW67933 standard; protein; 33 AA.  
DE Fragment of human secreted protein encoded by gene 5.  
PN WO9842738-A1.  
PD 01-OCT-1998.  
PA (HUMA-) HUMA GENOME SCI INC.  
Query Match 9.9%; Score 175; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2.5e-09;  
RESULT 906  
ID ADS11838 standard; protein; 148 AA.  
DE Human therapeutic contig protein - SEQ ID 2075.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NIVE-) NIVELO INC.  
Query Match 9.6%; Score 170.5; DB 8; Length 148;  
Best Local Similarity 29.9%; Pred. No. 6.2e-08;  
RESULT 907  
ID AAY43138 standard; protein; 365 AA.  
DE Human NAIL protein sequence.  
PN WO9950297-A1.  
PD 07-OCT-1999.  
PA (IMNV ) IMMUNEX CORP.  
Query Match 9.6%; Score 170; DB 2; Length 365;  
Best Local Similarity 21.9%; Pred. No. 2.6e-07;  
RESULT 908  
ID AAM23942 standard; protein; 365 AA.  
DE Human EST encoded protein SEQ ID NO: 1467.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.6%; Score 170; DB 4; Length 365;  
Best Local Similarity 21.9%; Pred. No. 2.6e-07;  
RESULT 909  
ID AAU11929 standard; protein; 365 AA.  
DE Human protein sequence #2, related to isolation of genes within SLR-1B.  
PN WO200188200-A2.  
PD 22-NOV-2001.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 9.6%; Score 170; DB 5; Length 365;  
Best Local Similarity 21.9%; Pred. No. 2.6e-07;  
RESULT 910  
ID ADP56168 standard; protein; 365 AA.



DE Human PRO protein sequence SEQ ID NO:2144.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 9.6%; Score 170; DB 8; Length 365;  
Best Local Similarity 21.9%; Pred. No. 2.6e-07;  
RESULT 911  
ID ADP25183 standard; protein; 365 AA.  
DE PRO polypeptide SEQ ID NO:2361.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 9.6%; Score 170; DB 8; Length 365;  
Best Local Similarity 21.9%; Pred. No. 2.6e-07;  
RESULT 912  
ID ABP41447 standard; protein; 391 AA.  
DE Human ovarian antigen HMAGN71, SEQ ID NO:2579.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HOMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 170; DB 5; Length 391;  
Best Local Similarity 21.9%; Pred. No. 2.9e-07;  
RESULT 913  
ID AAR97630 standard; protein; 305 AA.  
DE Human SLAMF3 T-cell co-stimulatory protein.  
PN WO9617060-A1.  
PD 06-JUN-1996.  
PA (SCHE ) SCHERING CORP.  
Query Match 9.3%; Score 164.5; DB 2; Length 305;  
Best Local Similarity 21.7%; Pred. No. 6.8e-07;  
RESULT 914  
ID ABB90777 standard; protein; 305 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 286.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 9.3%; Score 164.5; DB 5; Length 305;  
Best Local Similarity 21.7%; Pred. No. 6.8e-07;  
RESULT 915  
ID ABU54484 standard; protein; 305 AA.  
DE Human normal endothelial marker NEM 23 secreted.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 9.3%; Score 164.5; DB 6; Length 305;  
Best Local Similarity 21.7%; Pred. No. 6.8e-07;  
RESULT 916  
ID AAR97633 standard; protein; 329 AA.  
DE Mouse SLAMF2 T-cell co-stimulatory protein.  
PN WO9617060-A1.  
PD 06-JUN-1996.  
PA (SCHE ) SCHERING CORP.  
Query Match 8.9%; Score 158.5; DB 2; Length 329;  
Best Local Similarity 27.0%; Pred. No. 2.9e-06;  
RESULT 917  
ID AAU11928 standard; protein; 329 AA.  
DE Mouse protein sequence #1, related to isolation of genes within SLF-1B.  
PN WO200188200-A2.  
PD 22-NOV-2001.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 8.9%; Score 158.5; DB 5; Length 329;  
Best Local Similarity 27.0%; Pred. No. 2.9e-06;  
RESULT 918  
ID AAR97629 standard; protein; 298 AA.  
DE Human SLAMF2 T-cell co-stimulatory protein.  
PN WO9617060-A1.  
PD 06-JUN-1996.  
PA (SCHE ) SCHERING CORP.  
Query Match 8.6%; Score 152; DB 2; Length 298;  
Best Local Similarity 23.4%; Pred. No. 1.1e-05;  
RESULT 919  
ID ABB90778 standard; protein; 298 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 287.

PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 8.6%; Score 152; DB 5; Length 298;  
Best Local Similarity 23.4%; Pred. No. 1.1e-05;  
RESULT 920  
ID ABU54485 standard; protein; 298 AA.  
DE Human normal endothelial marker NEM 23 short.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 8.6%; Score 152; DB 6; Length 298;  
Best Local Similarity 23.4%; Pred. No. 1.1e-05;  
RESULT 921  
ID AAY52479 standard; protein; 285 AA.  
DE Human D-SLAM.  
PN WO9940184-A1.  
PD 12-AUG-1999.  
PA (HOMA-) HUMAN GENOME SCI INC.  
Query Match 8.5%; Score 150.5; DB 3; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 922  
ID AAM93287 standard; protein; 285 AA.  
DE Human polypeptide, SEQ ID NO: 2773.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 8.5%; Score 150.5; DB 4; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 923  
ID AAB71852 standard; protein; 285 AA.  
DE Human D-SLAM protein.  
PN WO20011046-A1.  
PD 15-FEB-2001.  
PA (HOMA-) HUMAN GENOME SCI INC.  
Query Match 8.5%; Score 150.5; DB 4; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 924  
ID AAB47323 standard; protein; 285 AA.  
DE APEX-3.  
PN WO200146260-A2.  
PD 28-JUN-2001.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 8.5%; Score 150.5; DB 4; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 925  
ID AAR12075 standard; protein; 285 AA.  
DE Dendritic cell (DC) DCIGR protein.  
PN WO200172773-A2.  
PD 04-OCT-2001.  
PA (NOVS ) NOVARTIS AG.  
Query Match 8.5%; Score 150.5; DB 4; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 926  
ID ABG32412 standard; protein; 285 AA.  
DE Dendritic enriched secreted lymphocyte activation molecule (D-SLAM).  
PN WO200262955-A2.  
PD 15-AUG-2002.  
PA (HOMA-) HUMAN GENOME SCI INC.  
Query Match 8.5%; Score 150.5; DB 5; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 927  
ID ADC78929 standard; protein; 285 AA.  
DE Human PRO protein #79.  
PN WO2003034984-A2.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.5%; Score 150.5; DB 7; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 928  
ID ADD18914 standard; protein; 285 AA.  
DE Human disease related protein SegId403.



PN WO2003018621-A2.  
PD 06-MAR-2003.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 8.5%; Score 150.5; DB 7; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 929  
ID ADP15146 standard; protein; 285 AA.  
DE Human albumin fusion protein-related protein SegID444.  
PN WO2003060071-A2.  
PD 24-JUL-2003.  
PA (HUMA-) HUMAN GENOME SCI. INC.  
PA (DELT-) DELTA BIOTECHNOLOGY LTD.  
PA (PRIN-) PRINCIPAL PHARM CORP.  
Query Match 8.5%; Score 150.5; DB 7; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 930  
ID ADL30740 standard; protein; 285 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 2773.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 8.5%; Score 150.5; DB 8; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 931  
ID ADQ21161 standard; protein; 285 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3981.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 8.5%; Score 150.5; DB 8; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 932  
ID ADP14157 standard; protein; 285 AA.  
DE Human NF-kappaB pathway-associated protein SegID158.  
PN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
Query Match 8.5%; Score 150.5; DB 8; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 933  
ID ADP25075 standard; protein; 285 AA.  
DE PRO polypeptide SEQ ID NO:2253.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GERTH-) GENENTECH INC.  
Query Match 8.5%; Score 150.5; DB 8; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 934  
ID ADU06615 standard; protein; 285 AA.  
DE Novel bronchial cancer-associated human protein SegID841.  
PN DE10316701-A1.  
PD 04-NOV-2004.  
PA (HINZ/) HINZMANN B.  
PA (HERM/) HERMANN K.  
PA (CAST/) HEIDEN CASTANOS-VELEZ E.  
Query Match 8.5%; Score 150.5; DB 8; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 935  
ID ADY17598 standard; protein; 285 AA.  
DE PRO polypeptide SEQ ID NO 3404.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GERTH-) GENENTECH INC.  
Query Match 8.5%; Score 150.5; DB 9; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 936  
ID ADZ10066 standard; protein; 285 AA.  
DE Human breast cancer marker BLMB protein.  
PN EP1522594-A2.  
PD 13-APR-2005.  
PA (FARB-) BAYER HEALTHCARE AG.  
Query Match 8.5%; Score 150.5; DB 9; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.4e-05;  
RESULT 937  
ID AEW01429 standard; protein; 211 AA.  
DE Murine TANGO 195 protein extracellular domain.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.3%; Score 146.5; DB 7; Length 211;  
Best Local Similarity 28.6%; Pred. No. 2.2e-05;  
RESULT 938  
ID AAY92180 standard; protein; 312 AA.  
DE Partial human TANGO 195 protein.  
PN WO20010800-A1.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHEAPRUTICS INC.  
Query Match 8.2%; Score 146; DB 3; Length 312;  
Best Local Similarity 24.5%; Pred. No. 4.4e-05;  
RESULT 939  
ID ABG74265 standard; protein; 312 AA.  
DE Human transmembrane protein TANGO 195 form 1.  
PN US2002155526-A1.  
PD 24-OCT-2002.  
PA (BUSF/) BUSFIELD S J.  
Query Match 8.2%; Score 146; DB 6; Length 312;  
Best Local Similarity 24.5%; Pred. No. 4.4e-05;  
RESULT 940  
ID AEW01412 standard; protein; 312 AA.  
DE Human TANGO 195 form 1 protein.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.2%; Score 146; DB 7; Length 312;  
Best Local Similarity 24.5%; Pred. No. 4.4e-05;  
RESULT 941  
ID AAM24013 standard; protein; 318 AA.  
DE Human EST encoded protein SEQ ID NO: 1538.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 8.2%; Score 146; DB 4; Length 318;  
Best Local Similarity 24.5%; Pred. No. 4.5e-05;  
RESULT 942  
ID AAY92182 standard; protein; 320 AA.  
DE Human partial TANGO 195 from clone T195Atbpb93f1.  
PN WO200018800-A1.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHEAPRUTICS INC.  
Query Match 8.2%; Score 146; DB 3; Length 320;  
Best Local Similarity 24.5%; Pred. No. 4.5e-05;  
RESULT 943  
ID ABG74267 standard; protein; 320 AA.  
DE Human transmembrane protein TANGO 195, full length.  
PN US2002155526-A1.  
PD 24-OCT-2002.  
PA (BUSF/) BUSFIELD S J.  
Query Match 8.2%; Score 146; DB 6; Length 320;  
Best Local Similarity 24.5%; Pred. No. 4.5e-05;  
RESULT 944  
ID AEW01436 standard; protein; 320 AA.  
DE Human TANGO 195 form 2 protein.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.2%; Score 146; DB 7; Length 320;  
Best Local Similarity 24.5%; Pred. No. 4.5e-05;  
RESULT 945  
ID ADR10254 standard; protein; 211 AA.  
DE Human protein useful for treating neurological disease Seq 3760.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 8.2%; Score 145; DB 8; Length 211;  
Best Local Similarity 30.2%; Pred. No. 3.1e-05;  
RESULT 946



ID AAY92183 standard; protein; 285 AA.  
DE Full-length human TANGO 195 protein.  
PN WO200018800-A1.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 8.2%; Score 144.5; DB 3; Length 285;  
Best Local Similarity 22.5%; Pred. No. 5.4e-05;  
RESULT 947  
ID ABG74268 standard; protein; 285 AA.  
DE Mouse transmembrane protein TANGO 195.  
PN US2002155526-A1.  
PD 24-OCT-2002.  
PA (BUSF/) BUSFTELD S J.  
Query Match 8.2%; Score 144.5; DB 6; Length 285;  
Best Local Similarity 22.5%; Pred. No. 5.4e-05;  
RESULT 948  
ID ABW01442 standard; protein; 285 AA.  
DE Human TANGO 195 protein.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.2%; Score 144.5; DB 7; Length 285;  
Best Local Similarity 22.5%; Pred. No. 5.4e-05;  
RESULT 949  
ID ADZ13290 standard; protein; 344 AA.  
DE Murine cancer-associated protein #90.  
PN WO2005031001-W2.  
PD 07-APR-2005.  
PA (CHIR) CHIRON CORP.  
Query Match 8.1%; Score 144; DB 9; Length 344;  
Best Local Similarity 21.4%; Pred. No. 7.9e-05;  
RESULT 950  
ID AEM85810 standard; protein; 358 AA.  
DE Mouse protein sequence MCP3002.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 8.1%; Score 144; DB 7; Length 358;  
Best Local Similarity 21.4%; Pred. No. 8.4e-05;  
RESULT 951  
ID ABG75379 standard; protein; 416 AA.  
DE Predicted INSP052 protein.  
PN WO2003093316-A2.  
PD 13-NOV-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 8.0%; Score 142.5; DB 7; Length 416;  
Best Local Similarity 22.1%; Pred. No. 0.00015;  
RESULT 952  
ID ABG75377 standard; protein; 416 AA.  
DE Human INSP052 complete protein.  
PN WO2003093316-A2.  
PD 13-NOV-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 8.0%; Score 142.5; DB 7; Length 416;  
Best Local Similarity 22.1%; Pred. No. 0.00015;  
RESULT 953  
ID ADO47892 standard; protein; 416 AA.  
DE Human protein SEQ ID NO:9.  
PN WO2004007672-A2.  
PD 22-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 8.0%; Score 142.5; DB 8; Length 416;  
Best Local Similarity 22.1%; Pred. No. 0.00015;  
RESULT 954  
ID ADS11056 standard; protein; 416 AA.  
DE Human therapeutic protein - SEQ ID 1293.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 8.0%; Score 142.5; DB 8; Length 416;  
Best Local Similarity 22.1%; Pred. No. 0.00015;  
RESULT 955  
ID AEA27921 standard; protein; 416 AA.

DE Cell surface recognition molecule INSP052.  
PN WO2005046714-A2.  
PD 26-MAY-2005.  
PA (ARES-) ARES TRADING SA.  
Query Match 8.0%; Score 142.5; DB 9; Length 416;  
Best Local Similarity 22.1%; Pred. No. 0.00015;  
RESULT 956  
ID ADO65357 standard; protein; 367 AA.  
DE Novel human protein sequence #330.  
PN EPI440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 8.0%; Score 142; DB 8; Length 367;  
Best Local Similarity 22.2%; Pred. No. 0.00014;  
RESULT 957  
ID ADA07622 standard; peptide; 149 AA.  
DE Human secreted protein from gene 43, peptide #2.  
PN US2003064412-A1.  
PD 03-APR-2003.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAF/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
Query Match 8.0%; Score 141; DB 7; Length 149;  
Best Local Similarity 30.7%; Pred. No. 4.5e-05;  
RESULT 958  
ID ADN41449 standard; protein; 149 AA.  
DE Novel human secreted protein fragment seqid 571.  
PN US2004044191-A1.  
PD 04-MAR-2004.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAF/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Query Match 8.0%; Score 141; DB 8; Length 149;  
Best Local Similarity 30.7%; Pred. No. 4.5e-05;  
RESULT 959  
ID ADA57556 standard; protein; 142 AA.  
DE Human secreted protein #504.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.9%; Score 140.5; DB 6; Length 142;  
Best Local Similarity 31.0%; Pred. No. 4.7e-05;  
RESULT 960  
ID ADA41448 standard; protein; 142 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.9%; Score 140.5; DB 6; Length 142;  
Best Local Similarity 31.0%; Pred. No. 4.7e-05;  
RESULT 961  
ID ADC74567 standard; protein; 142 AA.  
DE Human secreted protein - SEQ ID 1200.



PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.9%; Score 140.5; DB 7; Length 142;  
RESULT 962  
ID ADD38086 standard; protein; 142 AA.  
PN WO200290526-A2.  
PD 14-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.9%; Score 140.5; DB 7; Length 142;  
RESULT 963  
ID ADN41130 standard; protein; 142 AA.  
PN US200404191-A1.  
PD 04-MAR-2004.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAFL/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIT/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Query Match  
Best Local Similarity 7.9%; Score 140.5; DB 8; Length 142;  
RESULT 964  
ID AAY02692 standard; protein; 143 AA.  
PN WO9902546-A1.  
PD 21-JAN-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.9%; Score 140.5; DB 2; Length 143;  
RESULT 965  
ID ADA07371 standard; protein; 143 AA.  
PN US2003064412-A1.  
PD 03-APR-2003.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAFL/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIT/) SHI Y.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
Query Match  
Best Local Similarity 7.9%; Score 140.5; DB 7; Length 143;  
RESULT 966  
ID AEW01419 standard; protein; 290 AA.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 7.9%; Score 140.5; DB 7; Length 290;  
RESULT 967  
ID AEW01438 standard; protein; 298 AA.  
PN US2003113865-A1.  
PD 18-MAR-2004.

PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 7.9%; Score 140.5; DB 7; Length 298;  
RESULT 968  
ID AAW67932 standard; protein; 28 AA.  
PN WO9842738-A1.  
PD 01-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.1e-06;  
RESULT 969  
ID AEW01444 standard; protein; 263 AA.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 7.8%; Score 139; DB 7; Length 263;  
RESULT 970  
ID ABG75378 standard; protein; 418 AA.  
PN WO2003093316-A2.  
PD 13-NOV-2003.  
PA (MURR-) MURRINE INSP052 complete protein.  
Query Match  
Best Local Similarity 22.9%; Pred. No. 0.00036;  
RESULT 971  
ID AEA27923 standard; protein; 418 AA.  
PN WO2005046714-A2.  
PD 26-MAY-2005.  
PA (ARES-) ARES TRADING SA.  
Query Match  
Best Local Similarity 7.8%; Score 138.5; DB 9; Length 418;  
RESULT 972  
ID AAR26255 standard; protein; 70 AA.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 7.8%; Score 138; DB 5; Length 70;  
RESULT 973  
ID AEW01635 standard; protein; 70 AA.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 7.8%; Score 138; DB 7; Length 70;  
RESULT 974  
ID ADO47895 standard; protein; 383 AA.  
PN WO2004007672-A2.  
PD 22-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match  
Best Local Similarity 7.8%; Score 137.5; DB 8; Length 383;  
RESULT 975  
ID AEA27931 standard; protein; 383 AA.  
PN WO2005046714-A2.  
PD 26-MAY-2005.  
PA (ARES-) ARES TRADING SA.  
Query Match  
Best Local Similarity 7.8%; Score 137.5; DB 9; Length 383;  
RESULT 976  
ID ADW72195 standard; protein; 327 AA.  
PN WO2004022097-A1.  
PD 18-MAR-2004.



PA (MEDI-) MEDIMUNE INC.  
 PA (USSR) US NAT CANCER INST.  
 Query Match 7.7%; Score 136.5; DB 8; Length 327;  
 Best Local Similarity 23.9%; Pred. No. 0.00039;  
 RESULT 977  
 ID AAY83135 standard; protein; 351 AA.  
 DE Human CD2.  
 PN W0200012113-A2.  
 PD 09-MAR-2000.  
 PA (BIOC) BIOGEN INC.  
 Query Match 7.7%; Score 136.5; DB 3; Length 351;  
 Best Local Similarity 23.9%; Pred. No. 0.00043;  
 RESULT 978  
 ID AAB61159 standard; protein; 351 AA.  
 DE Human CD2.  
 PN US6162432-A.  
 PD 19-DEC-2000.  
 PA (UNMT) UNIV MICHIGAN.  
 Query Match 7.7%; Score 136.5; DB 4; Length 351;  
 Best Local Similarity 23.9%; Pred. No. 0.00043;  
 RESULT 979  
 ID ABB81993 standard; protein; 351 AA.  
 DE Human CD2 polypeptide.  
 PN W0200260480-A1.  
 PD 08-AUG-2002.  
 PA (BIOC) BIOGEN INC.  
 Query Match 7.7%; Score 136.5; DB 5; Length 351;  
 Best Local Similarity 23.9%; Pred. No. 0.00043;  
 RESULT 980  
 ID AAU76227 standard; protein; 351 AA.  
 DE Mammalian CD2 antigen protein.  
 PN US2002009449-A1.  
 PD 24-JAN-2002.  
 PA (BIOC) BIOGEN INC.  
 Query Match 7.7%; Score 136.5; DB 8; Length 351;  
 Best Local Similarity 23.9%; Pred. No. 0.00043;  
 RESULT 981  
 ID ABM85811 standard; protein; 351 AA.  
 DE Human protein sequence hcp48906.  
 PN W02003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Query Match 7.7%; Score 136.5; DB 7; Length 351;  
 Best Local Similarity 23.9%; Pred. No. 0.00043;  
 RESULT 982  
 ID ADG60208 standard; protein; 351 AA.  
 DE Human CD2 protein.  
 PN US2004136987-A1.  
 PD 15-JUL-2004.  
 PA (BIOC) BIOGEN INC.  
 Query Match 7.7%; Score 136.5; DB 8; Length 351;  
 Best Local Similarity 23.9%; Pred. No. 0.00043;  
 RESULT 983  
 ID ADZ13293 standard; protein; 351 AA.  
 DE Human cancer-associated protein #249.  
 PN W02005031001-A2.  
 PD 07-APR-2005.  
 PA (CHIR) CHIRON CORP.  
 Query Match 7.7%; Score 136.5; DB 9; Length 351;  
 Best Local Similarity 23.9%; Pred. No. 0.00043;  
 RESULT 984  
 ID AAR06365 standard; protein; 353 AA.  
 DE Soluble two domain human CD2 glycoprotein.  
 PN W09008187-A.  
 PD 26-JUL-1990.  
 PA (DAND) DANA FARBER CANCER INST INC.  
 Query Match 7.7%; Score 136.5; DB 2; Length 353;  
 Best Local Similarity 23.9%; Pred. No. 0.00044;  
 RESULT 985  
 ID AAU29274 standard; protein; 198 AA.  
 DE Human PRO polypeptide sequence #251.  
 PN W0200168848-A2.  
 PD 20-SEP-2001.  
 PA (GETH) GENENTECH INC.  
 Query Match 7.6%; Score 134.5; DB 4; Length 198;  
 Best Local Similarity 30.7%; Pred. No. 0.00029;  
 RESULT 986  
 ID ABU58650 standard; protein; 198 AA.  
 DE Human PRO polypeptide #251.  
 PN US2003027272-A1.  
 PD 06-FEB-2003.  
 Query Match 7.6%; Score 134.5; DB 6; Length 198;  
 Best Local Similarity 30.7%; Pred. No. 0.00029;  
 RESULT 987  
 ID ABU88198 standard; protein; 198 AA.  
 DE Novel human secreted and transmembrane protein PRO4421.  
 PN US2003032127-A1.  
 PD 13-FEB-2003.  
 Query Match 7.6%; Score 134.5; DB 6; Length 198;  
 Best Local Similarity 30.7%; Pred. No. 0.00029;  
 RESULT 988  
 ID ABU84513 standard; protein; 198 AA.  
 DE Human secreted/transmembrane protein (PRO) #251.  
 PN US2003032112-A1.  
 PD 13-FEB-2003.  
 Query Match 7.6%; Score 134.5; DB 6; Length 198;  
 Best Local Similarity 30.7%; Pred. No. 0.00029;  
 RESULT 989  
 ID ABR66387 standard; protein; 198 AA.  
 DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
 PN US2003027278-A1.  
 PD 06-FEB-2003.  
 Query Match 7.6%; Score 134.5; DB 6; Length 198;  
 Best Local Similarity 30.7%; Pred. No. 0.00029;  
 RESULT 990  
 ID ABR65777 standard; protein; 198 AA.  
 DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
 PN US2003036159-A1.  
 PD 20-FEB-2003.  
 Query Match 7.6%; Score 134.5; DB 6; Length 198;  
 Best Local Similarity 30.7%; Pred. No. 0.00029;  
 RESULT 991  
 ID ABU99717 standard; protein; 198 AA.  
 DE Human secreted/transmembrane protein (PRO) #251.  
 PN US2003040070-A1.  
 PD 27-FEB-2003.  
 Query Match 7.6%; Score 134.5; DB 6; Length 198;  
 Best Local Similarity 30.7%; Pred. No. 0.00029;  
 RESULT 992  
 ID ABU82956 standard; protein; 198 AA.  
 DE Human PRO polypeptide #251.  
 PN US2003032113-A1.  
 PD 13-FEB-2003.  
 Query Match 7.6%; Score 134.5; DB 6; Length 198;  
 Best Local Similarity 30.7%; Pred. No. 0.00029;  
 RESULT 993  
 ID ABU90077 standard; protein; 198 AA.  
 DE Novel human secreted and transmembrane protein PRO4421.  
 PN US2003036147-A1.  
 PD 20-FEB-2003.  
 Query Match 7.6%; Score 134.5; DB 6; Length 198;  
 Best Local Similarity 30.7%; Pred. No. 0.00029;  
 RESULT 994  
 ID ABR68326 standard; protein; 198 AA.  
 DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
 PN US2003027264-A1.  
 PD 06-FEB-2003.  
 Query Match 7.6%; Score 134.5; DB 6; Length 198;  
 Best Local Similarity 30.7%; Pred. No. 0.00029;  
 RESULT 995  
 ID ABU96379 standard; protein; 198 AA.  
 DE Novel human secreted and transmembrane protein PRO4421.  
 PN US2003036144-A1.  
 PD 20-FEB-2003.



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Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 996
ID ABU92810 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 997
ID AB008887 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 998
ID AB002939 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 999
ID ABR75093 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1000
ID ABR94855 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1001
ID ABU85828 standard; protein: 198 AA.
DE Human PRO polypeptide #251.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1002
ID ABU98988 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1003
ID ABU98203 standard; protein: 198 AA.
DE Human secreted and transmembrane protein PRO4421.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1004
ID ABU91909 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1005
ID ABU89602 standard; protein: 198 AA.
DE Human PRO polypeptide #251.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1006
ID ABU86443 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1007
ID ABU67656 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1008
ID ABU80684 standard; protein: 198 AA.
DE Human PRO protein #251.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1009
ID ABR99602 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1010
ID ABR98992 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1011
ID AB016515 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1012
ID ABR92415 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1013
ID AB019056 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1014
ID ABR78477 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1015
ID ABR85213 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
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Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1016
ID ABO00352 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1017
ID ABO11684 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1018
ID ABO02329 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1019
ID AB08903 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1020
ID AB08359 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1021
ID ABO06399 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1022
ID ABR59435 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1023
ID ABO09497 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1024
ID ABO19361 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1025
ID ABO11379 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1026
ID ABR6997 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1027
ID ABO16210 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1028
ID ABO13916 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1029
ID AB05819 standard; protein: 198 AA.
DE Human secreted/transmembrane protein, SEQ ID 502.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1030
ID ABO07667 standard; protein: 198 AA.
DE Human PRO polypeptide #251.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1031
ID ABO03854 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1032
ID ABR67302 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1033
ID ABO15905 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1034
ID ABUS6186 standard; protein: 198 AA.
DE Human secreted/transmembrane protein, PRO4421.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1035
ID ABUS514 standard; protein: 198 AA.
DE Human PRO polypeptide #251.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1036
ID AB095459 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
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PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1037  
ID ABR71362 standard; protein; 198 AA.  
DE Human PRO4421 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1038  
ID ABR07972 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1039  
ID ABR70213 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1040  
ID ABR9546 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1041  
ID ABR01687 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1042  
ID ABR01687 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1043  
ID ABR60286 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1044  
ID ABR68021 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1045  
ID ABR5409 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1046  
ID ABR6831 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027274-A1.

PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1047  
ID ABR72043 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1048  
ID ABR5523 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1049  
ID ABR89213 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1050  
ID ABR83293 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1051  
ID ABR95149 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1052  
ID ABR90697 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1053  
ID ABR84208 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1054  
ID ABR93859 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1055  
ID ABR5104 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1056  
ID ABR68936 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027271-A1.  
PD 06-FEB-2003.



Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1057  
ID ABO06752 standard; protein; 198 AA.  
DE Human secreted/cranmembrane protein (PRO) #251.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1058  
ID ABR99297 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1059  
ID ABU57181 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1060  
ID ABU86133 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1061  
ID ABU82420 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1062  
ID ABU87431 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1063  
ID ABU83903 standard; protein; 198 AA.  
DE Human secreted/cranmembrane protein (PRO) #251.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1064  
ID ABO08277 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1065  
ID ABU81988 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1066  
ID ABU66152 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1067

ID ABR5981 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1068  
ID ABU94169 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1069  
ID ABO00042 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1070  
ID ABR66592 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1071  
ID ABR91110 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1072  
ID ABU94537 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1073  
ID ABU79419 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1074  
ID ABU86748 standard; protein; 198 AA.  
DE Human secreted/cranmembrane protein (PRO) #251.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1075  
ID ABU87053 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1076  
ID ABU94842 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1077  
ID ABO04769 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.



PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1078  
ID ABR70518 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1079  
ID ABR98683 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1080  
ID ABR66082 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1081  
ID ABR64799 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1082  
ID ABR979724 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1083  
ID ABR93115 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1084  
ID ABR96074 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1085  
ID ABR91294 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1086  
ID ABR90387 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1087  
ID ABR09802 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1088  
ID ABR11074 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1089  
ID ABR71128 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1090  
ID ABR67736 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1091  
ID ABR91604 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1092  
ID ABR84818 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1093  
ID ABR69908 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1094  
ID ABR80285 standard; protein; 198 AA.  
DE Human PRO protein #251.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1095  
ID ABR93554 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1096  
ID ABR01017 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1097  
ID ABR009192 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1098



ID ABU10760 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein #251.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1099  
ID ABU95769 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1100  
ID ABU96978 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1101  
ID ABR70882 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1102  
ID ABO05174 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US200308352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1103  
ID ABO08582 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1104  
ID ABO05789 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1105  
ID ABR4178 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1106  
ID ABR5770 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1107  
ID ABR1067 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;

Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1108  
ID ABR81372 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1109  
ID ABM01068 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1110  
ID ABR88670 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1111  
ID ABM77491 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1112  
ID ABO28975 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1113  
ID ABO31720 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1114  
ID ABM08137 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1115  
ID ABO40617 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1116  
ID ABO36042 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;



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RESULT 1117
ID ABO44181 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1118
ID ADA78254 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1119
ID ABM24976 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1120
ID ABO03244 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1121
ID ABR90500 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1122
ID ABM17414 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1123
ID ABR95160 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1124
ID ABR95465 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1125
ID ABO21703 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1126
ID ABR97967 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1127
ID ABR87755 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1128
ID ABM77796 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1129
ID ABM28026 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1130
ID ABM06307 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1131
ID ABM03813 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1132
ID ABM35264 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1133
ID ABM26501 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1134
ID ABO48283 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1135
ID ABR93025 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
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Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1136
ID ABO24786 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1137
ID ABM11797 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1138
ID ABM02898 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1139
ID ABM16194 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1140
ID ABO27755 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1141
ID ABM29246 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1142
ID ABM07222 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1143
ID ABM21316 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1144
ID ABM09662 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1145
ID ABO41532 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1146
ID ABO36347 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1147
ID ABO43876 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1148
ID ABM76576 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1149
ID ABM76272 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1150
ID ABM25891 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1151
ID ABM26196 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1152
ID ABO03549 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1153
ID ABO02634 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1154
ID ABR30805 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
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Best Local Similarity 30.7%; Pred. No. 0.00029;
ID ABR73873 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1156
ID ABO17125 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1157
ID ABR94550 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1158
ID ABR76057 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1159
ID ABR71433 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059860-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1160
ID ABR93330 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1161
ID ABR93635 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1162
ID ABR88060 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1163
ID ABO28060 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1164
ID ABO30195 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1165
ID ABO33404 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1166
ID ABO05092 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1167
ID ABO09052 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1168
ID ABO36652 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1169
ID ABO35737 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1170
ID ABO39702 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1171
ID ABO10577 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1172
ID ABO12102 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1173
ID ABO52248 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
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PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1174  
ID ABO52553 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1175  
ID ABO23871 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1176  
ID ABR97357 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1177  
ID ABR97145 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1178  
ID ABM1187 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1179  
ID ABM28331 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1180  
ID ABO32330 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1181  
ID ABM15457 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1182  
ID ABM06612 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1183  
ID ABM04423 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1184  
ID ABM22536 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1185  
ID ABM07832 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1186  
ID ABO40922 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1187  
ID ABM35569 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1188  
ID ABM33332 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1189  
ID ABO52858 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1190  
ID ABO50418 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1191  
ID ABU99412 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;



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RESULT 1192
ID ABO04464 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1193
ID ABM18634 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1194
ID ABR97662 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1195
ID ABR80762 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1196
ID ABM01373 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1197
ID ABR88975 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1198
ID ABM13627 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1199
ID ABM21011 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1200
ID ABO42142 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1201
ID ABO42752 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1202
ID ABM10272 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1203
ID ABO38787 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1204
ID ABM33027 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1205
ID ABM22841 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1206
ID ABM75052 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1207
ID ADA80046 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1208
ID ABR96442 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1209
ID ABM02593 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1210
ID ABR86535 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
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[illegible]

DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003082716-A1.	
PD	01-MAY-2003.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1221		
ID	ABM6585 standard; protein; 198 AA.	
DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003068737-A1.	
PD	10-APR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1222		
ID	ABM75967 standard; protein; 198 AA.	
DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003104547-A1.	
PD	05-JUN-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1223		
ID	ABM34247 standard; protein; 198 AA.	
DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003093659-A1.	
PD	22-MAY-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1224		
ID	ABM34552 standard; protein; 198 AA.	
DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003100061-A1.	
PD	29-MAY-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1225		
ID	ABO20483 standard; protein; 198 AA.	
DE	Human secreted/transmembrane protein (PRO) #251.	
PN	US2003032125-A1.	
PD	13-FEB-2003.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1226		
ID	ABO21398 standard; protein; 198 AA.	
DE	Human secreted/transmembrane protein (PRO) #251.	
PN	US2003054454-A1.	
PD	20-MAR-2003.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1227		
ID	ABO22313 standard; protein; 198 AA.	
DE	Human secreted/transmembrane protein (PRO) #251.	
PN	US2003054477-A1.	
PD	20-MAR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1228		
ID	ABR96747 standard; protein; 198 AA.	
DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003054460-A1.	
PD	20-MAR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1229		
ID	ABR85925 standard; protein; 198 AA.	
DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003049753-A1.	
PD	13-MAR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1230		
ID	ABR85925 standard; protein; 198 AA.	
DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003049753-A1.	
PD	13-MAR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1231		
ID	ABR85925 standard; protein; 198 AA.	
DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003049753-A1.	
PD	13-MAR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1232		
ID	ABR85925 standard; protein; 198 AA.	
DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003049753-A1.	
PD	13-MAR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1233		
ID	ABR85925 standard; protein; 198 AA.	
DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003049753-A1.	
PD	13-MAR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1234		
ID	ABR85925 standard; protein; 198 AA.	
DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003049753-A1.	
PD	13-MAR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1235		
ID	ABR85925 standard; protein; 198 AA.	
DE	Human secreted polypeptide PRO4421,	SEQ ID NO:502.
PN	US2003049753-A1.	
PD	13-MAR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	7.6%; Score 134.5; DB 6;	Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;	
RESULT 1236		
ID	ABR85925 standard; protein; 198 AA.	
DE	Human	



Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1230  
ID ABR99907 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1231  
ID ABM00458 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1232  
ID ABM00763 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1233  
ID ABO29890 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1234  
ID ABM23756 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1235  
ID ABM29551 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1236  
ID ABO38482 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1237  
ID ABO45782 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1238  
ID ABM20706 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1239

ID ADA81773 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1240  
ID ABO16820 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1241  
ID ABO18446 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1242  
ID ABO22873 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1243  
ID ABO23178 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1244  
ID ABR92720 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1245  
ID ABR81677 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1246  
ID ABM78101 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1247  
ID ABR9890 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1248  
ID ABM26806 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;



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Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1249
ID ABM13932 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1250
ID ABO28670 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1251
ID ABO30500 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1252
ID ABM07527 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1253
ID ABM04118 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1254
ID ABO37262 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1255
ID ABO41837 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1256
ID ABO35432 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1257
ID ABM5281 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1258
ID ABO47673 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1259
ID ABO47978 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1260
ID ABO4858 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1261
ID ABO51638 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1262
ID ABO51943 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1263
ID ABO50723 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1264
ID ABR79847 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1265
ID ABM17109 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1266
ID ABO18141 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1267
ID ABO21093 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032132-A1.
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PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1268  
ID ABR97052 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1269  
ID ABM12407 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1270  
ID ABM16499 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1271  
ID ABM43366 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1272  
ID ABM14847 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1273  
ID ABM04728 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1274  
ID ABM06917 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1275  
ID ABM09357 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1276  
ID ABO39397 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;

RESULT 1277  
ID ABM75662 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1278  
ID ABM25586 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1279  
ID ABM20096 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1280  
ID ABO47002 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1281  
ID ABO47307 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1282  
ID ADA63571 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1283  
ID ABR71738 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1284  
ID ABR72348 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1285  
ID ABR98687 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1286  
ID ABO07057 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003040053-A1.  
PD 27-FEB-2003.



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Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1287
ID ABR85010 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1288
ID ABR73568 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1289
ID ABR76662 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1290
ID ABR73263 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1291
ID ABR18329 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1292
ID ABO20788 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1293
ID ABO25531 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1294
ID ABO25836 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1295
ID ABR94245 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1296
ID ABR0152 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1297
ID ABR11492 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1298
ID ABO33099 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1299
ID ABO30805 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1300
ID ABO31110 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1301
ID ABR27416 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1302
ID ABR30161 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1303
ID ABR05697 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1304
ID ABR15762 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1305
ID ABR08747 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068759-A1.
PD 10-APR-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1306  
ID ABO42447 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1307  
ID ABO38177 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1308  
ID ABO46087 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1309  
ID ABM66890 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1310  
ID ADB20614 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1311  
ID ABM19791 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1312  
ID ABO49503 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1313  
ID ABO49808 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1314  
ID ADA78666 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;

Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1315  
ID ABR88365 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1316  
ID ABM27111 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1317  
ID ABM03508 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1318  
ID ABO40007 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1319  
ID ABO50113 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1320  
ID ABO51028 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1321  
ID ABO05484 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1322  
ID ABR74788 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1323  
ID ABR77267 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1324  
ID ABM18024 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.



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PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1325
ID ABR66075 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1326
ID ABO22008 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1327
ID ABO20178 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1328
ID ABO24481 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1329
ID ABR6230 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1330
ID ABM10882 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1331
ID ABM16881 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1332
ID ABR69585 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1333
ID ABM12712 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1334
ID ABM06002 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1335
ID ABO35127 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1336
ID ABM03203 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1337
ID ABM19181 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1338
ID ABM19486 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1339
ID ABO46697 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1340
ID ABO49198 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1341
ID ABR69241 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1342
ID ABR69280 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1343
ID ABR72653 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
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PN US2003036120-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1344
ID ABR74483 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1345
ID ABO18751 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1346
ID ABR80457 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1347
ID ABM01678 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1348
ID ABM02288 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1349
ID ABR87450 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1350
ID ABM13017 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1351
ID ABM10771 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1352
ID ABM24671 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1353
ID ABO29585 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1354
ID ABO31415 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1355
ID ABM14542 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1356
ID ABM09967 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1357
ID ABO39092 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1358
ID ABM34857 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1359
ID ABO51333 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1360
ID ABO04159 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1361
ID ABO10629 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1362
ID ABR77872 standard; protein; 198 AA.
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DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1363  
ID ABR79082 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1364  
ID ABO24176 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1365  
ID ABR3940 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1366  
ID ABR01983 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1367  
ID ABR78406 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1368  
ID ABR0195 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1369  
ID ABR27721 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1370  
ID ABR13322 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1371  
ID ABO32025 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1372  
ID ABR14237 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1373  
ID ABR08442 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1374  
ID ABO40312 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1375  
ID ABR74747 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1376  
ID ABR3942 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1377  
ID ABR20401 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1378  
ID ABO48893 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1379  
ID ABR72958 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1380  
ID ABO15600 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1381



[illegible]

Query Match	7.6%;	Score 134.5;	DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1391				
ID	ABM21621 standard; protein; 198 AA.			
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.			
PN	US2003068744-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	7.6%;	Score 134.5;	DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1392				
ID	ABM15152 standard; protein; 198 AA.			
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.			
PN	US2003068766-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	7.6%;	Score 134.5;	DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1393				
ID	ABO41227 standard; protein; 198 AA.			
DE	Human secreted/transmembrane protein (PRO) #251.			
PN	US2003068694-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	7.6%;	Score 134.5;	DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1394				
ID	ABO36957 standard; protein; 198 AA.			
DE	Human secreted/transmembrane protein (PRO) #251.			
PN	US2003068715-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	7.6%;	Score 134.5;	DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1395				
ID	ABO37567 standard; protein; 198 AA.			
DE	Human secreted/transmembrane protein (PRO) #251.			
PN	US2003068726-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	7.6%;	Score 134.5;	DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1396				
ID	ABM75357 standard; protein; 198 AA.			
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.			
PN	US2003104544-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	7.6%;	Score 134.5;	DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1397				
ID	ABM33637 standard; protein; 198 AA.			
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.			
PN	US2003096357-A1.			
PD	22-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	7.6%;	Score 134.5;	DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1398				
ID	ABO46392 standard; protein; 198 AA.			
DE	Human PRO polypeptide #251.			
PN	US2003049760-A1.			
PD	13-MAR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	7.6%;	Score 134.5;	DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1399				
ID	ADA82937 standard; protein; 198 AA.			
DE	Human secreted/transmembrane protein (PRO) #251.			
PN	US2003049755-A1.			
PD	13-MAR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	7.6%;	Score 134.5;	DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1399				
ID	ADA82937 standard; protein; 198 AA.			
DE	Human secreted/transmembrane protein (PRO) #251.			
PN	US2003049755-A1.			
PD	13-MAR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	7.6%;	Score 134.5;	DB 7;	Length 198;



Best Local Similarity	30.7%;	Pred. No. 0.00029;	
RESULT 1400			
ID	ABM311991 standard; protein; 198 AA.		
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.		
PN	US2003068680-A1.		
PD	10-APR-2003.		
Query Match	7.6%;	Score 134.5; DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;	
RESULT 1401			
ID	ABM31381 standard; protein; 198 AA.		
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.		
PN	US2003068762-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	7.6%;	Score 134.5; DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;	
RESULT 1402			
ID	ADBB6245 standard; protein; 198 AA.		
DE	Human secreted/transmembrane protein (PRO) #251.		
PN	US2003054472-A1.		
PD	20-MAR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	7.6%;	Score 134.5; DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;	
RESULT 1403			
ID	ABM32296 standard; protein; 198 AA.		
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.		
PN	US2003068708-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	7.6%;	Score 134.5; DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;	
RESULT 1404			
ID	ABM32601 standard; protein; 198 AA.		
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.		
PN	US2003068713-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	7.6%;	Score 134.5; DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;	
RESULT 1405			
ID	ABM31686 standard; protein; 198 AA.		
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.		
PN	US2003068761-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	7.6%;	Score 134.5; DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;	
RESULT 1406			
ID	ABM31076 standard; protein; 198 AA.		
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.		
PN	US2003068771-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	7.6%;	Score 134.5; DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;	
RESULT 1407			
ID	ADD05975 standard; protein; 198 AA.		
DE	Human secreted/transmembrane protein (PRO) #251.		
PN	US2003087376-A1.		
PD	08-MAY-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	7.6%;	Score 134.5; DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;	
RESULT 1408			
ID	ADG02970 standard; protein; 198 AA.		
DE	Novel human secreted and transmembrane protein PRO4421.		
PN	US2003207397-A1.		
PD	06-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	7.6%;	Score 134.5; DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;	
RESULT 1409			
ID	ABM311991 standard; protein; 198 AA.		
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.		
PN	US2003068680-A1.		
PD	10-APR-2003.		
Query Match	7.6%;	Score 134.5; DB 7;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;	
RESULT 1409			

ID	ADG01677 standard; protein; 198 AA.
DE	Novel human secreted and transmembrane protein PRO4421.
PN	US2003207399-A1.
PD	06-NOV-2003.
PA	( GETH ) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1410	
ID	ADP95852 standard; protein; 198 AA.
DE	Novel human secreted and transmembrane protein PRO4421.
PN	US2003207398-A1.
PD	06-NOV-2003.
PA	( GETH ) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1411	
ID	ADG12667 standard; protein; 198 AA.
DE	Novel human secreted and transmembrane protein PRO4421.
PN	US2003207392-A1.
PD	06-NOV-2003.
PA	( GETH ) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1412	
ID	ADH09327 standard; protein; 198 AA.
DE	Human PRO polypeptide #251.
PN	US2003207395-A1.
PD	06-NOV-2003.
PA	( GETH ) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1413	
ID	ADI33106 standard; protein; 198 AA.
DE	Novel human secreted and transmembrane protein PRO4421.
PN	US2003207396-A1.
PD	06-NOV-2003.
PA	( GETH ) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1414	
ID	ADM030642 standard; protein; 198 AA.
DE	Novel human secreted and transmembrane protein PRO4421.
PN	US2003073813-A1.
PD	17-APR-2003.
PA	( GETH ) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1415	
ID	ADE74639 standard; protein; 198 AA.
DE	Human secreted/transmembrane protein (PRO) #251.
PN	US2003211572-A1.
PD	13-NOV-2003.
PA	( GETH ) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1416	
ID	ADE75251 standard; protein; 198 AA.
DE	Human secreted/transmembrane protein (PRO) #251.
PN	US2003211574-A1.
PD	13-NOV-2003.
PA	( GETH ) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1417	
ID	ADP96464 standard; protein; 198 AA.
DE	Novel human secreted and transmembrane protein PRO4421.
PN	US2003215909-A1.
PD	20-NOV-2003.
PA	( GETH ) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1418	
ID	ADG04735 standard; protein; 198 AA.
DE	Novel human secreted and transmembrane protein PRO4421.
PN	US2003215912-A1.
PD	20-NOV-2003.
PA	( GETH ) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity	30.7%; Pred. No. 0.00029;



Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1419  
ID ADG00895 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1420  
ID ADG8151 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1421  
ID ADH26432 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1422  
ID ADH33401 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1423  
ID ADJ55140 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1424  
ID ADJ64911 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1425  
ID ADM31807 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1426  
ID ADM36854 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1427  
ID ADM4659 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;

Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1428  
ID ADN38267 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1429  
ID ADE63380 standard; protein; 240 AA.  
DE Rat Protein p10252, SEQ ID NO 9319.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GENO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 7.6%; Score 134; DB 7; Length 240;  
Best Local Similarity 24.6%; Pred. No. 0.00043;  
RESULT 1430  
ID ADV90298 standard; protein; 327 AA.  
DE Protease-hydrolysed polypeptide #75.  
PN WO2004113522-A1.  
PD 29-DEC-2004.  
PA (DIRE) DIREVO BIOTECH AG.  
Query Match 7.5%; Score 133.5; DB 9; Length 327;  
Best Local Similarity 22.7%; Pred. No. 0.00076;  
RESULT 1431  
ID AAR74221 standard; protein; 332 AA.  
DE Epitope on the primary CD2 sequence.  
PN US5411861-A.  
PD 02-MAY-1995.  
PA (GENO) GEN HOSPITAL CORP.  
Query Match 7.5%; Score 133.5; DB 2; Length 332;  
Best Local Similarity 22.7%; Pred. No. 0.00078;  
RESULT 1432  
ID AAY30457 standard; protein; 332 AA.  
DE Predicted sequence of the mature CD2 protein.  
PN US5955264-A.  
PD 21-SEP-1999.  
PA (GENO) GEN HOSPITAL CORP.  
Query Match 7.5%; Score 133.5; DB 2; Length 332;  
Best Local Similarity 22.7%; Pred. No. 0.00078;  
RESULT 1433  
ID ADA25185 standard; protein; 332 AA.  
DE Mature CD2 protein.  
PN US6579676-B1.  
PD 17-JUN-2003.  
PA (GENO) GEN HOSPITAL CORP.  
Query Match 7.5%; Score 133.5; DB 6; Length 332;  
Best Local Similarity 22.7%; Pred. No. 0.00078;  
RESULT 1434  
ID AAR11921 standard; protein; 351 AA.  
DE Human T11 sugar protein.  
PN JP03035782-A.  
PD 15-FEB-1991.  
PA (DAND) DANA FARBER CANCER INST INC.  
Query Match 7.5%; Score 133.5; DB 2; Length 351;  
Best Local Similarity 24.4%; Pred. No. 0.00085;  
RESULT 1435  
ID AAR20803 standard; protein; 351 AA.  
DE Human CD2 antigen.  
PN WO9201049-A.  
PD 23-JAN-1992.  
PA (GENO) GEN HOSPITAL CORP.  
Query Match 7.5%; Score 133.5; DB 2; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1436  
ID AAR34223 standard; protein; 351 AA.  
DE Amino acid sequence of CD2.  
PN WO9306852-A2.  
PD 15-APR-1993.  
PA (BIOC) BIOGEN INC.  
Query Match 7.5%; Score 133.5; DB 2; Length 351;



Best Local Similarity 23.6%; Pred. No. 0.00085;  
RESULT 1437  
ID AAR91431 standard; protein; 351 AA.  
DE Human CD2.  
PN US5506126-A.  
PD 09-APR-1996.  
PA (GHEO) GEN HOSPITAL CORP.  
Query Match 7.5%; Score 133.5; DB 2; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1438  
ID AAW60440 standard; protein; 351 AA.  
DE Human CD2 antigen.  
PN US5830731-A.  
PD 03-NOV-1998.  
PA (GHEO) GEN HOSPITAL CORP.  
Query Match 7.5%; Score 133.5; DB 2; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1439  
ID AAW6188 standard; protein; 351 AA.  
DE Human CD2 antigen.  
PN US5849898-A.  
PD 15-DEC-1998.  
PA (GHEO) GEN HOSPITAL CORP.  
Query Match 7.5%; Score 133.5; DB 2; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1440  
ID AAY96126 standard; protein; 351 AA.  
DE Human cell surface antigen CD2.  
PN US6111093-A.  
PD 29-AUG-2000.  
PA (GHEO) GEN HOSPITAL CORP.  
Query Match 7.5%; Score 133.5; DB 3; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1441  
ID AAU02435 standard; protein; 351 AA.  
DE Human lymphocyte cell surface antigen CD2 polypeptide.  
PN US6218525-B1.  
PD 17-APR-2001.  
PA (GHEO) GEN HOSPITAL CORP.  
Query Match 7.5%; Score 133.5; DB 4; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1442  
ID ADD25530 standard; protein; 351 AA.  
DE Binding domain-immunoglobulin fusion protein-associated protein #42.  
PN US200318592-A1.  
PD 26-JUN-2003.  
PA (GENE)- GENECRAFT INC.  
Query Match 7.5%; Score 133.5; DB 7; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1443  
ID ADF76723 standard; protein; 351 AA.  
DE Novel human secreted and transmembrane protein Segid 398.  
PN WO2003072035-A2.  
PD 04-SEP-2003.  
PA (GHEH) GENENTECH INC.  
Query Match 7.5%; Score 133.5; DB 7; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1444  
ID ADO49339 standard; protein; 351 AA.  
DE Human CD2 antigen.  
PN US2004072283-A1.  
PD 15-APR-2004.  
PA (SEED)/ SEED B.  
PA (ALIE)/ ALLEN J.  
PA (ARUF)/ ARUFFO A.  
PA (CAME)/ CAMERINI D.  
PA (LAUF)/ LAUFER L.  
PA (OOUJ)/ OOUENDO C.  
PA (STIM)/ STIMONS D.  
PA (STAM)/ STAMENKOVIC I.  
PA (STEN)/ STENGLIN S.  
PA (AMTO)/ AMTOT M.  
Query Match 7.5%; Score 133.5; DB 8; Length 351;

Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1445  
ID ADQ18464 standard; protein; 351 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1283.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT)- PROTEIN DESIGN LABS INC.  
Query Match 7.5%; Score 133.5; DB 8; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1446  
ID ADP56034 standard; protein; 351 AA.  
DE Human PRO protein sequence SEQ ID NO:2010.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GHEH) GENENTECH INC.  
Query Match 7.5%; Score 133.5; DB 8; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1447  
ID ADY19602 standard; protein; 351 AA.  
DE PRO polypeptide SEQ ID NO 5408.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GHEH) GENENTECH INC.  
Query Match 7.5%; Score 133.5; DB 9; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1448  
ID ADY15634 standard; protein; 351 AA.  
DE PRO polypeptide SEQ ID NO 1440.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GHEH) GENENTECH INC.  
Query Match 7.5%; Score 133.5; DB 9; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00085;  
RESULT 1449  
ID AAP1178 standard; protein; 360 AA.  
DE Sequence of human T11 sheep erythrocyte glycoprotein (T11) cDNA deduced from FBI.  
PN EP260880-A.  
PD 23-MAR-1988.  
PA (DAND) DANA FARBER CANCER INST INC.  
Query Match 7.5%; Score 133.5; DB 1; Length 360;  
Best Local Similarity 23.9%; Pred. No. 0.00088;  
RESULT 1450  
ID AAB4368 standard; protein; 737 AA.  
DE Human cancer associated protein sequence SEQ ID NO:1133.  
PN WO20005350-A1.  
PD 21-SEP-2000.  
PA (HUMA)- HUMAN GENOME SCI INC.  
Query Match 7.5%; Score 133.5; DB 3; Length 737;  
Best Local Similarity 22.3%; Pred. No. 0.0025;  
RESULT 1451  
ID ABU04810 standard; protein; 737 AA.  
DE Human expressed protein tag (EPT) #1476.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCO INC.  
Query Match 7.5%; Score 133.5; DB 6; Length 737;  
Best Local Similarity 22.3%; Pred. No. 0.0025;  
RESULT 1452  
ID AAR28366 standard; protein; 225 AA.  
DE Sheep LFA-3 protein.  
PN EP517174-A2.  
PD 09-DEC-1992.  
PA (KANP) KANEGAFUCHI KAGAKU KOGYO KK.  
Query Match 7.4%; Score 131; DB 2; Length 225;  
Best Local Similarity 25.0%; Pred. No. 0.00077;  
RESULT 1453  
ID AAR43473 standard; protein; 351 AA.  
DE Sequence encoded by a naturally occurring human CD2.  
PN WO9306866-A2.  
PD 15-APR-1993.  
PA (BIOC) BIOGEN INC.  
Query Match 7.4%; Score 130.5; DB 2; Length 351;



Best Local Similarity 23.2%; Pred. No. 0.0017;  
RESULT 1454  
ID AAR54714 standard; protein; 526 AA.  
DE Carcinoembryonic antigen CEA-(c).  
PN US5274087-A.  
PD 28-DEC-1993.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match  
Best Local Similarity 7.4%; Score 130.5; DB 2; Length 526;  
RESULT 1455  
ID AAR60314 standard; protein; 225 AA.  
DE Sheep LFA-3.  
PN JP06157334-A.  
PD 03-JUN-1994.  
PA (KAMF) KAMBUCHI KAGAKU KOGYO KK.  
Query Match  
Best Local Similarity 7.2%; Score 128; DB 2; Length 225;  
RESULT 1456  
ID AAR06434 standard; protein; 321 AA.  
DE SPI-like protein encoded by clone h1s1.  
PN WO9007937-A.  
PD 26-JUL-1990.  
PA (OKLA-) OKLAHOMA MED RES FO.  
Query Match  
Best Local Similarity 7.2%; Score 128; DB 2; Length 321;  
RESULT 1457  
ID ABU05236 standard; protein; 321 AA.  
DE Human expressed protein tag (EPT) #1902.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 7.2%; Score 128; DB 6; Length 321;  
RESULT 1458  
ID AAY43139 standard; protein; 451 AA.  
DE NAIL-Fc protein sequence.  
PN WO9950297-A1.  
PD 07-OCT-1999.  
PA (IMMV) IMMUNEX CORP.  
Query Match  
Best Local Similarity 7.2%; Score 128; DB 2; Length 451;  
RESULT 1459  
ID ADE08687 standard; protein; 697 AA.  
DE Novel protein (useful for identifying genetic disorders) #842.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 7.2%; Score 128; DB 7; Length 697;  
RESULT 1460  
ID AAU74427 standard; protein; 240 AA.  
DE Mouse protein sequence #4, related to isolation of genes within SLF-1B.  
PN WO200188200-A2.  
PD 22-NOV-2001.  
PA (TEXA) UNIV TEXAS SYSTEM.  
Query Match  
Best Local Similarity 7.1%; Score 126.5; DB 5; Length 240;  
RESULT 1461  
ID AAY43140 standard; protein; 243 AA.  
DE NAIL-Flag-polyHis protein sequence.  
PN WO9950297-A1.  
PD 07-OCT-1999.  
PA (IMMV) IMMUNEX CORP.  
Query Match  
Best Local Similarity 7.1%; Score 126.5; DB 2; Length 243;  
RESULT 1462  
ID AAY43141 standard; protein; 272 AA.  
DE NAIL-12-polyHis protein sequence.  
PN WO9950297-A1.  
PD 07-OCT-1999.  
PA (IMMV) IMMUNEX CORP.  
Query Match  
Best Local Similarity 7.1%; Score 126.5; DB 2; Length 272;  
Best Local Similarity 23.8%; Pred. No. 0.0028;

RESULT 1463  
ID AAB71855 standard; protein; 427 AA.  
DE Human D-SLAM extracellular domain carrying C-terminal HIS tag.  
PN WO20011046-A1.  
PD 15-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.1%; Score 126; DB 4; Length 427;  
RESULT 1464  
ID ABG32414 standard; protein; 427 AA.  
DE D-SLAM protein with C-terminal His tag.  
PN WO200262955-A2.  
PD 15-AUG-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.1%; Score 126; DB 5; Length 427;  
RESULT 1465  
ID AAM82480 standard; protein; 856 AA.  
DE Mammalian ZAP-70 protein #1.  
PN JP10313868-A.  
PD 02-DEC-1998.  
PA (KAGA-) KAGAKU GIYUTSU SHINKO JIGYODAN.  
Query Match  
Best Local Similarity 7.1%; Score 126; DB 2; Length 856;  
RESULT 1466  
ID AAR22045 standard; protein; 321 AA.  
DE Carcino embryonic antigen-related antigen encoded by clone W233.  
PN JP04045788-A.  
PD 14-FEB-1992.  
PA (SUNR) SUNTORY LTD.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 2; Length 321;  
RESULT 1467  
ID ABU04836 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1502.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 6; Length 344;  
RESULT 1468  
ID ABU04804 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1470.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 6; Length 344;  
RESULT 1469  
ID ABU04839 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1505.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 6; Length 344;  
RESULT 1470  
ID AEC04936 standard; protein; 344 AA.  
DE Human breast cancer marker protein SBQ ID NO 13 variant.  
PN WO2005072050-A2.  
PD 11-AUG-2005.  
PA (COMP-) COMPUEN USA INC.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 9; Length 344;  
RESULT 1471  
ID AAR22318 standard; protein; 351 AA.  
DE Carcino embryonic antigen-related antigen encoded by clone W239.  
PN JP04045788-A.  
PD 14-FEB-1992.  
PA (SUNR) SUNTORY LTD.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 2; Length 351;  
RESULT 1472  
Best Local Similarity 25.1%; Pred. No. 0.0051;



ID AAP93996 standard; protein; 368 AA.  
DE Transmembrane-4 carcinoembryonic antigen amino acid sequence.  
PN EP346710-A.  
PD 20-DEC-1989.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match 7.1%; Score 125.5; DB 1; Length 368;  
Best Local Similarity 25.1%; Pred. No. 0.0054;  
RESULT 1473  
ID AAP2044 standard; protein; 417 AA.  
DE Carcino embryonic antigen-related antigen encoded by clone W211.  
PN JP04045788-A.  
PD 14-FEB-1992.  
PA (SUNR) SUNTORY LTD.  
Query Match 7.1%; Score 125.5; DB 2; Length 417;  
Best Local Similarity 25.1%; Pred. No. 0.0065;  
RESULT 1474  
ID AAP93994 standard; protein; 430 AA.  
DE Sequence of transmembrane (TM)-2 carcinoembryonic antigen (CEA) - (c).  
PN EP346710-A.  
PD 20-DEC-1989.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match 7.1%; Score 125.5; DB 1; Length 430;  
Best Local Similarity 25.1%; Pred. No. 0.0068;  
RESULT 1475  
ID AEA23827 standard; protein; 430 AA.  
DE Human PRO polypeptide SEQ ID NO 369.  
PN WO2005051988-A2.  
PD 09-JUN-2005.  
PA (GENH) GENENTECH INC.  
Query Match 7.1%; Score 125.5; DB 9; Length 430;  
Best Local Similarity 25.1%; Pred. No. 0.0069;  
RESULT 1476  
ID AAP93995 standard; protein; 464 AA.  
DE Transmembrane-3 carcinoembryonic antigen amino acid sequence.  
PN EP346710-A.  
PD 20-DEC-1989.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match 7.1%; Score 125.5; DB 1; Length 464;  
Best Local Similarity 25.1%; Pred. No. 0.0076;  
RESULT 1477  
ID AAR65166 standard; protein; 464 AA.  
DE Biliary glycoprotein.  
PN WO9506067-A1.  
PD 02-MAR-1995.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.  
Query Match 7.1%; Score 125.5; DB 2; Length 464;  
Best Local Similarity 25.1%; Pred. No. 0.0076;  
RESULT 1478  
ID AAR77436 standard; protein; 468 AA.  
DE BGP (1-314)/CEA (490-643) chimeric protein.  
PN WO9506067-A1.  
PD 02-MAR-1995.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.  
Query Match 7.1%; Score 125.5; DB 2; Length 468;  
Best Local Similarity 25.1%; Pred. No. 0.0077;  
RESULT 1479  
ID AAR77435 standard; protein; 493 AA.  
DE BGP (1-314)/CEA (490-C-terminal) chimeric protein.  
PN WO9506067-A1.  
PD 02-MAR-1995.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.  
Query Match 7.1%; Score 125.5; DB 2; Length 493;  
Best Local Similarity 25.1%; Pred. No. 0.0083;  
RESULT 1480  
ID AAR77437 standard; protein; 509 AA.  
DE BGP (1-314)/CEA (490-644)/BGP (391-430) chimeric protein.  
PN WO9506067-A1.  
PD 02-MAR-1995.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.  
Query Match 7.1%; Score 125.5; DB 2; Length 509;  
Best Local Similarity 25.1%; Pred. No. 0.0087;  
RESULT 1481  
ID AAR77438 standard; protein; 511 AA.

DE BGP (1-314)/CEA (490-642)/BGP (387-430) chimeric protein.  
PN WO9506067-A1.  
PD 02-MAR-1995.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.  
Query Match 7.1%; Score 125.5; DB 2; Length 511;  
Best Local Similarity 25.1%; Pred. No. 0.0088;  
RESULT 1482  
ID AAP81223 standard; protein; 526 AA.  
DE FL-CEA or carcinoembryonic antigen-C.  
PN EP263933-A.  
PD 20-APR-1988.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match 7.1%; Score 125.5; DB 1; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0091;  
RESULT 1483  
ID AAM06873 standard; protein; 526 AA.  
DE Carcinoembryonic antigen CEA-C.  
PN US5571710-A.  
PD 05-NOV-1996.  
PA (FARB) BAYER CORP.  
Query Match 7.1%; Score 125.5; DB 2; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0091;  
RESULT 1484  
ID AAW83138 standard; protein; 526 AA.  
DE FL-CEA protein.  
PN US5843761-A.  
PD 01-DEC-1998.  
PA (FARB) BAYER CORP FORMERLY MOLECULAR DIAGNOSTIC.  
Query Match 7.1%; Score 125.5; DB 2; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0091;  
RESULT 1485  
ID ADL15001 standard; protein; 526 AA.  
DE Human carcinoembryonic antigen BGPa protein for cancer treatment.  
PN WO2003068268-A2.  
PD 21-AUG-2003.  
PA (BIOI) BIOINVENT INT AB.  
Query Match 7.1%; Score 125.5; DB 7; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0091;  
RESULT 1486  
ID ADN95238 standard; protein; 526 AA.  
DE Human BGC/DEC-related protein sequence SeqID160.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDM-) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
Query Match 7.1%; Score 125.5; DB 7; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0091;  
RESULT 1487  
ID ADQ17310 standard; protein; 526 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 127.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 7.1%; Score 125.5; DB 8; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0091;  
RESULT 1488  
ID ADQ17232 standard; protein; 526 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 48.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 7.1%; Score 125.5; DB 8; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0091;  
RESULT 1489  
ID ADQ29706 standard; protein; 526 AA.  
DE Human colorectal cancer-associated protein #61.  
PN EP1439393-A2.  
PD 21-JUN-2004.  
PA (FARB) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 7.1%; Score 125.5; DB 8; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0091;  
RESULT 1490



ID AD67261 standard; protein; 526 AA.  
DE Human bladder cancer associated amino acid sequence.  
PN WO2004076613-A2.  
PD 10-SEP-2004.  
PA (HERR/) HERR A.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (STAU/) STAU B.  
PA (PILA/) PILARSKY C.  
PA (SPEC/) SPEC T.  
Query Match 7.1%; Score 125.5; DB 8; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0091;  
RESULT 1491  
ID AEA04517 standard; protein; 526 AA.  
DE Human protein from gene under-expressed in cancer, CEACAM1.  
PN WO2005044990-A2.  
PD 19-MAY-2005.  
PA (FAR) BAYER HEALTHCARE LLC.  
PA (MAYO) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 7.1%; Score 125.5; DB 9; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0091;  
RESULT 1492  
ID AEB08040 standard; protein; 526 AA.  
DE Human CEACAM1 protein, SEQ ID NO: 2.  
PD 30-JUN-2005.  
PA (UTKU/) UTKU N.  
Query Match 7.1%; Score 125.5; DB 9; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0091;  
RESULT 1493  
ID ABJ7104 standard; protein; 437 AA.  
DE Concatameric immunoadhesion human protein sequence SEQ ID NO 14.  
PN WO2003010202-A1.  
PD 06-FEB-2003.  
PA (MEDE-) MEDEXGEN CO LTD.  
Query Match 7.1%; Score 125; DB 6; Length 437;  
Best Local Similarity 23.5%; Pred. No. 0.0078;  
RESULT 1494  
ID ADQ79912 standard; protein; 437 AA.  
DE Human CD2/Ig construct.  
PN KR2004009997-A.  
PD 31-JAN-2004.  
PA (MEDE-) MEDEXGEN INC.  
Query Match 7.1%; Score 125; DB 8; Length 437;  
Best Local Similarity 23.5%; Pred. No. 0.0078;  
RESULT 1495  
ID ABJ7106 standard; protein; 617 AA.  
DE Concatameric immunoadhesion human protein sequence SEQ ID NO 18.  
PN WO2003010202-A1.  
PD 06-FEB-2003.  
PA (MEDE-) MEDEXGEN CO LTD.  
Query Match 7.1%; Score 125; DB 6; Length 617;  
Best Local Similarity 23.5%; Pred. No. 0.013;  
RESULT 1496  
ID ABJ7108 standard; protein; 617 AA.  
DE Concatameric immunoadhesion human protein sequence SEQ ID NO 22.  
PN WO2003010202-A1.  
PD 06-FEB-2003.  
PA (MEDE-) MEDEXGEN CO LTD.  
Query Match 7.1%; Score 125; DB 6; Length 617;  
Best Local Similarity 23.5%; Pred. No. 0.013;  
RESULT 1497  
ID ADQ7916 standard; protein; 617 AA.  
DE Human CD2-CD2/Ig construct.  
PN KR2004009997-A.  
PD 31-JAN-2004.  
PA (MEDE-) MEDEXGEN INC.  
Query Match 7.1%; Score 125; DB 8; Length 617;  
Best Local Similarity 23.5%; Pred. No. 0.013;  
RESULT 1498  
ID ADQ79920 standard; protein; 617 AA.  
DE Human mgCD2-CD2/Ig construct.  
PN KR2004009997-A.

PD 31-JAN-2004.  
PA (MEDE-) MEDEXGEN INC.  
Query Match 7.1%; Score 125; DB 8; Length 617;  
Best Local Similarity 23.5%; Pred. No. 0.013;  
RESULT 1499  
ID ADP14932 standard; protein; 820 AA.  
DE Human albumin therapeutic fusion protein Seqid228.  
PN WO2003060071-A2.  
PD 24-JUL-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (DELZ) DELTA BIOTECHNOLOGY LTD.  
PA (PRIN-) PRINCIPIA PHARM CORP.  
Query Match 7.1%; Score 125; DB 7; Length 820;  
Best Local Similarity 25.1%; Pred. No. 0.02;  
RESULT 1500  
ID AEC03856 standard; protein; 344 AA.  
DE Human breast cancer marker protein SEQ ID NO 13.  
PN WO2005072050-A2.  
PD 11-AUG-2005.  
PA (COMP-) COMPUTEN USA INC.  
Query Match 7.0%; Score 124.5; DB 9; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0061;



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OM protein - protein search, using sw model

Run on: December 16, 2005, 10:34:37 ; Search time 39 Seconds

(without alignments)  
826,477 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 1772

Sequence: 1 MAGSPCTCLTYIIMQLTGS.....PHSLITMPDTRLPAYENVVI 335

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	343	19.4	629	2 A46500	Ly-9.2 antigen - m
2	182.5	10.3	335	2 S58892	signaling lymphocy
3	144	8.1	344	2 B28967	T-cell surface gly
4	138	7.8	344	2 I49585	CD2 antigen protei
5	136.5	7.7	351	1 RWHUC2	T-cell surface gly
6	134	7.6	240	2 S01299	OX-45 membrane gly
7	130	7.3	344	1 RWHUC2	T-cell surface gly
8	126.5	7.1	240	2 J10143	antigen BCM1 precu
9	125.5	7.1	321	2 JH0395	biliary glycoprote
10	125.5	7.1	351	2 JH0396	biliary glycoprote
11	125.5	7.1	417	2 JH0394	biliary glycoprote
12	125.5	7.1	464	2 C30127	transmembrane carc
13	125.5	7.1	526	1 A32164	biliary glycoprote
14	124.5	7.0	344	2 A27681	nonspecific cross-
15	122.5	6.9	521	2 S34338	biliary glycoprote
16	119	6.5	458	2 JCI509	carcinoembryonic a
17	114.5	6.5	702	2 A36319	biliary glycoprote
18	113.5	6.4	458	1 WMM5R1	biliary glycoprote
19	113.5	6.4	521	2 JCI508	biliary glycoprote
20	109.5	6.2	432	2 S30193	T-cell surface gly
21	108.5	6.1	365	2 JCI780	coxsackie- and ade
22	107.5	6.1	398	2 I49443	gene 2B4 protein -
23	106	6.0	897	2 G84613	hypothetical prote
24	105.5	6.0	329	1 A48754	B7-2 antigen - hum
25	104	5.9	349	2 A34815	carcinoembryonic a
26	102.5	5.8	458	2 S23969	cell-adhesion mole
27	102.5	5.8	526	2 A37821	butyrophilin - bov
28	101.5	5.7	761	2 T00940	hypothetical prote
29	101	5.7	587	2 JH0464	DM-GRASP precursor

30	101	5.7	588	2 JH0506	adhesion molecule
31	100.5	5.6	259	2 A86822	hypothetical prote
32	100	5.6	392	2 B44194	poliovirus recepto
33	99	5.6	417	2 A44194	poliovirus recepto
34	99	5.6	588	2 A45254	surface glycoprote
35	98.5	5.6	1227	2 T23004	hypothetical prote
36	98	5.5	347	2 S41638	T-cell surface gly
37	98	5.5	503	2 UC5287	SHP substrate-1 pr
38	97	5.5	523	2 I50478	neuroilin - goldfis
39	97	5.5	773	1 QRRBG	secretory componen
40	96.5	5.4	402	2 A40678	T-cell adhesion re
41	96	5.4	210	2 S36297	T-cell receptor ga
42	96	5.4	526	2 S70587	butyrophilin precu
43	96	5.4	1087	2 I51552	platelet-derived g
44	96	5.4	1451	2 S42167	190K protein - hum
45	95.5	5.4	341	2 JCI512	biliary glycoprote
46	95.5	5.4	417	1 RWHUPA	poliovirus recepto
47	95.5	5.4	458	2 S68177	C-CAM2a protein is
48	95.5	5.4	519	2 A44783	ecto-ATPase precu
49	95.5	5.4	700	1 S12053	protein-tyrosine-p
50	94.5	5.3	218	2 A36198	T-cell receptor be
51	94	5.3	233	2 JH0372	42K surface glycop
52	94	5.3	1088	1 IJXLNL	neural cell adhesi
53	93.5	5.3	2409	1 A60979	versican precursor
54	93	5.2	419	2 B54312	pregnancy-specific
55	93	5.2	419	2 A36109	pregnancy-specific
56	93	5.2	419	2 UC4123	pregnancy-specific
57	92.5	5.2	299	2 S56749	pregnancy-specific
58	92.5	5.2	330	2 I46691	junctional adhesio
59	92.5	5.2	761	2 A96810	CD86 precursor - r
60	92	5.2	822	2 T01095	probable Mutator-1
61	91.5	5.2	1079	2 T28197	hypothetical prote
62	91	5.1	417	2 A28277	probable DNA-direc
63	91	5.1	419	2 A33258	pregnancy-specific
64	91	5.1	426	2 B33258	pregnancy-specific
65	91	5.1	467	1 HLMSP3	poliovirus recepto
66	90	5.1	250	2 A28564	lymphocyte functio
67	90	5.1	395	2 D43354	pregnancy-specific
68	90	5.1	397	2 C43354	pregnancy-specific
69	90	5.1	406	2 B43354	pregnancy-specific
70	90	5.1	419	2 A31135	pregnancy-specific
71	90	5.1	426	2 A35964	pregnancy-specific
72	90	5.1	426	2 A35341	pregnancy-specific
73	90	5.1	428	2 A27658	pregnancy-specific
74	89.5	5.1	243	2 A53244	leukocyte antigen
75	89.5	5.1	349	2 B84968	outer membrane pro
76	89.5	5.1	428	2 T36555	probable penicilli
77	89	5.0	309	2 I49522	gene B7-2 protein
78	89	5.0	341	2 JCI511	biliary glycoprote
79	89	5.0	821	2 C1H0H3	calpain (EC 3.4.22
80	89	5.0	5175	1 T20992	hypothetical prote
81	89	5.0	5198	2 T43290	hemikentn precurs
82	88.5	5.0	1390	1 T7H0M6	hepatocyte growth
83	88	5.0	363	2 F70195	UDP-N-acetylglucos
84	88	5.0	422	2 A71147	hypothetical prote
85	88	5.0	530	2 A53437	poliovirus recepto
86	88	5.0	668	2 S56909	polymyxin B resist
87	88	5.0	699	2 UC6132	protein-tyrosine-p
88	88	5.0	821	1 B34488	calpain (EC 3.4.22
89	88	5.0	1092	1 JN0635	neural cell adhesi
90	88	5.0	6669	2 S55024	nebulin, skeletal
91	87.5	4.9	265	2 A55811	carcinoembryonic a
92	87.5	4.9	276	2 S20660	31.6K hypothetical
93	87.5	4.9	392	1 RWHUPD	poliovirus recepto
94	87.5	4.9	769	1 QRRBS	secretory componen
95	87.5	4.9	2340	2 I48310	kinase-related pro
96	87.5	4.9	4162	2 T42633	connectin/titin -
97	87	4.9	457	1 RWM5T4	T-cell surface gly
98	87	4.9	583	2 I39428	alcam - human
99	87	4.9	1666	2 A48594	skelentin - mouse
100	87	4.9	1907	2 S50893	protein-tyrosine-p
101	87	4.9	3707	2 S18252	heparan sulfate pr
102	86.5	4.9	528	2 B75364	extracellular solu



103	86	4.9	212	2	C33258	pregnancy-specific
104	86	4.9	354	1	VCBB67	glycoprotein D pre
105	86	4.9	428	2	I57486	pregnancy-specific
106	86	4.9	885	2	B86257	NBS/LRR disease re
107	86	4.9	1327	2	T09402	immunoglobulin-lik
108	85.5	4.8	324	2	G43354	pregnancy-specific
109	85.5	4.8	326	2	F43354	pregnancy-specific
110	85.5	4.8	333	2	A43354	pregnancy-specific
111	85.5	4.8	335	2	H43354	pregnancy-specific
112	85.5	4.8	941	1	TVMVMD	protein-tyrosine k
113	85.5	4.8	2588	2	T14342	NS1 protein - mou
114	85	4.8	428	2	JS0032	pregnancy-specific
115	85	4.8	731	2	T16524	hypothetical prote
116	85	4.8	757	1	S48841	secretory componen
117	84.5	4.8	656	2	A96724	hypothetical prote
118	84	4.7	275	2	UC7604	CD86 spliced varia
119	84	4.7	851	2	D90216	hypothetical prote
120	84	4.7	1379	1	S01254	hepatocyte growth
121	84	4.7	1499	2	I50212	protein-tyrosine-p
122	84	4.7	3034	2	T14119	seven-pass transme
123	83.5	4.7	315	2	H71009	probable prolifera
124	83.5	4.7	392	2	T33444	hypothetical prote
125	83.5	4.7	656	2	B49423	semaphorin I - fru
126	83.5	4.7	775	2	T21436	hypothetical prote
127	83.5	4.7	1501	2	I58148	protein-tyrosine-p
128	83.5	4.7	1863	2	S46217	pregnancy-specific
129	83	4.7	335	2	A33514	pregnancy-specific
130	83	4.7	757	2	I45956	polymeric immunogl
131	83	4.7	873	1	A49729	VDL receptor prec
132	83	4.7	925	2	T37475	lipoprotein recept
133	83	4.7	1106	2	T29496	hypothetical prote
134	83	4.7	2489	2	S59782	probable membrane
135	82.5	4.7	393	2	B96780	hypothetical prote
136	82.5	4.7	826	2	B36203	iron-responsive el
137	82.5	4.7	1004	2	A71617	SSEA antigen/papai
138	82.5	4.7	2692	1	T18344	ritin, cardiac mus
139	82	4.6	386	2	B69666	Na+ ABC transporte
140	82	4.6	609	2	S43009	hemagglutinin - ri
141	82	4.6	880	2	B53743	protein-tyrosine k
142	82	4.6	3562	2	A47171	chondroitin sulfat
143	82	4.6	278	1	TDRTOX	OX-2 membrane glyc
144	81.5	4.6	352	2	T77374	pregnancy-specific
145	81.5	4.6	355	2	T06122	cysteine proteinas
146	81.5	4.6	378	2	S00842	leukostallin precu
147	81.5	4.6	497	2	D97264	galactose-1-phosph
148	81.5	4.6	524	2	S44982	flagellin - Shigel
149	81.5	4.6	708	2	T48022	hypothetical prote
150	81	4.6	335	2	B33251	nonspecific cross-
151	81	4.6	338	2	UC4776	limbic-system-asso
152	81	4.6	374	2	S57750	naringenin 3-dioxy
153	81	4.6	760	2	S19374	probable membrane
154	81	4.6	769	2	B97092	glycosyltransferas
155	81	4.6	829	1	IYHUCP	cadherin 3 precurs
156	81	4.6	1898	2	S46216	leukocyte antigen-
157	81	4.6	1941	2	T30554	ubiquitin-protein
158	80.5	4.5	346	2	S46993	elk ligand - human
159	80.5	4.5	376	2	B85435	cysteine proteinas
160	80.5	4.5	462	2	H97292	UDP-N-acetylmuramo
161	80.5	4.5	473	2	AG0612	probable transport
162	80.5	4.5	475	2	I76668	pregnancy-specific
163	80.5	4.5	540	2	B64829	membrane protein b
164	80.5	4.5	540	2	H90751	probable transport
165	80.5	4.5	540	2	P85615	probable transport
166	80.5	4.5	721	2	T09631	probable acylamino
167	80.5	4.5	823	2	T08092	plus fringe glycop
168	80.5	4.5	823	2	S44887	ZK112.7 protein -
169	80.5	4.5	6642	1	T29757	protein UNC-89 - C
170	80	4.5	307	1	RWMSBC	T-cell receptor as
171	80	4.5	341	2	I61725	natural killer as
172	80	4.5	341	2	G90680	probable periplasm
173	80	4.5	343	2	C85531	periplasmic ferric
174	80	4.5	454	2	A46532	Ig mu chain C regi
175	80	4.5	482	2	JH0110	arginine/ornithine
176	80	4.5	1040	2	A49356	transient axonal g
177	80	4.5	1170	2	A40558	thrombospondin 1 p
178	79.5	4.5	134	2	I46627	rearranged T-cell
179	79.5	4.5	244	2	UC8019	CD58 protein - pig
180	79.5	4.5	249	1	A61087	myelin po glycopro
181	79.5	4.5	273	2	B28928	pregnancy-specific
182	79.5	4.5	275	2	A28928	pregnancy-specific
183	79.5	4.5	282	2	C28928	pregnancy-specific
184	79.5	4.5	289	2	G90314	cytochrome proteinas
185	79.5	4.5	328	2	Q01121	oxidoreductase (im
186	79.5	4.5	400	2	A10104	probable galactosi
187	79.5	4.5	430	2	T28143	tapasin 1 homolog,
188	79.5	4.5	446	2	T34782	probable signal pe
189	79.5	4.5	490	2	I41293	EcO5 type I restrit
190	79.5	4.5	769	2	S16236	fibroblast growth
191	79.5	4.5	822	2	A45081	fibroblast growth
192	79.5	4.5	822	2	A41794	keratinocyte growt
193	79.5	4.5	873	1	I48952	VDL receptor prec
194	79.5	4.5	980	1	TYCTMD	macrophage colony-
195	79.5	4.5	1465	2	S43529	16Sk protein, skel
196	79.5	4.5	2491	1	A28372	insulin-like growt
197	79	4.5	210	2	C87256	hypothetical prote
198	79	4.5	244	2	AC1765	B. subtilis TagA p
199	79	4.5	438	2	G64513	hypothetical prote
200	79	4.5	479	2	C84039	carboxy-terminal p
201	79	4.5	584	2	T08678	hypothetical prote
202	79	4.5	657	2	S77543	short-chain alcoho
203	79	4.5	903	2	T20804	hypothetical prote
204	79	4.5	1228	2	G96751	hypothetical prote
205	79	4.5	1361	2	T30984	neural specific DN
206	78.5	4.4	235	2	S25750	Ig lambda chain -
207	78.5	4.4	429	1	BHRT	Ig epsilon chain C
208	78.5	4.4	497	2	C91225	probable oxidoredu
209	78.5	4.4	497	2	A86072	probable oxidoredu
210	78.5	4.4	539	2	T01513	Cmp synthase (EC 6
211	78.5	4.4	588	2	I37202	B-CAM protein - hu
212	78.5	4.4	628	2	I38000	Lutheran blood gro
213	78.5	4.4	638	2	T51383	receptor protein k
214	78.5	4.4	831	2	S39835	hypothetical prote
215	78.5	4.4	847	2	JH0371	B-cell adhesion pr
216	78.5	4.4	1036	2	S22383	axomin 1 precursor
217	78.5	4.4	1038	2	AG2187	hypothetical prote
218	78.5	4.4	1468	2	T05672	hypothetical prote
219	78	4.4	257	2	A97121	undecaprenyl pyrop
220	78	4.4	282	2	I48268	bilialy glycoprote
221	78	4.4	286	2	A28333	carcinoembryonic a
222	78	4.4	335	2	C54312	pregnancy-specific
223	78	4.4	402	2	T09062	probable advanced
224	78	4.4	490	2	T43184	DEAD box ATP-depen
225	78	4.4	604	2	T41249	DEAD box ATP-depen
226	78	4.4	608	2	AB3562	gfp-binding protei
227	78	4.4	608	2	AB3562	hemagglutinin - ri
228	78	4.4	609	1	HMNZKA	neural cell adhesi
229	78	4.4	836	1	IYHUNG	hypothetical prote
230	78	4.4	836	1	T42323	cadherin - African
231	78	4.4	905	2	S43064	probable vacuolar
232	77.5	4.4	172	2	T34227	hypothetical prote
233	77.5	4.4	214	2	C89833	hypothetical prote
234	77.5	4.4	236	2	T41012	conserved hypotnet
235	77.5	4.4	239	2	I46082	C08 alpha-chain -
236	77.5	4.4	448	2	H98007	exodeoxyribonuclea
237	77.5	4.4	509	2	UC5288	SHP substrate-1 pr
238	77.5	4.4	513	2	UC5289	SHP substrate-1 pr
239	77.5	4.4	539	2	G86465	flutG12.2 protein -
240	77.5	4.4	591	2	H83362	glucuronate dehydrog
241	77.5	4.4	717	2	AD3037	ferrienterobactin-
242	77.5	4.4	717	2	B98189	ferrienterobactin-
243	77.5	4.4	739	2	A41288	vascular cell adhe
244	77.5	4.4	757	1	S64742	dynamin-related pr
245	77.5	4.4	863	2	S06017	neuraxin - rat
246	77.5	4.4	881	2	S03068	eny protein - huma
247	77.5	4.4	968	2	T25667	hypothetical prote
248	77.5	4.4	991	2	T48631	polynucleotide pho



249	77.5	4.4	1015	2	T32186	hypothetical prote
250	77.5	4.4	1099	2	T18713	hypothetical prote
251	77.5	4.4	1205	2	T13959	limeless protein r
252	77.5	4.4	1262	1	B48758	protein-tyrosine-p
253	77.5	4.4	1496	1	A48758	protein-tyrosine-p
254	77.5	4.4	1894	2	C54689	protein-tyrosine-p
255	77.5	4.4	1892	2	A56178	protein-tyrosine-p
256	77.5	4.4	1950	2	S12332	ubiquitin-protein
257	77	4.3	327	2	S06611	Ig gamma-2 chain c
258	77	4.3	328	2	I47158	Ig gamma 1 chain c
259	77	4.3	338	2	JCS519	50K glycoprotein p
260	77	4.3	398	2	B86353	protein P2B2.6 (im
261	77	4.3	439	2	S51378	probable membrane
262	77	4.3	491	2	JE0276	voltage-gated pota
263	77	4.3	502	2	S61935	SKS1 protein - yea
264	77	4.3	523	2	T05946	cytochrome P450 78
265	77	4.3	796	2	JC7966	xylian 1,4-beta-xy1
266	77	4.3	873	1	ORRBD	VLDL receptor prec
267	77	4.3	1021	2	I39207	leukocyte surface
268	77	4.3	1029	2	D83120	probable RND efflu
269	77	4.3	1041	2	S55862	probable membrane
270	77	4.3	1897	1	TDHULK	leukocyte antigen-
271	77	4.3	2167	2	AP1489	cell wall-associat
272	77	4.3	4836	2	T14346	herc2 protein - mo
273	76.5	4.3	177	1	C40428	non-specific cross-
274	76.5	4.3	191	2	E75132	molybdopterin-guan
275	76.5	4.3	238	2	T24314	hypothetical prote
276	76.5	4.3	251	2	S75312	hypothetical prote
277	76.5	4.3	296	2	G82131	conserved hypothet
278	76.5	4.3	390	2	D86291	hypothetical prote
279	76.5	4.3	394	2	S20905	hypothetical prote
280	76.5	4.3	402	2	A54312	pregnancy-specific
281	76.5	4.3	423	2	AB1142	N-carbamyl-L-amino
282	76.5	4.3	426	2	C55181	pregnancy-specific
283	76.5	4.3	426	2	S09016	pregnancy-specific
284	76.5	4.3	426	2	B35334	pregnancy-specific
285	76.5	4.3	436	2	B55181	pregnancy-specific
286	76.5	4.3	495	2	A55181	pregnancy-specific
287	76.5	4.3	497	2	D65189	YicG protein - Bac
288	76.5	4.3	582	2	A71906	DNA polymerase III
289	76.5	4.3	727	2	T23585	hypothetical prote
290	76.5	4.3	788	2	S17906	hypothetical prote
291	76.5	4.3	839	2	B96538	hypothetical prote
292	76.5	4.3	876	2	D85350	hypothetical prote
293	76.5	4.3	876	2	S71277	serine/threonine-s
294	76.5	4.3	1005	2	T18537	Ig heavy chain - c
295	76.5	4.3	1043	2	T19734	hypothetical prote
296	76.5	4.3	1071	2	T18307	suppressor protein
297	76.5	4.3	1089	1	PFHUGA	platelet-derived g
298	76.5	4.3	1124	2	JX0293	zinc finger protei
299	76.5	4.3	1154	2	A56242	E-box-binding repr
300	76.5	4.3	1328	2	S62467	ATP-dependent DNA
301	76.5	4.3	1461	2	B70588	probable polyketid
302	76.5	4.3	1802	2	S69703	HK1 protein precu
303	76.5	4.3	2039	2	T15347	ankyrin-related un
304	76.5	4.3	138	2	S16199	phocovsytam I prot
305	76	4.3	144	2	AH1172	mannose-specific p
306	76	4.3	230	2	S49449	Ig lambda chain -
307	76	4.3	239	2	T23147	hypothetical prote
308	76	4.3	262	2	A64882	probable carboxype
309	76	4.3	262	2	H85751	probable carboxype
310	76	4.3	262	2	A99867	probable carboxype
311	76	4.3	286	2	B97010	prephenate dehydro
312	76	4.3	305	2	H69759	conserved hypothet
313	76	4.3	333	2	A31923	amalgam protein pr
314	76	4.3	378	2	I46268	brevian precursor
315	76	4.3	487	1	S55194	DNA-directed DNA p
316	76	4.3	507	2	T47021	hypothetical prote
317	76	4.3	508	2	AD0236	L-asparagine perme
318	76	4.3	550	2	G90497	hypothetical prote
319	76	4.3	758	2	T15577	hypothetical prote
320	76	4.3	841	2	T01011	hypothetical prote
321	76	4.3	964	2	T15746	hypothetical prote
322	76	4.3	978	2	S16385	macrophage colony-
323	76	4.3	1018	2	JC4211	neural adhesion pr
324	76	4.3	1093	2	T51503	valine-tRNA ligase
325	76	4.3	2029	1	TDFFLK	protein-tyrosine-p
326	75.5	4.3	246	2	A47712	myelin/oligodentro
327	75.5	4.3	326	2	JC4124	pregnancy-specific
328	75.5	4.3	419	2	S42989	T48 protein - frui
329	75.5	4.3	421	2	T40614	G beta repeat prot
330	75.5	4.3	432	2	T30130	hypothetical prote
331	75.5	4.3	446	2	A95140	exodeoxyribonuclea
332	75.5	4.3	462	2	A84689	chloroplast membra
333	75.5	4.3	485	2	T28076	hypothetical prote
334	75.5	4.3	819	2	T05744	hypothetical prote
335	75.5	4.3	933	2	S05944	neuronal cell surf
336	75.5	4.3	1020	2	S05944	aggrean precursor
337	75.5	4.3	2109	1	I50421	hypothetical prote
338	75	4.2	150	2	D95131	probable anthranil
339	75	4.2	208	2	D71529	probable beta-keto
340	75	4.2	466	2	D84906	glucose-6-phosphat
341	75	4.2	491	2	AC2650	glucose-6-phosphat
342	75	4.2	503	2	B97432	glutamate/asparat
343	75	4.2	543	2	S26609	Ig y heavy chain (
344	75	4.2	572	2	B46529	Ig mu chain precu
345	75	4.2	573	2	S12838	hypothetical prote
346	75	4.2	622	2	B96751	hypothetical prote
347	75	4.2	686	2	A55665	microtubule-associ
348	75	4.2	747	1	ORCFPE	ferrichrome-iron r
349	75	4.2	747	2	B85499	outer membrane rec
350	75	4.2	747	2	B90648	outer membrane rec
351	75	4.2	821	1	TYMSBK	fibroblast growth
352	75	4.2	976	1	TYMSKD	macrophage colony-
353	75	4.2	1091	1	IUCHNL	neutral cell adhesi
354	75	4.2	1256	2	T03096	CD0 protein - rat
355	75	4.2	1338	2	T02206	hypothetical prote
356	75	4.2	7962	2	I38346	elastic titin - hu
357	74.5	4.2	232	1	DXCH	ovalbumin-related
358	74.5	4.2	278	2	A39037	carcinoembryonic a
359	74.5	4.2	309	2	T31908	hypothetical prote
360	74.5	4.2	321	2	S10006	hypothetical prote
361	74.5	4.2	379	2	D91078	probable lipoprote
362	74.5	4.2	379	2	B85923	lipoprotein D prec
363	74.5	4.2	379	2	B55522	hypothetical prote
364	74.5	4.2	463	2	T14884	conserved hypothet
365	74.5	4.2	518	2	D69539	protein-tyrosine k
366	74.5	4.2	544	2	I51593	triacylglycerol li
367	74.5	4.2	688	2	A47705	fibroblast growth
368	74.5	4.2	705	2	S51635	probable transport
369	74.5	4.2	741	2	B90739	probable transport
370	74.5	4.2	741	2	H85589	irregular chiasm C
371	74.5	4.2	764	2	A49448	hypothetical prote
372	74.5	4.2	771	2	T34376	hypothetical prote
373	74.5	4.2	786	2	H64817	probable membrane
374	74.5	4.2	795	2	T20609	hypothetical prote
375	74.5	4.2	889	1	VCLJ05	env polyprotein -
376	74.5	4.2	984	2	T00326	hypothetical prote
377	74.5	4.2	1003	2	T19638	hypothetical prote
378	74.5	4.2	1007	2	PM0156	glutamate receptor
379	74.5	4.2	1008	2	S28858	glutamate receptor
380	74.5	4.2	1021	2	A57112	contactin precurs
381	74.5	4.2	1178	2	B87145	[beta] subunit of
382	74.5	4.2	1179	2	S31145	DNA-directed RNA p
383	74.5	4.2	1522	2	T00028	brain-specific ang
384	74.5	4.2	1723	2	S58880	receptor DEC-205 -
385	74.5	4.2	1896	2	T08851	Down syndrome cell
386	74.5	4.2	2256	2	AD1018	large repetitive p
387	74.5	4.2	2256	2	A56577	microtubule-associ
388	74.5	4.2	2364	2	A34416	hypothetical prote
389	74.5	4.2	2783	2	S36291	T-cell receptor ga
390	74	4.2	203	2	S01320	Ig kappa chain pre
391	74	4.2	278	2	JC1506	biliary glycoprote
392	74	4.2	333	2	B50018	Ig gamma-2b chain
393	74	4.2	334	2	T19637	hypothetical prote
394	74	4.2	349	2	S68092	protein-glutamine



395	74	4.2	384	2	H64161	hypothetical prote
396	74	4.2	403	2	I52590	m3-B isoform - mo
397	74	4.2	424	2	T43498	hypothetical prote
398	74	4.2	463	2	CG9997	probable prolina t
399	74	4.2	468	2	S70297	SP22 protein homol
400	74	4.2	502	2	T40792	hypothetical prote
401	74	4.2	548	2	M44302	protein-glutamine
402	74	4.2	586	2	T15259	hypothetical prote
403	74	4.2	611	2	F82442	kinase-binding pro
404	74	4.2	645	2	T39614	hypothetical prote
405	74	4.2	673	2	T48701	ErbB kinase activa
406	74	4.2	860	2	JC5702	differentiation an
407	74	4.2	862	2	T49583	probable receptor
408	74	4.2	876	2	B96693	probable disease r
409	74	4.2	900	2	B96617	calcium, zinc, cob
410	74	4.2	1063	2	A33830	hypothetical prote
411	74	4.2	1063	2	JC4700	hypothetical prote
412	74	4.2	1130	2	T23104	hypothetical prote
413	74	4.2	1133	2	T23103	chitin synthase (E
414	74	4.2	1165	1	S45879	probable RNA helic
415	74	4.2	1237	2	E86457	hypothetical prote
416	74	4.2	1367	2	T33819	hypothetical prote
417	74	4.2	1582	2	T15308	dysnein heavy chain
418	74	4.2	4344	1	A53489	HC-toxin synthetas
419	74	4.2	5232	2	M45086	protectin - fruit
420	74	4.2	6658	2	T13931	cysteine proteinas
421	74	4.1	325	2	S49451	myeloid cell surfa
422	73.5	4.1	364	2	A30521	dhidroocortase pyr
423	73.5	4.1	428	2	B83967	hypothetical prote
424	73.5	4.1	647	2	T33773	probable membrane
425	73.5	4.1	740	2	M06600	ErbB kinase activa
426	73.5	4.1	797	2	T27518	env polypeptide pr
427	73.5	4.1	880	1	VCLJ52	probable ligand-ga
428	73.5	4.1	923	2	F84732	glucan 1,4-beta-gl
429	73.5	4.1	925	2	D83888	type I restriction
430	73.5	4.1	957	2	CG9463	ubiquitin-tumor sup
431	73.5	4.1	1166	2	S37692	probable peptidogl
432	73.5	4.1	1225	2	T48251	CDO protein - huma
433	73.5	4.1	1240	2	T03097	probable peptidogl
434	73.5	4.1	2013	2	AD1129	variant-specific s
435	73.5	4.1	2301	1	GNNYTN	genome polypeptide
436	73.5	4.1	2301	1	GNNYTN	adherence factor T
437	73.5	4.1	3255	1	G81702	alpha-2-macroglobu
438	73.5	4.1	4544	1	S02392	hypothetical prote
439	73.5	4.1	4544	1	T34265	conserved hypothet
440	73	4.1	147	2	G69047	Ig lambda chain -
441	73	4.1	220	1	S14675	hypothetical prote
442	73	4.1	235	2	S37544	hypothetical prote
443	73	4.1	250	2	H96906	hypothetical prote
444	73	4.1	293	2	H84095	hypothetical prote
445	73	4.1	322	2	T27712	conserved hypothet
446	73	4.1	354	2	T46722	F611.9 protein - A
447	73	4.1	389	2	E86304	hemolin - cecropia
448	73	4.1	397	2	S65948	hemolin precursor
449	73	4.1	413	2	A37778	T-cell surface gly
450	73	4.1	413	2	RMWQ74	probable fatty aci
451	73	4.1	432	1	H84524	interleukin 1 prece
452	73	4.1	476	2	S38921	kinasin-related pr
453	73	4.1	519	2	S38921	hypothetical prote
454	73	4.1	590	2	I56526	probable receptor-
455	73	4.1	666	1	A36026	neural cell adhesi
456	73	4.1	730	2	S64998	penicillin-binding
457	73	4.1	735	2	T00850	core protein VP3 -
458	73	4.1	853	1	IJBONC	hypothetical prote
459	73	4.1	864	2	JH0438	integrin alpha-6 c
460	73	4.1	901	1	P3XR17	hypothetical prote
461	73	4.1	1014	2	T13476	cadmium resistance
462	73	4.1	1072	2	A38457	unconventional myo
463	73	4.1	1171	2	T13635	hypothetical prote
464	73	4.1	1179	2	T05673	hypothetical prote
465	73	4.1	1515	1	S51863	hypothetical prote
466	73	4.1	1737	2	A59235	hypothetical prote
467	73	4.1	1806	2	T23298	hypothetical prote
468	73	4.1	3788	2	T30851	lysosomal traffick
469	72.5	4.1	202	2	S36293	r-cell receptor ga
470	72.5	4.1	221	2	T31620	hypothetical prote
471	72.5	4.1	334	2	G01650	malate dehydrogena
472	72.5	4.1	336	2	C27658	pregnancy-specific
473	72.5	4.1	342	2	AG1729	protein gp19 (Bact
474	72.5	4.1	351	2	B34595	pregnancy-specific
475	72.5	4.1	363	2	I39726	manopine biosynth
476	72.5	4.1	371	2	T40287	hypothetical prote
477	72.5	4.1	399	2	A11114	hypothetical prote
478	72.5	4.1	424	2	A34595	surface protein (p
479	72.5	4.1	435	2	D33258	pregnancy-specific
480	72.5	4.1	435	2	S52885	TYA protein - yea
481	72.5	4.1	440	2	AE3294	tolB protein limpo
482	72.5	4.1	443	2	A35969	tryptan-like prote
483	72.5	4.1	478	2	A49228	hypothetical cell
484	72.5	4.1	487	2	A11146	hypothetical prote
485	72.5	4.1	491	2	T22844	hypothetical prote
486	72.5	4.1	527	2	D75127	Sirt protein - yea
487	72.5	4.1	666	2	A39610	heparin-binding gr
488	72.5	4.1	682	2	A35969	glucose-regulated
489	72.5	4.1	687	2	T39838	hypothetical prote
490	72.5	4.1	768	2	JC7352	hypothetical prote
491	72.5	4.1	769	2	T45854	hypothetical prote
492	72.5	4.1	842	2	E96641	hypothetical prote
493	72.5	4.1	851	2	S44880	ncl-1 ZK112.2 prot
494	72.5	4.1	876	2	A49508	protein-tyrosine k
495	72.5	4.1	895	2	T11979	receptor tyrosine
496	72.5	4.1	913	2	A48280	receptor tyrosine
497	72.5	4.1	1057	2	S45801	exodeoxyribonuclea
498	72.5	4.1	1123	2	AB0125	membrane nuclease
499	72.5	4.1	1138	2	A82939	neurotactin - chic
500	72.5	4.1	1272	2	S26180	transmembrane prot
501	72.5	4.1	1434	2	T30172	lysosactin synthet
502	72.5	4.1	1575	2	T18545	dynein heavy chain
503	72.5	4.1	4367	1	B54802	probable peptidase
504	72.5	4.1	4924	2	T50176	hypothetical prote
505	72.5	4.1	4936	2	AH2515	purine nucleoside
506	72	4.1	265	2	H72233	searcrow-like pro
507	72	4.1	320	2	C89867	hypothetical prote
508	72	4.1	378	2	T51237	hypothetical prote
509	72	4.1	423	2	T29549	hypothetical prote
510	72	4.1	437	2	AP3613	hypothetical prote
511	72	4.1	442	2	E71553	hypothetical prote
512	72	4.1	446	2	B89922	conserved hypothet
513	72	4.1	469	2	CG9628	gamma-aminobutyrat
514	72	4.1	505	2	F69867	two-component sens
515	72	4.1	510	2	A84707	probable pseudouri
516	72	4.1	521	2	E82377	ABC transporter, p
517	72	4.1	543	2	S38353	glutamate transpor
518	72	4.1	549	2	T33517	hypothetical prote
519	72	4.1	558	2	T01343	hypothetical prote
520	72	4.1	565	2	C82280	sensor kinase cItA
521	72	4.1	585	2	S48929	hypothetical prote
522	72	4.1	599	2	T16774	hypothetical prote
523	72	4.1	617	2	T23197	hypothetical prote
524	72	4.1	646	2	I38049	cell surface glyco
525	72	4.1	783	2	T45899	receptor protein k
526	72	4.1	808	2	F81180	conserved hypothet
527	72	4.1	868	2	JC5701	ErbB kinase activa
528	72	4.1	873	2	H96503	protein P9C16.17 [
529	72	4.1	885	2	D86151	F22M8.8 protein -
530	72	4.1	900	2	T04839	core protein p3 -
531	72	4.1	901	2	S07419	androgen receptor
532	72	4.1	911	2	B34721	hypothetical prote
533	72	4.1	1038	2	H90053	hypothetical prote
534	72	4.1	1186	2	T19334	Smad interacting p
535	72	4.1	1214	2	UC7259	hypothetical prote
536	72	4.1	1216	2	H85023	sax-3 protein - Ca
537	72	4.1	1273	2	T42405	vascular endotheli
538	72	4.1	1348	2	S51656	myosin-light-chain
539	72	4.1	1906	1	S68235	probable membrane
540	72	4.1	2383	2	D64962	probable membrane



541	72	4.1	4872	2	S27272	ryanodine receptor
542	71.5	4.0	145	2	S25743	Ig lambda chain -
543	71.5	4.0	229	1	B43685	nonstructural prot
544	71.5	4.0	238	2	A49633	Ig lambda-like cha
545	71.5	4.0	299	2	S50803	hypothetical prote
546	71.5	4.0	312	2	A64461	hypothetical prote
547	71.5	4.0	338	2	A64303	conserved hypocat
548	71.5	4.0	339	2	S08981	malate dehydrogena
549	71.5	4.0	362	2	T05167	hypothetical prote
550	71.5	4.0	443	2	T14916	mitosis-specific c
551	71.5	4.0	498	2	G90067	malate quinone oxi
552	71.5	4.0	500	2	T11946	ribosomal protein
553	71.5	4.0	542	2	AP2587	MFS permease [limp
554	71.5	4.0	549	2	F97369	hypothetical prote
555	71.5	4.0	582	2	T50385	hypothetical colle
556	71.5	4.0	603	2	H64442	hypothetical prote
557	71.5	4.0	669	2	T48466	hypothetical prote
558	71.5	4.0	707	2	A38429	keratinocyte growt
559	71.5	4.0	707	2	A54846	secretory componen
560	71.5	4.0	764	1	ORHUGS	fibroblast growth
561	71.5	4.0	822	2	B54846	hexon protein - hu
562	71.5	4.0	919	2	S33942	probable yopC/gen
563	71.5	4.0	921	2	F71486	acetylflavine resist
564	71.5	4.0	1032	2	H64100	platelet-derived g
565	71.5	4.0	1089	1	S33727	hypothetical prote
566	71.5	4.0	1180	2	B86719	probable epidermal
567	71.5	4.0	1348	2	S27812	probable epidermal
568	71.5	4.0	1348	2	A43917	probable epidermal
569	71.5	4.0	1374	2	S62524	probable RNA helic
570	71.5	4.0	1374	2	C70148	DNA-directed RNA p
571	71.5	4.0	1413	2	D84481	probable retroelem
572	71.5	4.0	1462	2	T11648	probable mitotic s
573	71.5	4.0	2397	1	A55535	versican precursor
574	71	4.0	61	2	C82536	hypothetical prote
575	71	4.0	142	2	S38392	T-cell receptor be
576	71	4.0	189	2	G64496	hypothetical prote
577	71	4.0	207	2	T50206	hypothetical zinc
578	71	4.0	221	2	T21117	hypothetical prote
579	71	4.0	224	2	H81568	conserved hypocat
580	71	4.0	231	2	B86520	CT181 hypothetical
581	71	4.0	231	2	G72102	ct181 hypothetical
582	71	4.0	258	2	S73803	MG356 homolog H91
583	71	4.0	329	1	DEDFLM	L-lactate dehydrog
584	71	4.0	333	2	AP0407	lipoprotein limpor
585	71	4.0	343	2	A10358	probable fimbrial
586	71	4.0	344	2	I56551	neurotrophin - rat
587	71	4.0	345	2	I48780	Stral/Ep1g2 protei
588	71	4.0	346	2	AP1820	siatoglycoproteina
589	71	4.0	387	2	B71611	hypothetical prote
590	71	4.0	389	2	S68155	ubiquinol-cytochro
591	71	4.0	390	2	T27033	hypothetical prote
592	71	4.0	407	2	T34442	hypothetical prote
593	71	4.0	423	1	EHMS5	Ig epsilon chain C
594	71	4.0	455	2	S50391	hypothetical prote
595	71	4.0	462	2	JN0719	drought-inducible
596	71	4.0	463	2	AH1758	amino acid transpo
597	71	4.0	509	1	MMVZMX	Mg-R protein - myx
598	71	4.0	570	2	T11647	probable pyruvate
599	71	4.0	609	2	H82039	GRP-binding protei
600	71	4.0	615	2	B38575	glucuronate 2-dehyd
601	71	4.0	682	2	T22064	hypothetical prote
602	71	4.0	687	2	A49636	soluble vascular e
603	71	4.0	690	2	A24545	triacylglycerol 1i
604	71	4.0	691	2	B89797	glycerol ester hyd
605	71	4.0	765	2	E96558	hypothetical prote
606	71	4.0	821	1	TVHUF2	fibroblast growth
607	71	4.0	876	1	T51507	WD40-repeat protei
608	71	4.0	902	1	S54495	probable carrier p
609	71	4.0	940	2	T41992	hypothetical prote
610	71	4.0	956	2	C70327	isoletucine-tRNA 1i
611	71	4.0	1018	2	A54744	contractin 1 precu
612	71	4.0	1027	2	B85089	receptor protein k
613	71	4.0	1082	2	S64903	regulatory protein
614	71	4.0	1217	2	T22672	hypothetical prote
615	71	4.0	1251	2	T21389	hypothetical prote
616	71	4.0	1338	2	S09982	protein-tyrosine k
617	71	4.0	4391	2	A38096	perlecan precursor
618	71	4.0	5107	2	T29144	partial CDS - Caen
619	70.5	4.0	203	2	F69381	flagellin (flaB1-1
620	70.5	4.0	223	2	A81068	hypothetical prote
621	70.5	4.0	238	2	D86302	hypothetical prote
622	70.5	4.0	246	2	B82764	hypothetical prote
623	70.5	4.0	332	2	T45770	hypothetical prote
624	70.5	4.0	338	1	DSRTMW	malate dehydrogena
625	70.5	4.0	358	2	B89588	protein R09P10.8 l
626	70.5	4.0	429	1	B41902	arsenical pump mem
627	70.5	4.0	455	2	G01923	KIR (c1-5) NK rece
628	70.5	4.0	502	2	T19108	hypothetical prote
629	70.5	4.0	505	2	T15159	hypothetical prote
630	70.5	4.0	522	2	T26319	hypothetical prote
631	70.5	4.0	526	1	TVFV60	protein-tyrosine k
632	70.5	4.0	533	1	TVCHS1	protein-tyrosine k
633	70.5	4.0	537	1	A45501	protein-tyrosine k
634	70.5	4.0	545	2	S52313	protein-tyrosine k
635	70.5	4.0	546	2	S52314	protein-tyrosine k
636	70.5	4.0	557	1	TVFVS2	protein-tyrosine k
637	70.5	4.0	558	1	MMXKRT	RNA 10 protein - r
638	70.5	4.0	568	1	TVFVS1	protein-tyrosine k
639	70.5	4.0	569	2	A45624	trichozoite cystei
640	70.5	4.0	587	1	TVFVPR	protein-tyrosine k
641	70.5	4.0	627	2	S14683	Ig mu chain precu
642	70.5	4.0	627	2	A59663	DNA mismatch repai
643	70.5	4.0	630	2	A39344	tumor-associated m
644	70.5	4.0	646	2	T48644	negative regulator
645	70.5	4.0	656	2	H84206	acetyl-CoA synthet
646	70.5	4.0	663	1	TVMVR	protein-tyrosine k
647	70.5	4.0	669	2	T13640	probable minor str
648	70.5	4.0	743	2	F71062	hypothetical prote
649	70.5	4.0	787	2	T41974	repliation origin
650	70.5	4.0	793	2	T41703	dipeptidyl aminope
651	70.5	4.0	844	2	S05988	transactin elonga
652	70.5	4.0	877	1	IUBOCN	N-cadherin precurs
653	70.5	4.0	878	2	S11842	hypothetical prote
654	70.5	4.0	895	2	A55413	triglyceride trans
655	70.5	4.0	906	1	IUMSCN	N-cadherin precurs
656	70.5	4.0	928	2	G86546	polymorphic oute
657	70.5	4.0	928	2	G81591	polymorphic membra
658	70.5	4.0	938	2	F86548	polymorphic oute
659	70.5	4.0	938	2	H72074	polymorphic membra
660	70.5	4.0	1088	2	B56715	calcium receptor (
661	70.5	4.0	1200	2	T17440	hyalin - sea urchi
662	70.5	4.0	1356	2	UC1402	protein-tyrosine k
663	70.5	4.0	1402	2	F84480	probable retroelem
664	70.5	4.0	1427	2	I51669	tumor suppressor -
665	70.5	4.0	1694	2	S50065	siatodhesin - mou
666	70.5	4.0	2051	2	T30938	receptor tyrosine
667	70.5	4.0	2303	1	GNNYRP	genome polypotein
668	70.5	4.0	2303	1	S13554	genome polypotein
669	70.5	4.0	2464	1	ORMSP1	microtubule-associ
670	70.5	4.0	6831	2	A88852	protein unc-22 lim
671	70.5	4.0	6839	2	S57242	twitcllin [similari
672	70.5	4.0	7160	2	T27935	hypothetical prote
673	70	4.0	115	1	KVMSL6	Ig kappa chain pre
674	70	4.0	203	2	S23043	T-cell receptor ga
675	70	4.0	224	2	I37243	CMRF-35 antigen -
676	70	4.0	236	2	S25746	Ig lambda chain -
677	70	4.0	283	2	AB0105	probable maltodext
678	70	4.0	292	2	T44230	hypothetical prote
679	70	4.0	299	2	DB3010	probable binding p
680	70	4.0	304	2	G71624	rtifin PFB0025C - m
681	70	4.0	347	2	T29415	hypothetical prote
682	70	4.0	356	2	G82938	hemlin transport sy
683	70	4.0	374	2	A46352	ORP1 protein - Chl
684	70	4.0	403	2	B36151	tryptophan synthas
685	70	4.0	410	2	I50494	serine proteinase
686	70	4.0	469	2	T46929	hypothetical prote



687	70	4.0	491	2	T27661	hypothetical prote
688	70	4.0	517	2	T09860	hypothetical prote
689	70	4.0	536	2	T37544	hypothetical serin
690	70	4.0	548	2	B71549	hypothetical prote
691	70	4.0	550	2	T03714	5-epi-aristolochen
692	70	4.0	576	2	A32604	interleukin-1 rece
693	70	4.0	599	2	T48450	hypothetical prote
694	70	4.0	609	2	A82062	gamma-glutamyltran
695	70	4.0	611	1	W1MLEP	E1 protein - Europ
696	70	4.0	611	1	H70938	probable fad5 pro
697	70	4.0	648	2	T08856	hypothetical prote
698	70	4.0	687	1	A39045	protein-glutamine
699	70	4.0	790	2	T01537	S-receptor kinase
700	70	4.0	805	2	S68441	leptin receptor, s
701	70	4.0	810	1	S57196	calpain (EC 3.4.22
702	70	4.0	818	2	T32154	hypothetical prote
703	70	4.0	828	2	AD2004	hypothetical prote
704	70	4.0	837	2	A34898	granulocyte colony
705	70	4.0	838	2	AC1064	outer membrane fil
706	70	4.0	849	2	T22306	hypothetical prote
707	70	4.0	892	2	S68439	leptin receptor, s
708	70	4.0	894	2	S68437	leptin receptor, s
709	70	4.0	900	2	S68440	leptin receptor, s
710	70	4.0	933	2	H90247	ATP-dependent heli
711	70	4.0	990	2	T16554	hypothetical prote
712	70	4.0	1040	2	A34695	axonal glycoprotei
713	70	4.0	1086	2	T40354	hypothetical prote
714	70	4.0	1092	2	T30214	fibrinogen-binding
715	70	4.0	1162	2	S68438	leptin receptor, s
716	70	4.0	1190	2	T00842	probable histidine
717	70	4.0	1317	2	B41950	retrovirus-related
718	70	4.0	1456	1	WMMGPV	RNA-directed RNA p
719	70	4.0	1456	2	JQ2294	hypothetical 16S.1
720	70	4.0	2004	2	AC0314	probable membrane
721	70	4.0	2183	2	T42764	coagulation factor
722	70	4.0	2199	2	S76412	hypothetical prote
723	69.5	3.9	219	2	S74483	hypothetical prote
724	69.5	3.9	285	1	I38548	alcohol sulfoxtrans
725	69.5	3.9	332	2	E71105	hypothetical prote
726	69.5	3.9	338	1	DEMSMW	malate dehydrogena
727	69.5	3.9	346	2	T49148	nitrilase (EC 3.5.
728	69.5	3.9	366	2	E97304	iron-regulated ABC
729	69.5	3.9	407	2	T08732	hypothetical prote
730	69.5	3.9	427	2	C23703	ribose-bisphosph
731	69.5	3.9	437	2	D70353	adenylosuccinate 1
732	69.5	3.9	442	2	H66144	hypothetical prote
733	69.5	3.9	444	2	E97750	toB protein precu
734	69.5	3.9	447	2	B81519	UDP-N-acetylmuram
735	69.5	3.9	447	2	A86603	muramoyl-DAP ligas
736	69.5	3.9	447	2	F72021	muramoyl-dap ligas
737	69.5	3.9	453	2	B88040	protein lin-42 [im
738	69.5	3.9	461	2	T47782	hypothetical prote
739	69.5	3.9	503	2	S63257	probable membrane
740	69.5	3.9	506	2	T05272	fatty acid elongas
741	69.5	3.9	523	1	TYFVMT	protein-tyrosine k
742	69.5	3.9	548	1	A26511	amds protein - Eme
743	69.5	3.9	548	2	S27958	transcription fact
744	69.5	3.9	568	2	T39840	conserved hypocht
745	69.5	3.9	585	2	A39395	delayed rectifier
746	69.5	3.9	616	2	D64569	conserved hypocht
747	69.5	3.9	633	2	S19352	amino acid transpo
748	69.5	3.9	640	2	T43724	dnak-type molecula
749	69.5	3.9	682	2	D90946	hypothetical prote
750	69.5	3.9	682	2	H85794	hypothetical prote
751	69.5	3.9	682	2	A41798	carboxy-terminal p
752	69.5	3.9	710	1	I51283	hepatocyte growth
753	69.5	3.9	736	2	T40904	pombe specific hyp
754	69.5	3.9	757	2	T24266	hypothetical prote
755	69.5	3.9	776	2	A41704	genome polypeptid
756	69.5	3.9	776	2	F81289	probable sugar tra
757	69.5	3.9	846	2	T04533	hypothetical prote
758	69.5	3.9	849	1	UTPVAD	noncapped protein
759	69.5	3.9	1034	2	H86399	protein F17L21.26
760	69.5	3.9	1045	2	G69167	cobalamin biosynth
761	69.5	3.9	1102	2	T28666	protein kinase C-r
762	69.5	3.9	1172	2	F70535	probable rpoB prot
763	69.5	3.9	1199	2	C71500	probable swi/snf h
764	69.5	3.9	1260	1	S05479	neural cell adhesi
765	69.5	3.9	1463	2	T30290	AAS surface protei
766	69.5	3.9	1832	2	AC2594	glutamate synthase
767	69.5	3.9	1858	2	D97376	hypothetical prote
768	69	3.9	115	2	C90907	hypothetical prote
769	69	3.9	139	2	AH1847	photosystem I reac
770	69	3.9	222	2	A64548	conserved hypocht
771	69	3.9	279	2	S04693	T-cell receptor de
772	69	3.9	289	2	T18048	carbohydrate prote
773	69	3.9	291	2	A87153	hypothetical prote
774	69	3.9	306	2	T25625	hypothetical prote
775	69	3.9	330	2	AD1533	hypothetical prote
776	69	3.9	348	2	D96815	probable gamma-glu
777	69	3.9	363	2	AG0675	probable secreted
778	69	3.9	390	2	F72863	AcOrf-109 protein
779	69	3.9	391	2	T41849	AcMNPV orf109 - Bo
780	69	3.9	396	2	T36678	probable septum si
781	69	3.9	418	2	T35753	gene ND4L introm 1
782	69	3.9	428	2	S09134	hypothetical prote
783	69	3.9	461	2	F83772	SERINE CARBOXYPEPT
784	69	3.9	465	2	B85358	hypothetical prote
785	69	3.9	469	2	T46930	cytochrome P450 2C
786	69	3.9	490	2	B28516	hypothetical prote
787	69	3.9	493	2	E71008	hypothetical prote
788	69	3.9	501	1	PLMB2	H+-transporting tw
789	69	3.9	505	1	PMYCA	hypothetical prote
790	69	3.9	542	2	T20457	alpha-glucosidase
791	69	3.9	584	1	ALBY	rab binding prote
792	69	3.9	613	2	EB0358	proteinase IV Xf26
793	69	3.9	633	2	D82527	hypothetical prote
794	69	3.9	644	2	A25684	sodium/phosphate c
795	69	3.9	653	2	A54366	hypothetical prote
796	69	3.9	657	2	S25184	cap1 protein - Cor
797	69	3.9	715	2	I45832	scinderin - bovine
798	69	3.9	715	2	T10049	adeaverin - mouse
799	69	3.9	773	2	T46283	hypothetical prote
800	69	3.9	824	2	T51057	related to tol pro
801	69	3.9	919	2	C66578	type III secretion
802	69	3.9	919	2	F72045	vacuolar carboxype
803	69	3.9	1049	2	S67613	ribonuclease E VC2
804	69	3.9	1052	2	A82127	hypothetical prote
805	69	3.9	1244	2	T19615	hypothetical Serin
806	69	3.9	1283	2	T39174	probable membrane
807	69	3.9	1357	2	S61187	hypothetical prote
808	69	3.9	1360	2	T32833	hypothetical prote
809	69	3.9	1442	2	T18538	patched protein -
810	69	3.9	1656	2	S54520	probable membrane
811	69	3.9	1802	2	S52611	tyB protein - yeas
812	69	3.9	2132	1	A55182	aggreacan precursor
813	69	3.9	2437	2	T18482	hypothetical prote
814	69	3.9	4563	1	LEPHUB	apolipoprotein B-1
815	69	3.9	5188	2	B85547	probable RTX fami
816	69	3.9	5291	2	F90636	hypothetical prote
817	69	3.9	10797	2	T30192	probable peptidase
818	68.5	3.9	134	2	J11245	Ig kappa chain pre
819	68.5	3.9	135	2	J00472	T-cell receptor be
820	68.5	3.9	145	2	S36324	T-cell receptor de
821	68.5	3.9	227	2	T33766	hypothetical prote
822	68.5	3.9	228	2	A82200	two-component resp
823	68.5	3.9	234	2	S25757	Ig lambda chain -
824	68.5	3.9	234	2	S14237	Ig kappa chain pre
825	68.5	3.9	240	2	A39016	T-cell surface gly
826	68.5	3.9	267	2	G90579	hypothetical prote
827	68.5	3.9	268	2	S48942	hypothetical prote
828	68.5	3.9	292	2	C64699	proteinase IV (EC
829	68.5	3.9	296	2	G65002	hypothetical prote
830	68.5	3.9	299	2	T32094	syndecan 1 precurs
831	68.5	3.9	310	2	A41776	replication protei
832	68.5	3.9	327	2	A81192	



833	68.5	3.9	328	2	147161	Ig gamma 3 chain c
834	68.5	3.9	329	2	T19872	hypothetical prote
835	68.5	3.9	362	2	A70852	hypothetical prote
836	68.5	3.9	375	2	B96567	hypothetical prote
837	68.5	3.9	393	2	B48965	subtilin biosynthe
838	68.5	3.9	423	2	AG0451	maltopectin (import
839	68.5	3.9	448	1	G69960	exodeoxyribonuclea
840	68.5	3.9	458	1	RWHUT4	T-cell surface gly
841	68.5	3.9	463	1	T19343	ribulose-bisphosph
842	68.5	3.9	464	2	T06176	DNA damage inducib
843	68.5	3.9	493	2	T41397	glycoprotein E pre
844	68.5	3.9	498	2	JQ2353	flagella-related p
845	68.5	3.9	513	2	H90401	SRP1 protein - yea
846	68.5	3.9	522	2	S30884	dihydroxyacid dehy
847	68.5	3.9	555	2	P70372	probable membrane
848	68.5	3.9	561	2	SC3388	protein-tyrosine k
849	68.5	3.9	561	2	AS9182	aldehyde-ferredoxi
850	68.5	3.9	581	2	C71078	hypothetical prote
851	68.5	3.9	589	2	T40252	phosphoribosylamin
852	68.5	3.9	592	2	SS4489	DNA mismatch repai
853	68.5	3.9	601	2	AD1250	GMP-binding tyrosi
854	68.5	3.9	606	2	AP2903	hypothetical prote
855	68.5	3.9	606	2	H97678	hypothetical prote
856	68.5	3.9	630	2	S77346	protein T23J18.9 l
857	68.5	3.9	636	2	A86248	methy1-accepting c
858	68.5	3.9	654	2	A69656	type III secretion
859	68.5	3.9	672	2	D81746	transferrin-bindin
860	68.5	3.9	689	2	S70661	S-receptor kinase
861	68.5	3.9	772	1	T05753	genome polyprotein
862	68.5	3.9	776	2	B41704	SHB4 protein - yea
863	68.5	3.9	789	2	S62172	hypothetical prote
864	68.5	3.9	818	2	B83537	S-layer protein -
865	68.5	3.9	827	2	A37849	prolactin receptor
866	68.5	3.9	831	2	JQ1655	cadherin 2 precurs
867	68.5	3.9	906	1	I0HUCN	ionotropic glutama
868	68.5	3.9	950	2	T51134	macrophage colony-
869	68.5	3.9	972	1	TVHUMD	alpha-amyliase (BC
870	68.5	3.9	976	2	A42466	DNA-binding protei
871	68.5	3.9	1043	2	AS6037	conserved hypothet
872	68.5	3.9	1074	2	F72217	Ca2+-transporting
873	68.5	3.9	1086	2	T18294	hypothetical prote
874	68.5	3.9	1134	2	SS3955	neural cell adhesi
875	68.5	3.9	1257	1	A41060	proteinase related
876	68.5	3.9	1269	2	A90267	SP2 protein - yea
877	68.5	3.9	1466	2	A35426	polymorphic membra
878	68.5	3.9	1520	2	A81731	hypothetical prote
879	68.5	3.9	1767	2	T20766	probable peptidogl
880	68.5	3.9	2013	2	A11489	acetyl-CoA carboxy
881	68.5	3.9	2288	2	T30568	probable cell-surf
882	68.5	3.9	3229	2	S27852	calo protein - fru
883	68.5	3.9	4116	2	T13719	T-cell receptor de
884	68	3.8	1442	2	S36307	mannose-specific p
885	68	3.8	144	2	A11529	PA1 cross-reacting
886	68	3.8	155	2	I64130	pathogenesis-relat
887	68	3.8	157	2	T09659	hypothetical prote
888	68	3.8	180	2	A71634	adhesin p1 precurs
889	68	3.8	221	2	S73349	hypothetical prote
890	68	3.8	231	2	D64461	NAPC membrane prot
891	68	3.8	233	2	H95345	intercellular adhe
892	68	3.8	266	2	G69483	conserved hypothet
893	68	3.8	275	2	S03967	hypothetical prote
894	68	3.8	276	2	D82169	transmembrane sens
895	68	3.8	286	2	A82159	protein farnesyltr
896	68	3.8	311	2	AH3197	probable aliphatic
897	68	3.8	326	2	T51811	oligopeptide ABC t
898	68	3.8	330	2	B96027	farnesyltransferas
899	68	3.8	338	2	C83653	permease protein o
900	68	3.8	340	2	T49006	synaptotagmin VII
901	68	3.8	341	2	A81824	probable DNA polym
902	68	3.8	355	2	SS8401	probable elongatio
903	68	3.8	371	2	A71378	
904	68	3.8	378	2	E84806	
905	68	3.8	385	2	T27626	
906	68	3.8	401	2	B89863	argininosuccinate
907	68	3.8	409	1	PAWTF	fructose-bisphosph
908	68	3.8	412	2	T35664	probable prokaryot
909	68	3.8	431	2	F64072	multidrug oxidoredu
910	68	3.8	444	2	D87296	multidrug resistanc
911	68	3.8	459	2	S76138	hypothetical prote
912	68	3.8	459	2	T21105	hypothetical prote
913	68	3.8	465	2	T46054	hypothetical prote
914	68	3.8	471	2	A81680	conserved hypothet
915	68	3.8	479	1	S22542	transcription fact
916	68	3.8	525	1	P5XR10	outer capsid prote
917	68	3.8	528	2	T38027	hypothetical prote
918	68	3.8	541	2	B96789	protein T23J18.10
919	68	3.8	582	2	S46183	alpha-glucosidase
920	68	3.8	602	2	D90557	hypothetical prote
921	68	3.8	632	2	T37810	RNA-binding post-t
922	68	3.8	637	2	D82816	fibrinial assembly
923	68	3.8	638	2	SS4418	fibrinectin-bindin
924	68	3.8	640	2	S35734	DNA topoisomerase
925	68	3.8	645	2	B96631	probable receptor
926	68	3.8	649	1	C2CLDM	cellulase (BC 3.2.
927	68	3.8	656	2	F71675	hypothetical prote
928	68	3.8	690	2	JC4185	proteinase II (BC
929	68	3.8	710	2	T82432	GAD6R family prote
930	68	3.8	721	2	T27570	hypothetical prote
931	68	3.8	789	2	S28259	androgen-regulated
932	68	3.8	793	2	D38992	cadherin 8 - human
933	68	3.8	795	2	T21487	hypothetical prote
934	68	3.8	796	2	T39962	catomer complex b
935	68	3.8	814	1	C40618	fimbrial outer mem
936	68	3.8	896	2	AH2075	ferrichrome-iron r
937	68	3.8	896	2	S26984	probable DNA-direc
938	68	3.8	901	2	JE0062	core protein VP3 -
939	68	3.8	905	1	I1XLC2	N-cadherin 2 precu
940	68	3.8	912	2	AS4423	brevian precursor
941	68	3.8	940	2	AB1744	internalin protein
942	68	3.8	962	2	S03818	carboxymethylcellu
943	68	3.8	963	2	A57238	iron-responsive el
944	68	3.8	963	2	D88473	protein F40H6.2 [i
945	68	3.8	997	2	T13039	tyrosine kinase re
946	68	3.8	1019	2	T52306	methionine S-methy
947	68	3.8	1071	2	S64930	serine/threonine-s
948	68	3.8	1147	2	T38140	protein-tyrosine-p
949	68	3.8	1174	2	I81010	protein ZK250.10 f
950	68	3.8	1192	2	F88062	chitin synthase (B
951	68	3.8	1281	2	S61886	p-glycoprotein iso
952	68	3.8	1282	2	JC4353	microbial collagen
953	68	3.8	1291	2	T21694	hypothetical prote
954	68	3.8	1295	2	T30528	reverse transcript
955	68	3.8	1318	2	T05745	hypothetical prote
956	68	3.8	1458	2	A45665	adult-specific bru
957	68	3.8	1466	2	T32422	hypothetical prote
958	68	3.8	1664	2	H82601	conserved hypothet
959	68	3.8	1707	2	T18951	hypothetical prote
960	68	3.8	1786	1	H71527	probable exclucnle
961	68	3.8	1946	2	AE1449	hypothetical prote
962	68	3.8	2124	1	A28452	proteoglycan core
963	68	3.8	3341	1	A42996	genome polyprotein
964	67.5	3.8	134	2	T14454	cytochrome b5 - wi
965	67.5	3.8	177	2	H90493	hypothetical prote
966	67.5	3.8	212	2	S03964	stem bromelain (BC
967	67.5	3.8	221	1	B42521	hypothetical prote
968	67.5	3.8	229	2	A20969	outer capsid prote
969	67.5	3.8	261	2	S55139	hypothetical prote
970	67.5	3.8	267	2	T72882	hypothetical prote
971	67.5	3.8	277	2	B97703	hypothetical prote
972	67.5	3.8	278	2	JC1507	biliary glycoprote
973	67.5	3.8	299	2	F82975	hypothetical prote
974	67.5	3.8	315	2	G69785	mannose-6-phosphat
975	67.5	3.8	327	2	T22407	hypothetical prote
976	67.5	3.8	329	1	G2GP	Ig gamma-2 chain C
977	67.5	3.8	345	2	I58406	outer membrane pro
978	67.5	3.8	348	1	MMNHBP	



979	67.5	3.8	348	2	B70743	hypothetical prote	1052	67	3.8	127	2	S52447	Ig kappa chain V r
980	67.5	3.8	357	2	T34012	hypothetical prote	1053	67	3.8	128	2	S31468	Ig kappa chain pre
981	67.5	3.8	360	2	T27022	hypothetical prote	1054	67	3.8	131	2	S30552	T-cell activation
982	67.5	3.8	361	2	D83798	phosphoserine amin	1055	67	3.8	135	2	S49200	cytochrome b5 - co
983	67.5	3.8	362	2	A81397	conserved hypotet	1056	67	3.8	137	2	B70221	rev protein (rev)
984	67.5	3.8	364	2	T46630	cysteine proteinas	1057	67	3.8	182	2	T23259	hypothetical prote
985	67.5	3.8	364	2	T12039	hypothetical prote	1058	67	3.8	214	2	B71159	probable flagellin
986	67.5	3.8	367	2	AP2494	aggreccan - pig (fr	1059	67	3.8	239	2	AC2042	hypothetical prote
987	67.5	3.8	370	2	S29139	aggreccan - pig (fr	1060	67	3.8	255	2	B69692	amino acid ABC tra
988	67.5	3.8	402	2	T25732	hypothetical prote	1061	67	3.8	282	2	B84984	geranyltransferasi
989	67.5	3.8	426	2	T16948	Ig epsilon-chain -	1062	67	3.8	300	2	HE4050	glucose kinase hom
990	67.5	3.8	443	2	T19512	hypothetical prote	1063	67	3.8	302	2	AC1387	phosphate ABC tran
991	67.5	3.8	450	2	H71135	probable adenylosu	1064	67	3.8	302	2	AE1762	phosphate ABC tran
992	67.5	3.8	451	2	T06090	hypothetical prote	1065	67	3.8	311	2	C86638	glycosyl transfera
993	67.5	3.8	458	2	A83095	UDP-N-acetylmuramo	1066	67	3.8	358	2	G64461	biotin synthase (E
994	67.5	3.8	466	2	A11894	two-component sens	1067	67	3.8	373	1	PDBYB	RBP1 protein - yea
995	67.5	3.8	487	2	S65133	butyrophilin - mou	1068	67	3.8	430	2	T14420	S-lucos-specific g
996	67.5	3.8	510	2	A87482	conserved hypotet	1069	67	3.8	441	2	F71425	hypothetical prote
997	67.5	3.8	511	2	A46020	potassium channel	1070	67	3.8	450	2	S38424	S-lucos-specific g
998	67.5	3.8	511	2	S07095	59k antigen - Chla	1071	67	3.8	461	2	T09933	probable phosphodi
999	67.5	3.8	525	2	J00642	hypothetical prote	1072	67	3.8	474	2	I50830	Ig mu chain - Lep1
1000	67.5	3.8	527	2	G85760	hypothetical prote	1073	67	3.8	477	2	C86833	6-phospho-beta-glu
1001	67.5	3.8	527	2	H90858	hypothetical prote	1074	67	3.8	495	1	A26396	T-cell surface gly
1002	67.5	3.8	541	1	A43610	protein-tyrosine k	1075	67	3.8	518	2	JC4024	poliovirus recepto
1003	67.5	3.8	542	1	TVHUSC	protein-tyrosine k	1076	67	3.8	524	2	G64243	hypothetical prote
1004	67.5	3.8	547	2	B45808	B-lymphocyte antig	1077	67	3.8	532	2	C97228	probable peptide A
1005	67.5	3.8	547	2	T27253	hypothetical prote	1078	67	3.8	542	2	T41650	importin alpha sub
1006	67.5	3.8	567	2	S29498	flavoprotein limpo	1079	67	3.8	544	2	S41626	spike protein chai
1007	67.5	3.8	570	2	A11828	asparagine synthas	1080	67	3.8	569	2	S64957	aspergillopepsin I
1008	67.5	3.8	572	2	S55982	hypothetical prote	1081	67	3.8	599	2	S55363	maltase-like prote
1009	67.5	3.8	584	2	S48327	hypothetical prote	1082	67	3.8	619	2	S67067	probable membrane
1010	67.5	3.8	591	2	S73708	MG321 homolog H08	1083	67	3.8	622	2	HE4447	hypothetical prote
1011	67.5	3.8	619	2	A13336	potassium/proton a	1084	67	3.8	623	1	AE4774	ybaU protein - Bsc
1012	67.5	3.8	621	2	A72091	metalloproteinase	1085	67	3.8	625	1	S52485	glucokinase regula
1013	67.5	3.8	621	2	D81578	zinc proteinase CP	1086	67	3.8	661	1	H71237	probable ferrous i
1014	67.5	3.8	627	2	D46956	nuc family transc	1087	67	3.8	690	2	T25431	hypothetical prote
1015	67.5	3.8	651	2	T49986	lectin-like protei	1088	67	3.8	717	2	A12447	hypothetical prote
1016	67.5	3.8	697	2	E95196	neuraminidase B [i	1089	67	3.8	721	2	A75018	transport protein
1017	67.5	3.8	726	2	AG0837	Tomb-dependent out	1090	67	3.8	746	2	T23607	hypothetical prote
1018	67.5	3.8	732	1	JU0132	acylaminoacyl-pept	1091	67	3.8	747	2	T19080	cell surface glyco
1019	67.5	3.8	748	2	T48744	semaphorin A - mou	1092	67	3.8	750	2	B84417	hypothetical trans
1020	67.5	3.8	759	2	S67164	probable membrane	1093	67	3.8	836	2	B84417	cell surface glyco
1021	67.5	3.8	776	2	S67053	cadherin-14 - huma	1094	67	3.8	850	2	AE3484	hypothetical trans
1022	67.5	3.8	790	2	G02678	protein-tyrosine k	1095	67	3.8	852	2	A28459	cell surface glyco
1023	67.5	3.8	790	2	A39627	intermalin protein	1096	67	3.8	871	2	G66586	DNA topoisomerase
1024	67.5	3.8	832	2	AD1096	protein K07E3.2 [i	1097	67	3.8	875	2	S62177	HIR2 protein - yea
1025	67.5	3.8	837	2	B89583	hypothetical prote	1098	67	3.8	876	2	I49152	protein-tyrosine k
1026	67.5	3.8	855	2	T10587	serine/threonine-s	1100	67	3.8	898	2	T19492	hypothetical prote
1027	67.5	3.8	866	2	S73757	hypothetical prote	1101	67	3.8	920	2	UC7313	aryl hydrocarbon r
1028	67.5	3.8	879	2	AG1957	hypothetical prote	1102	67	3.8	939	2	AE2275	hypothetical prote
1029	67.5	3.8	906	2	D86897	hypothetical prote	1103	67	3.8	974	2	B86613	zinc metalloprotei
1030	67.5	3.8	926	2	D66897	hypothetical prote	1104	67	3.8	974	2	T29545	hypothetical prote
1031	67.5	3.8	933	2	AD3309	hypothetical membr	1105	67	3.8	976	2	T29583	hypothetical prote
1032	67.5	3.8	944	2	T47246	chitin synthase (E	1106	67	3.8	980	2	I57936	glutamate receptor
1033	67.5	3.8	956	2	JH0826	glutamate ionotro	1107	67	3.8	981	2	T18234	beta transducin ho
1034	67.5	3.8	992	2	JQ1165	Env protein - Maed	1108	67	3.8	1040	2	DB1379	transmembrane effl
1035	67.5	3.8	1036	2	A29832	HPI layer surface	1109	67	3.8	1048	2	HE4459	hypothetical prote
1036	67.5	3.8	1042	2	E85968	evolved beta-D-gal	1110	67	3.8	1070	2	JC4593	protein-tyrosine k
1037	67.5	3.8	1042	2	P91123	conserved hypotet	1111	67	3.8	1115	1	TYMSNL	neural cell adhesi
1038	67.5	3.8	1061	2	D98008	hypothetical prote	1112	67	3.8	1134	2	T04587	hypothetical prote
1039	67.5	3.8	1118	2	T27865	probable pyrolysin	1113	67	3.8	1151	2	AG1717	probable peptidogl
1040	67.5	3.8	1155	2	H71456	chitinase A [impor	1114	67	3.8	1170	1	TSHUP1	type V adenyl-yl cy
1041	67.5	3.8	1215	2	T43916	P-glycoprotein-lik	1115	67	3.8	1264	2	S41603	type V adenyl-yl cy
1042	67.5	3.8	1229	2	D85023	protein-tyrosine-ik	1116	67	3.8	1309	1	BVBYP9	RAD9 protein - yea
1043	67.5	3.8	1229	2	T52319	P-glycoprotein-lik	1117	67	3.8	1328	2	T23007	hypothetical prote
1044	67.5	3.8	1260	1	TVRTNU	protein-tyrosine k	1118	67	3.8	1365	2	T45031	hypothetical prote
1045	67.5	3.8	1263	2	T13465	embryonic receptor	1119	67	3.8	1428	2	S62419	hypothetical prote
1046	67.5	3.8	1330	2	S49010	myosin-2 isoform -	1120	67	3.8	1441	1	T13717	CRAG protein - fru
1047	67.5	3.8	1471	2	T40117	beta-galactosidase	1121	67	3.8	1445	1	A48148	protein-tyrosine-P
1048	67.5	3.8	1928	2	J50610	kinase-related pro	1122	67	3.8	1533	2	F71274	hypothetical prote
1049	67.5	3.8	2338	2	T79597	variant surface pr	1123	67	3.8	1589	2	T22668	hypothetical prote
1050	67.5	3.8	3026	2	T28431	gp330 protein prec	1124	67	3.8	1680	2	T41628	probable transcrip



1125	67	3.8	1723	2	H86557	polymorphic membra	1198	66.5	3.8	1117	2	JC4934	delta-crystallin/B
1126	67	3.8	1723	2	E72067	polymorphic membra	1199	66.5	3.8	1160	2	T39898	carbamoyl-phosphat
1127	67	3.8	1732	2	C81601	polymorphic membra	1200	66.5	3.8	1181	2	T20386	hypothetical prote
1128	67	3.8	1742	2	S24600	prolectin - fruit	1201	66.5	3.8	1182	2	S59951	DNA-directed RNA p
1129	67	3.8	1790	1	S27772	vitellinogenin precu	1202	66.5	3.8	1183	2	H89821	RNA polymerase bet
1130	67	3.8	1813	2	T30564	resistance protein	1203	66.5	3.8	1184	2	A42904	adenylyl cyclase ty
1131	67	3.8	2095	2	S29529	genome polypotein	1204	66.5	3.8	1344	2	T14316	rig-1 protein - mo
1132	67	3.8	2380	2	T29551	hypothetical prote	1205	66.5	3.8	1376	2	F83711	exopolysaccharona
1133	67	3.8	2626	2	T31099	imosin-RhoGAP prot	1206	66.5	3.8	1447	2	A54100	tumor suppressor p
1134	67	3.8	136	2	C72524	hypothetical prote	1207	66.5	3.8	1462	2	T06819	DNA topoisomerase
1135	66.5	3.8	147	2	JC7237	receptor-activity-	1208	66.5	3.8	1471	2	F86218	protein F22013.8 [
1136	66.5	3.8	181	2	AC0686	hypothetical prote	1209	66.5	3.8	1484	2	T42632	breast cancer tumo
1137	66.5	3.8	191	2	AH0196	probable lipoprote	1210	66.5	3.8	1545	2	T26589	hypothetical prote
1138	66.5	3.8	218	2	D72494	probable thiosulfa	1211	66.5	3.8	1565	2	T01060	hypothetical prote
1139	66.5	3.8	228	2	AG2107	hypothetical prote	1212	66.5	3.8	1616	2	T00713	helicase homolog F
1140	66.5	3.8	245	2	T12334	L-ascorbate peroxi	1213	66.5	3.8	1643	2	T14274	versican precursor
1141	66.5	3.8	245	2	H71429	hypothetical prote	1214	66.5	3.8	2089	2	C85426	ARM-like protein [
1142	66.5	3.8	250	2	S64849	hypothetical prote	1215	66.5	3.8	2303	1	GNNYTM	genome polypotein
1143	66.5	3.8	285	2	T12156	nodulin, isoform N	1216	66.5	3.8	2470	2	I50726	catlon-independent
1144	66.5	3.8	301	2	S57531	transcription regu	1217	66.5	3.8	2588	2	A12136	peptide synthetase
1145	66.5	3.8	318	2	S61840	porin class PIB -	1218	66.5	3.8	3262	2	AH2137	hypothetical prote
1146	66.5	3.8	328	2	D69452	conserved hypothet	1219	66.5	3.8	3305	2	T18358	apolipoprotein prec
1147	66.5	3.8	335	2	A53434	cell surface glyco	1220	66.5	3.8	3381	2	T42389	versican precursor
1148	66.5	3.8	344	2	I51330	androgen receptor	1221	66.5	3.8	3738	2	T05501	hypothetical prote
1149	66.5	3.8	352	2	T09760	chymopapain (BC 3.	1222	66.5	3.8	4092	1	S38128	dysen heavy chain
1150	66.5	3.8	358	2	G70026	conserved hypothet	1223	66.5	3.8	4436	2	E71086	hypothetical prote
1151	66.5	3.8	362	2	T41842	AcNBPV orf101 - Bo	1224	66.5	3.8	4447	2	A69679	polyketide synthas
1152	66.5	3.8	367	2	T06529	cysteine proteinas	1225	66.5	3.8	5147	1	IJFPTM	cadherin-related p
1153	66.5	3.8	382	2	C86321	hypothetical prote	1226	66	3.7	118	2	S12627	Ig lambda chain pr
1154	66.5	3.8	384	2	F84675	hypothetical prote	1227	66	3.7	132	1	RWMS12	T-cell receptor ga
1155	66.5	3.8	394	2	AC3364	glutaryl-CoA dehyd	1228	66	3.7	134	2	T52469	cytochrome B5 [imp
1156	66.5	3.8	397	2	T34441	hypothetical prote	1229	66	3.7	167	2	S29579	Ig light chain - r
1157	66.5	3.8	404	1	I61596	advanced glycosyla	1230	66	3.7	182	2	A34647	pregnancy-specific
1158	66.5	3.8	413	2	H82270	hypothetical prote	1231	66	3.7	189	2	A31348	T-cell receptor CD
1159	66.5	3.8	417	2	A27775	phosphoglycerate k	1232	66	3.7	192	2	B75144	hypothetical prote
1160	66.5	3.8	422	1	BVBWMS	Ms11 protein - yea	1233	66	3.7	216	2	S69130	Ig lambda chain (D
1161	66.5	3.8	438	2	A97590	hypothetical prote	1234	66	3.7	226	2	T38234	hypothetical prote
1162	66.5	3.8	438	2	AH2811	Arpase, AAA family	1235	66	3.7	255	2	H72539	probable 4-nitroph
1163	66.5	3.8	438	2	A82262	conserved hypothet	1236	66	3.7	261	2	G87608	hypothetical prote
1164	66.5	3.8	442	2	BES211	chorismate lyase u	1237	66	3.7	272	2	T10116	replication protei
1165	66.5	3.8	453	2	A89873	hypothetical prote	1238	66	3.7	281	2	G71095	hypothetical prote
1166	66.5	3.8	461	2	D96835	probable cyclin, 4	1239	66	3.7	307	2	A71602	hypothetical prote
1167	66.5	3.8	463	2	T26655	hypothetical prote	1240	66	3.7	324	2	S66435	hypothetical prote
1168	66.5	3.8	475	2	A54879	pregnancy-specific	1241	66	3.7	362	2	T04079	ferredoxin 35.5k
1169	66.5	3.8	491	2	D91217	ketol-acid reducto	1242	66	3.7	376	2	T19186	hypothetical prote
1170	66.5	3.8	491	2	B86063	ketol-acid reducto	1243	66	3.7	381	2	AE2197	ABC transport prot
1171	66.5	3.8	497	2	JB0275	voltage-gated pola	1244	66	3.7	400	2	T24890	hypothetical prote
1172	66.5	3.8	532	2	T15354	hypothetical prote	1245	66	3.7	406	2	H64793	yeDn protein - Bsc
1173	66.5	3.8	542	2	A49114	protein-tyrosine k	1246	66	3.7	406	2	A99709	hypothetical prote
1174	66.5	3.8	549	2	H64992	hypothetical prote	1247	66	3.7	417	1	S22784	acetyl-CoA C-acylt
1175	66.5	3.8	553	2	T15220	hypothetical prote	1248	66	3.7	428	2	T14529	S-lucos-specific g
1176	66.5	3.8	557	2	S21596	extracellular prote	1249	66	3.7	432	2	T05236	hypothetical prote
1177	66.5	3.8	592	2	S25705	Ig mu chain - shae	1250	66	3.7	448	2	G83818	hypothetical prote
1178	66.5	3.8	616	2	G64160	GTP-binding protei	1251	66	3.7	451	2	T30603	perlecan homolog 2
1179	66.5	3.8	636	2	H87789	protein C34G6.1 [i	1252	66	3.7	457	2	D69059	glycanamide ribonu
1180	66.5	3.8	656	1	S59631	endo-1,4-beta-xyla	1253	66	3.7	459	2	T08594	probable sulfate a
1181	66.5	3.8	679	2	C71007	probable formate d	1254	66	3.7	466	2	T27120	hypothetical prote
1182	66.5	3.8	697	2	B98063	exo-alpha-stalida	1255	66	3.7	469	2	E70076	arabian endo-1,5-
1183	66.5	3.8	709	2	A53364	cacinoembryonic a	1256	66	3.7	471	2	S14165	cyclin B1 - yeast
1184	66.5	3.8	718	1	VCPVIM	coat protein VP1 -	1257	66	3.7	489	1	VGBETA	glycoprotein A - t
1185	66.5	3.8	773	2	S46011	probable pre-mRNA-	1258	66	3.7	495	2	C71679	UDP-n-acetylmutura
1186	66.5	3.8	848	2	C70203	DNA topoisomerase	1259	66	3.7	525	2	S55099	GMP synthase (glut
1187	66.5	3.8	862	2	B36786	hypothetical prote	1260	66	3.7	532	1	B34104	protein-tyrosine k
1188	66.5	3.8	917	2	I48950	telencephalin prec	1261	66	3.7	532	1	A34104	protein-tyrosine k
1189	66.5	3.8	921	2	T51136	ionotropic glutama	1262	66	3.7	538	2	UC2457	vascular cell adhe
1190	66.5	3.8	923	2	C86394	meiotic recombinat	1263	66	3.7	545	2	D81973	probable integrat
1191	66.5	3.8	969	2	C86394	protein T24P3.14	1264	66	3.7	550	2	I37579	Digeorge syndrome
1192	66.5	3.8	1005	2	S73711	probable lipoprote	1265	66	3.7	553	2	T48486	ABC transporter. A
1193	66.5	3.8	1009	2	JH0266	glutamate receptor	1266	66	3.7	580	2	H72270	hypothetical prote
1194	66.5	3.8	1044	2	T10050	integrin alpha-v c	1267	66	3.7	589	2	B90605	sulfur oxidation p
1195	66.5	3.8	1061	2	JC7116	Xeal-3 protein - A	1268	66	3.7	592	2	E70455	hypothetical prote
1196	66.5	3.8	1080	2	A35088	phycobilisome link	1269	66	3.7	603	2	S03020	dopamine beta-mono
1197	66.5	3.8	1097	2	T45622	hypothetical prote	1270	66	3.7				



1271	66	3.7	624	2	D84986	1344	65.5	3.7	237	2	G87286	conserved hypotet
1272	66	3.7	631	2	I52257	1345	65.5	3.7	254	1	VCCVTY	coat protein - tob
1273	66	3.7	640	2	B96784	1346	65.5	3.7	276	1	A69077	conserved hypotet
1274	66	3.7	662	2	T23271	1347	65.5	3.7	283	2	H90409	hypothetical prote
1275	66	3.7	687	2	G81970	1348	65.5	3.7	289	2	B82534	heat shock protei
1276	66	3.7	719	2	S44237	1349	65.5	3.7	290	2	A75497	UDP-N-acetylenolp
1277	66	3.7	738	2	A40096	1350	65.5	3.7	290	2	A34139	concanavalin A pre
1278	66	3.7	747	2	S66959	1351	65.5	3.7	290	2	G71623	rifin PRF0065w - m
1279	66	3.7	750	2	T04010	1352	65.5	3.7	309	2	A29812	sportulation protei
1280	66	3.7	751	2	T01449	1353	65.5	3.7	311	2	F69820	conserved hypotet
1281	66	3.7	754	2	JC4898	1354	65.5	3.7	312	2	G71864	probable chemotact
1282	66	3.7	808	2	D81924	1355	65.5	3.7	323	2	F71130	probable oligopept
1283	66	3.7	810	2	A81965	1356	65.5	3.7	321	2	AD2134	iron(III) dicitrat
1284	66	3.7	815	2	T35970	1357	65.5	3.7	336	2	S42632	Pit-1b protein pre
1285	66	3.7	833	2	T49782	1358	65.5	3.7	344	2	F83620	probable binding p
1286	66	3.7	839	2	T16755	1359	65.5	3.7	379	2	B64300	hypothetical dehydro
1287	66	3.7	851	2	T47495	1360	65.5	3.7	383	2	S47711	hypothetical 39.2K
1288	66	3.7	863	2	A80525	1361	65.5	3.7	383	2	C86020	hypothetical prote
1289	66	3.7	864	2	H85335	1362	65.5	3.7	382	2	C91174	hypothetical prote
1290	66	3.7	864	2	T04518	1363	65.5	3.7	386	2	T25755	hypothetical prote
1291	66	3.7	901	2	A80519	1364	65.5	3.7	393	2	D83589	glutaryl-CoA dehyd
1292	66	3.7	902	2	A60560	1365	65.5	3.7	398	1	G3MSM	Ig gamma-3 chain C
1293	66	3.7	912	1	IYCHCN	1366	65.5	3.7	399	2	B24698	formate dehydrogen
1294	66	3.7	920	2	B84640	1367	65.5	3.7	405	2	D82542	two-component syst
1295	66	3.7	961	2	G90053	1368	65.5	3.7	407	2	A71613	hypothetical prote
1296	66	3.7	974	2	A72012	1369	65.5	3.7	410	1	C69585	alanine transamina
1297	66	3.7	977	2	I45877	1370	65.5	3.7	410	1	B83930	antipeptidase amp
1298	66	3.7	979	2	JH0589	1371	65.5	3.7	410	1	B83930	antipeptidase BH2
1299	66	3.7	979	2	JH0592	1372	65.5	3.7	411	1	QOCVP2	PI polypeptide - m
1300	66	3.7	1006	2	AD2195	1373	65.5	3.7	411	2	F64224	hypothetical prote
1301	66	3.7	1043	2	T15191	1374	65.5	3.7	414	2	B90572	hypothetical prote
1302	66	3.7	1053	2	S72194	1375	65.5	3.7	429	2	S27793	hypothetical prote
1303	66	3.7	1065	2	H95321	1376	65.5	3.7	430	2	G89962	hypothetical prote
1304	66	3.7	1100	2	A35007	1377	65.5	3.7	440	2	S45737	TYA protein - yeas
1305	66	3.7	1105	2	S21173	1378	65.5	3.7	440	2	S49765	TYA protein - yeas
1306	66	3.7	1112	2	T30202	1379	65.5	3.7	447	2	T28207	hypothetical prote
1307	66	3.7	1118	2	S44641	1380	65.5	3.7	452	2	T39751	probable respirato
1308	66	3.7	1139	2	T22811	1381	65.5	3.7	486	2	A11505	conserved hypotet
1309	66	3.7	1207	2	T52459	1382	65.5	3.7	487	2	D70439	hypothetical cell
1310	66	3.7	1223	2	S29717	1383	65.5	3.7	489	2	A47200	EcoA system protei
1311	66	3.7	1232	2	T43027	1384	65.5	3.7	506	2	D71461	hypothetical prote
1312	66	3.7	1242	2	T39453	1385	65.5	3.7	527	2	S37899	hypothetical prote
1313	66	3.7	1248	2	C89874	1386	65.5	3.7	545	2	B88479	protein P470d2.9 l
1314	66	3.7	1335	2	T30211	1387	65.5	3.7	555	2	A30902	inositol-3-phospha
1315	66	3.7	1345	2	T26301	1388	65.5	3.7	561	2	S35637	high mobility grou
1316	66	3.7	1363	2	S44241	1389	65.5	3.7	564	2	A89956	hypothetical prote
1317	66	3.7	1367	2	A41228	1390	65.5	3.7	566	2	F84903	probable ubiquitin
1318	66	3.7	1549	2	D86338	1391	65.5	3.7	575	2	S46692	hypothetical prote
1319	66	3.7	1601	2	T18800	1392	65.5	3.7	582	2	H97326	methyl-accepting c
1320	66	3.7	1750	2	G84649	1393	65.5	3.7	585	2	B83218	hypothetical prote
1321	66	3.7	1792	2	T08878	1394	65.5	3.7	608	1	RD20K1	dihydrofolate redu
1322	66	3.7	1822	2	T14106	1395	65.5	3.7	615	2	T29223	hypothetical prote
1323	66	3.7	1828	2	T41455	1396	65.5	3.7	621	2	T20863	hypothetical prote
1324	66	3.7	1933	2	T30902	1397	65.5	3.7	623	2	AD2295	hypothetical prote
1325	66	3.7	2035	2	AC0233	1398	65.5	3.7	638	2	AH0340	putative autotransp
1326	66	3.7	2041	2	T17439	1399	65.5	3.7	647	1	HHXL70	dnak-type molecula
1327	66	3.7	2041	2	H89960	1400	65.5	3.7	659	2	T05630	hypothetical prote
1328	66	3.7	2186	2	T2347	1401	65.5	3.7	666	2	B86289	probable serine/ch
1329	66	3.7	2347	1	T30201	1402	65.5	3.7	672	2	S75001	hypothetical prote
1330	66	3.7	2352	2	T30201	1403	65.5	3.7	683	2	D82674	TonB-dependent rec
1331	66	3.7	2352	2	T30201	1404	65.5	3.7	683	2	D82674	exo-alpha-silidas
1332	66	3.7	2352	2	T30201	1405	65.5	3.7	694	2	I40866	probable portal pr
1333	66	3.7	2352	2	T30201	1406	65.5	3.7	714	2	B85642	probable portal pr
1334	66	3.7	2352	2	T30201	1407	65.5	3.7	714	2	B85642	probable bi-functi
1335	66	3.7	2352	2	T30201	1408	65.5	3.7	714	2	T34632	probable ABC trans
1336	66	3.7	2352	2	T30201	1409	65.5	3.7	714	2	G84791	hypothetical prote
1337	66	3.7	2352	2	T30201	1410	65.5	3.7	714	2	G84791	hypothetical prote
1338	66	3.7	2352	2	T30201	1411	65.5	3.7	714	2	G84791	hypothetical prote
1339	66	3.7	2352	2	T30201	1412	65.5	3.7	714	2	G84791	hypothetical prote
1340	66	3.7	2352	2	T30201	1413	65.5	3.7	714	2	G84791	hypothetical prote
1341	66	3.7	2352	2	T30201	1414	65.5	3.7	714	2	G84791	hypothetical prote
1342	66	3.7	2352	2	T30201	1415	65.5	3.7	714	2	G84791	hypothetical prote
1343	66	3.7	2352	2	T30201	1416	65.5	3.7	714	2	G84791	hypothetical prote











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Db      163 PORNMSQWNTNLSAPFKCAINPVSKSXTREV-----NCEPKGSPFYVTGAG 213
Qy      232 -LLVPLLSLFLVGLFWLFLKRRROEYLIEKKRVDCRETPNICHSGENTYDTIPT 290
Db      214 GLLVLVLVLF--FCICRRRRRRRRROBELEIASTST-----TYERGKPHS 261
Qy      291 NRTILKEDPANTVYSTEIPKIMENHSLTWEDTP 326
Db      262 T-----PMAAQNQSVLAQAPPPPHHQTPEHRP 290

RESULT 5
RHMUC2
T-cell surface glycoprotein CD2 precursor - human
N.Alternate names: E rosette receptor; erythrocyte receptor; erythrocyte-binding protein
C.Species: Homo sapiens (man)
C.Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C.Accession: A28967; A26486; B26486; A28416; A28023; S02292; A30430; S00829; A29874
R.Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988
A.Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)
A.Reference number: A28967; PMID:88144486; PMID:2894031
A.Accession: A28967
A.Molecule type: DNA
A.Cross-references: UNIPARC:UPI000062209; GB:M19806; GB:J03622; GB:J036
R.Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986
A.Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen.
A.Reference number: A26486; PMID:87041523; PMID:3490670
A.Accession: A26486
A.Molecule type: mRNA
A.Residues: 1-338, 'W', 340, 'QOKTCHPLPIKDKRNCLEF' <SE1>
A.Cross-references: UNIPARC:UPI000004D168
A.Accession: B26486
A.Molecule type: Protein
A.Residues: 25-46 'X', 50 <SE2>
A.Cross-references: UNIPARC:UPI000004D168
R.Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987
A.Reference number: A28416
A.Contents: revision
A.Accession: A28416
A.Molecule type: mRNA
A.Residues: 333-351 <SE3>
A.Cross-references: UNIPARC:UPI0000173764
R.Seed, B.; Aruffo, A.
Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987
A.Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a RAP
A.Reference number: A28023; PMID:87204137; PMID:2437578
A.Accession: A28023
A.Molecule type: mRNA
A.Residues: 1-265, 'Q', 267-351 <SE5>
A.Cross-references: UNIPARC:UPI0000127347; GB:M16445; NID:G178668; PIND:AAAS1738.1; PID:
R.Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; C
Proc. Natl. Acad. Sci. U.S.A. 84, 2941-2945, 1987
A.Title: Molecular cloning and expression of T11 cDNAs reveal a receptor-like structure
A.Reference number: S02292; PMID:87204243; PMID:2883656
A.Accession: S02292
A.Molecule type: mRNA
A.Residues: 1-338, 'W', 340, 'QOKTCHPLPIKDKRNCLEF' <SA1>
A.Cross-references: UNIPARC:UPI000004D168; GB:M16336; NID:G180093; PIND:AAAS1946.1; PID:
A.Accession: A30430
A.Molecule type: Protein
A.Residues: 25-43, 152-163 <SA2>
A.Cross-references: UNIPARC:UPI0000173765
R.Liang, G.; Morton, D.; Owen, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.Y.; Crumpton, M.
EMBO J. 7, 1675-1682, 1988
A.Title: The structure of the human CD2 gene and its expression in transgenic mice.
A.Reference number: S00829; PMID:89005055; PMID:2901953
A.Accession: S00829
A.Molecule type: DNA

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A.Residues: 1-351 <LAN>
A.Cross-references: UNIPARC:UPI0000062209; EMBL:X07871
C.Comment: CD2 is a surface antigen expressed on all peripheral blood T-cells. It appear
or is closely associated with, the erythrocyte receptor.
C.Genetics:
A.Gene: GDB:CD2
A.Cross-references: GDB:118735; OMIM:186990
A.Map position: 1p13.1-1p13.1
A.Introns: 21/1, 128/1, 205/1, 246/1
C.Superfamily: T-cell surface glycoprotein CD2
C.Keywords: glycoprotein; T-cell; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-351/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F:25-206/Domain: extracellular #status predicted <EXT>
F:210-234/Domain: transmembrane #status predicted <TM>
F:237-351/Domain: intracellular #status predicted <INT>
F:89,141,150/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match
Best Local Similarity 7.6%; Score 134; DB 1; Length 351;
Matches 71; Conservative 44; Mismatches 11; Indels 71; Gaps 15;

Qy      28 ELVSGVGAATPEPLAS--KVKQVDSIW--TNTPTVLTIOPEGTIIVTQNRNRVDF 83
Db      32 ERTGALGQDINDIDPSFQMSDDIDDIKWEKTSDDKKKIQFRKEKTF--KEDYTKL-F 87
Qy      84 PDGAGYSLKSLKKNDGSIYVGIYSSSLQGPSTOEYLVHVEHLSKPKVTGLQSNKNG 143
Db      86 KNG--TLKIKHLKTDODIYKVSITDTGKAVLAKIFDLKIERSKPKISM----- 137
Qy      144 TCV-TNLTCMEHGEVDIYTWKALQAANESHNGSLPISNR-----WGSS-DMTFICV 196
Db      138 TCINTTLTCEVNWNGTDPDL-----NLQDGHKLKSGRVITHKWTSLSAFKCT 187
Qy      197 ANNPVSKNPS-SPI-----LAKLCEGAADDPSSMTVLCILVPLLSLFLVGL 245
Db      188 AGNKVSKSVSPVASCPEKGLDIYLIIGCGGS-----LLMFVAL 230
Qy      246 FLMFLKREROBEYIEKKRVDCRETPNICHSGENTYDTIPTNRTILKEDPANT 302
Db      231 VYITTRKKQ-----RSRRNDELSTR--AHRVATBERGRPHQIPASTPQNPATS 279

RESULT 6
S01299
OX-45 membrane glycoprotein precursor - rat
N.Alternate names: MRC OX-45 antigen
C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C.Accession: S01299
R.Killeen, N.; Moesner, R.; Arvieux, J.; Willis, A.; Williams, A.F.
EMBO J. 7, 3087-3091, 1988
A.Title: The MRC OX-45 antigen of rat leukocytes and endothelium is in a subset of the i
A.Reference number: S01299; PMID:89030603; PMID:3181129
A.Accession: S01299
A.Molecule type: mRNA
A.Residues: 1-240 <LIU>
A.Cross-references: UNIPARC:P10252; UNIPARC:UPI0000127370; EMBL:X13016; NID:G56804; PIND:
C.Superfamily: B-cell surface glycoprotein blast-1
C.Keywords: glycoprotein; membrane protein; surface antigen
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-240/Product: OX-45 membrane glycoprotein (asn) (covalent) #status predicted
F:38,97,140,186,203/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match
Best Local Similarity 7.6%; Score 134; DB 2; Length 240;
Matches 48; Conservative 33; Mismatches 104; Indels 10; Gaps 4;

Qy      13 IIMOLTGSAAAGPVKELVSY-----GGAATPE-LNSKVVQVDSIYTWNTPTVLTIOPEG 67
Db      11 ILESLLSLVTFQDSVPVNAITGSNTTLTLKHPLASIYORLITWHTTNQKILEYFN 70
Qy      68 GTIIVTQNRNRERVDPPDGYSLSKLKNDGSIYVGIYSSSLQGPSTOEYLVHVEH 127

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Db      71 GKKTPESFVKORVDIDKTNGLARITVNSKEDGVDYMMHLHETEDQ---WKITMEVYL 127
      128 LSKPKVTMGLQSNKNGTCVTNLTCCEHGEEDVITYWKALGOANESHNGSILPISMRWG 187
      128 VSKPAIKIEKTKNLJDSCHLRLSCKVE--DQGVDTYTWYEDSGPFPQRNGYVLEITITPH 185
Qy      188 ESDMTFICVARNPV 202
      186 NKSTFYTCCVSNPV 200
      186 NKSTFYTCCVSNPV 200

RESULT 7
NRRTCT2
T-cell surface glycoprotein CD2 precursor - rat
N.Alternate names: CD2 antigen; OX-34 antigen
N.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text_change 25-Oct-1996
C.Accession: A33071; B27560; A27560; A32346
R.Barclay, A.N.; Williams, A.F.
submitted to the EMBL Data Library, May 1987
A.Reference number: A33071
A.Accession: A33071
A.Molecule type: mRNA
A.Residues: 1-344 <BAR>
A.Cross-references: UNIPARC:UPI0000173766
R.Williams, A.F.; Barclay, A.N.; Clark, S.J.; Paterson, D.J.; Willis, A.C.
J. Exp. Med. 165, 368-380, 1987
A.Title: Similarities in sequences and cellular expression between rat CD2 and CD4 antigen
A.Reference number: A27560; MUID:87139793; PMID:3102667
A.Accession: B27560
A.Molecule type: protein
A.Residues: 'X',24-52,'X',54-55,'X',57-62,93-109,119-150,238-245 <W1>
A.Cross-references: UNIPARC:UPI0000173767; UNIPARC:UPI0000173768; UNIPARC:UPI0000173769;
A.Accession: A27560
A.Molecule type: mRNA
A.Residues: 44-344 <W12>
A.Cross-references: UNIPARC:UPI0000173767; UNIPARC:UPI0000173768; UNIPARC:UPI0000173769;
A.Accession: A27560
A.Molecule type: mRNA
A.Residues: 1-33,'H',35-41 <HR1>
A.Cross-references: UNIPARC:UPI000017376C; GB:X05111
C.Keywords: T-cell surface glycoprotein CD2
C.Keywords: glycoprotein; T-cell; transmembrane protein
F.1-22/Domain: signal sequence #status predicted <Sig>
F.23-344/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F.23-199/Domain: extracellular #status predicted <EXT>
F.200-228/Domain: transmembrane #status predicted <TM>
F.229-344/Domain: intracellular #status predicted <INT>
F.99,106,134/Binding site: carbohydrate (Aan) (covalent) #status experimental

Query Match
Best Local Similarity 7.3%; Score 130; DB 1; Length 344;
Matches 65; Conservative 51; Mismatches 112; Indels 62; Gaps 13;

Qy      12 YILMOLVTSAA---SGPYKELVSGVAVTPELKSQVDSIVTFTPTPLVTIQPG 67
      10 FLLFSLSSKGDORDBDGTWVGALGR-GIMLNIPNFQMTDDIDBVRW-----BR 56
      68 GTIITQNRNRERVDPPDGY-----SLKSLKKNDSGIYVGYSSSLQDPSTQEV 121
      57 GSTLVAEPFRKMKPFKSGAFETILANGDKIKNLTDDSDGTYNVTVYSTNGRIILDKALD 116
      122 LHVYHLTSKPKVTMGLQSNKNGTCV---TNLTCCMEHGEEDVITYWKALGOANESHNG 177
      117 LRILEWVSGPMIYMEC-SNAITLTCEVLEBGTDAVKIKYQGEHL-----RSIRQKT----- 165
      178 SILPISMRWGESDMTFICVARNPVSRNFSPIIARLCEGAADDPDSMWLLCLLLVPL- 236
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Db      166 ---MSYQNTNLRAPDKCAVNRVSQSEMEVAV-----NCPKSGPLVLYIGVSG 212
      237 -LHSHFVLGLFLMFL-----KRERQEXYIEEK-KRVDICRETPNICPS 278
      213 GILLVFPFGALFIFCICRKRKRNRKRGSELEIKARMSVVERGPK--PHS 260
Qy      213 GILLVFPFGALFIFCICRKRKRNRKRGSELEIKARMSVVERGPK--PHS 260
      213 GILLVFPFGALFIFCICRKRKRNRKRGSELEIKARMSVVERGPK--PHS 260

RESULT 8
JL0143
antigen BCM1 precursor - mouse
N.Alternate names: CD48 antigen homolog sgp-60; OX45 antigen, Blast-1 antigen
C.Species: Mus musculus (house mouse)
C.Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C.Accession: JL0143; S21319; B47469
R.Wong, Y.W.; Williams, A.F.; Kingmore, S.F.; Seidlin, M.F.
J. Exp. Med. 171, 2115-2130, 1990
A.Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 or Blast-1) region on mouse chromosome 3.
A.Reference number: JL0143; MUID:90278362; PMID:1693656
A.Accession: JL0143
A.Molecule type: mRNA
A.Residues: 1-240 <MON>
A.Cross-references: UNIPROT:P18181; UNIPARC:UPI0000003BBF; EMBL:X17501; NID:950134; PIDN
R.Wong, Y.W.; Williams, A.F.; Kingmore, S.F.; Seidlin, M.F.
submitted to the EMBL Data Library, June 1990
A.Description: Structure, expression and genetic linkage of the mouse BCM1 (OX45 or Blast
3 region on mouse chromosome 3.
A.Reference number: S21319
A.Accession: S21319
A.Molecule type: preliminary
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-240 <MON2>
A.Cross-references: UNIPARC:UPI0000003BBF; EMBL:X53526; NID:950138; PIDN:CAA37604.1; PID
R.Cabreiro, J.G.; Freeman, G.J.; Lane, W.S.; Reiser, H.
Proc. Natl. Acad. Sci. U.S.A. 90, 3418-3422, 1993
A>Title: Identification, by protein sequencing and gene transfection, of sgp-60 as the m
A.Reference number: A47469; MUID:93234508; PMID:8475091
A.Accession: A47469
A.Molecule type: protein
A.Residues: 74-80 <CAB>
A.Cross-references: UNIPARC:UPI0000176785
A.Experimental source: EL-4 lymphoma cells
A>Note: sequence extracted from NCBI backbone (NCBIP:129658)
A.Accession: B47469
A.Molecule type: protein
A.Residues: 84-98 <CA2>
A.Cross-references: UNIPARC:UPI0000176786
A.Experimental source: EL-4 lymphoma cells
A>Note: sequence extracted from NCBI backbone (NCBIP:129660)
C.Comment: This antigen is widely expressed on leukocytes and is likely to be anchored t
C.Keywords: B-cell surface glycoprotein blast-1
C.Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F.1-22/Domain: signal sequence #status predicted <Sig>
F.23-217/Product: antigen BCM1 #status predicted <MAT>
F.218-240/Domain: carboxyl-terminal propeptide #status predicted <CPT>
F.32,38,70,136,186,203/Binding site: carbohydrate (Aan) (covalent) #status predicted
F.217/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match
Best Local Similarity 7.1%; Score 126.5; DB 2; Length 240;
Matches 52; Conservative 45; Mismatches 125; Indels 21; Gaps 8;

Qy      7 CLTIYIIMOLVGSAAASGPYKELVSGVAVTPEL-KSKVKQVDSIVTFTPTPLVTIQP 65
      9 CLVLELILPLDTGTGQGHISIPDINATTSNVTLKHKDPLGYKAITWLHTKQKILEYN 68
      66 EGGTIIVTQNRNRERVDPPDGYSLKSLKKNDSGIYVGYSSSLQDPSTQ-EXVLAV 124
      69 YNSTKTFSEPKGVYLEENNNGALHISVVRKEDGTYTMRV---LRTEHLEKLTLEV 124
      125 YHLSKPKVTMGLQSNKNGTCVTNLTCCEHGEEDVITYWKALGOANESHNGSILPISW 184
```



Db 125 FDPVPPKSEIEINKTEASTDSCHLRISC--EYKQDHVDYTWYSSGPPKSPGYVLDLIIV 182  
Qy 185 RWGSDMTFICVARNPVSARN-----FSSPI-LARK-LCEGAADPDSSWVLCLLIVPL 236  
Db 183 TPQNSTFYTCQVSNPVSXKDDTYFTLPCLDARSSGCMWA-----TWLVVTTLIHRI 237  
Qy 237 LLS 239  
Db 238 LLT 240

## RESULT 9

bilialy glycoprotein h precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: JH0395  
R:Kuraki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.  
Biochem. Biophys. Res. Commun. 176, 578-585, 1991  
A>Title: Three novel molecular forms of bilialy glycoprotein deduced from cDNA clones fr  
A:Reference number: JH0394; MUID:91222218; PMID:2025273  
A:Accession: JH0395  
A:Molecule type: mRNA  
A:Residues: 1-321 <KUR>  
A:Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A625; GB:M69176; NID:G179434; PIDN:  
A:Experimental source: leukocyte  
C:Comment: Bilialy glycoproteins belong to the carcinoembryonic antigen gene family.  
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi  
C:Keywords: glycoprotein; transmembrane protein  
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-321/Product: bilialy glycoprotein h #status predicted <MAT>  
F:160-217/Domain: immunoglobulin homology <IMM1>  
F:252-301/Domain: immunoglobulin homology <IMM2>  
Query Match 7.1%; Score 125.5; DB 2; Length 321;  
Best Local Similarity 25.1%; Pred. No. 0.01;  
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;  
Qy 68 GTIIIVTQ-----NRNRERDPDGYSLSKLKKNDSGIYVGYSSSL-QQPSIQE 119  
Db 81 GYALGTQATGPGANSGEETI-YRNA--SLIQNVNTQNDTFYTLQVTKSLDVNEBATGQ 137  
Qy 120 YVLHVEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHGEEDVITYWKALGQANESHNGSI 179  
Db 138 F--HYVPELPKPSISNSNSNPVEDKDAVAFTC--EPETQDTTYLMMI-----NNQS 184  
Qy 180 LPISMRW-----GESDMTFICVARN-----NPVSRNFSPIILARKLCEG-----A 218  
Db 185 LPVSPRLQLSNGNRTLLTSLVTRNDGPECEIQNPVSANRSDPV-TLVVYGPDPPTIS 243  
Qy 219 ADD-----PDSSMWLCLLL--VPLLSLFLVGLFLMFLKREGEYIEKKRVDCRPT 272  
Db 244 PSDTYRFGANLSISCYAASNPPAQSILWLTGTF---QOSTQELFLI-----P 287  
Qy 273 NI-CPHSGENTY--DTIPHTNRTILK 296  
Db 288 NITVNNSSSYTCNANNSVTGCRRTTVK 314  
RESULT 10  
JH0396  
bilialy glycoprotein i precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: JH0396  
R:Kuraki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.  
Biochem. Biophys. Res. Commun. 176, 578-585, 1991  
A>Title: Three novel molecular forms of bilialy glycoprotein deduced from cDNA clones fr  
A:Reference number: JH0394; MUID:91222218; PMID:2025273  
A:Accession: JH0396  
A:Molecule type: mRNA  
A:Residues: 1-351 <KUR>

A:Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A626; GB:M72238; NID:G179436; PIDN:  
A:Experimental source: leukocyte  
C:Comment: Bilialy glycoproteins belong to the carcinoembryonic antigen gene family.  
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi  
C:Keywords: glycoprotein; transmembrane protein  
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-351/Product: bilialy glycoprotein i #status predicted <MAT>  
F:160-217/Domain: immunoglobulin homology <IMM1>  
F:252-301/Domain: immunoglobulin homology <IMM2>

## Query Match 7.1%; Score 125.5; DB 2; Length 351;

Best Local Similarity 25.1%; Pred. No. 0.011;  
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

Qy 68 GTIIIVTQ-----NRNRERDPDGYSLSKLKKNDSGIYVGYSSSL-QQPSIQE 119  
Db 81 GYALGTQATGPGANSGEETI-YRNA--SLIQNVNTQNDTFYTLQVTKSLDVNEBATGQ 137  
Qy 120 YVLHVEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHGEEDVITYWKALGQANESHNGSI 179  
Db 138 F--HYVPELPKPSISNSNSNPVEDKDAVAFTC--EPETQDTTYLMMI-----NNQS 184  
Qy 180 LPISMRW-----GESDMTFICVARN-----NPVSRNFSPIILARKLCEG-----A 218  
Db 185 LPVSPRLQLSNGNRTLLTSLVTRNDGPECEIQNPVSANRSDPV-TLVVYGPDPPTIS 243  
Qy 219 ADD-----PDSSMWLCLLL--VPLLSLFLVGLFLMFLKREGEYIEKKRVDCRPT 272  
Db 244 PSDTYRFGANLSISCYAASNPPAQSILWLTGTF---QOSTQELFLI-----P 287  
Qy 273 NI-CPHSGENTY--DTIPHTNRTILK 296  
Db 288 NITVNNSSSYTCNANNSVTGCRRTTVK 314

## RESULT 11

bilialy glycoprotein g precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: JH0394  
R:Kuraki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.  
Biochem. Biophys. Res. Commun. 176, 578-585, 1991  
A>Title: Three novel molecular forms of bilialy glycoprotein deduced from cDNA clones fr  
A:Reference number: JH0394; MUID:91222218; PMID:2025273  
A:Accession: JH0394  
A:Molecule type: mRNA  
A:Residues: 1-417 <KUR>  
A:Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A624; GB:M72238; NID:G179436; PIDN:  
A:Experimental source: leukocyte  
C:Comment: Bilialy glycoproteins belong to the carcinoembryonic antigen gene family.  
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi  
C:Keywords: glycoprotein; transmembrane protein  
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-383/Product: bilialy glycoprotein g #status predicted <MAT>  
F:160-217/Domain: immunoglobulin homology <IMM1>  
F:252-301/Domain: immunoglobulin homology <IMM2>  
F:341-398/Domain: immunoglobulin homology <IMM3>  
Query Match 7.1%; Score 125.5; DB 2; Length 417;  
Best Local Similarity 25.1%; Pred. No. 0.014;  
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;  
Qy 68 GTIIIVTQ-----NRNRERDPDGYSLSKLKKNDSGIYVGYSSSL-QQPSIQE 119  
Db 81 GYALGTQATGPGANSGEETI-YRNA--SLIQNVNTQNDTFYTLQVTKSLDVNEBATGQ 137  
Qy 120 YVLHVEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHGEEDVITYWKALGQANESHNGSI 179  
Db 138 F--HYVPELPKPSISNSNSNPVEDKDAVAFTC--EPETQDTTYLMMI-----NNQS 184



Qy 180 LPISMRW---GESDMPTICVAR-----NPVSRRNPSSPILAKLCEG-----A 218  
 Db 185 LPVSPRLQLSGNRRNLTLTSLVRNDTGPCEBICQNPVANSNDPV-TLNVVYGPPTPTIS 243  
 Qy 219 ADD-----PDSSMWLLCLLL--VPLLSLFVLGLFLMFLKREKQOEYIEKKRVDCRETP 272  
 Db 244 PSDTYRRGANVLISCYAASNPAPYSWLNGTF---QOSTQELFI-----P 287  
 Qy 273 NI-CPHSGENTREY--DTIPHTNRITLK 296  
 Db 288 NITVNNSSGYTCNANNSTYGCNRTTVK 314

# RESULT 12 C30127

transmembrane carcinoembryonic antigen 3 precursor - human  
 N:Alternate names: CD66 splice form BGPC  
 C:Species: Homo sapiens (man)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C:Accession: C30127; 152597  
 J:Barnett, T.R.; Kreischer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; K  
 J. Cell Biol. 108, 267-276, 1989  
 A>Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs  
 A:Reference number: A92752; MUID:89139550; PMID:2537311  
 A:Accession: C30127  
 A:Molecule type: mRNA  
 A:Residues: 1-464 <BAR>  
 A:Cross-references: UNIPROT:O16170; UNIPARC:UPI0000072309; EMBL:X16356; EMBL:X14784  
 R:Watt, S.M.; Fawcett, J.; Murdoch, S.J.; Teixeira, A.M.; Geschmeissner, S.E.; Hajibagher  
 Blood 84, 200-210, 1994  
 A>Title: CD66 identifies the biliary glycoprotein (BGP) adhesion molecule: cloning, expr  
 A:Reference number: 152597; MUID:94289702; PMID:8018919  
 A:Accession: 152597  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-464 <RES>  
 A:Cross-references: UNIPARC:UPI0000072309; GB:S71326; NID:9550030; PIDN:AAB31183.1; PID:  
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi  
 C:Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein  
 F:1-38/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>  
 F:1-34/Domain: signal sequence #status predicted <SIG>  
 F:35-464/Product: transmembrane carcinoembryonic antigen 3 #status predicted <MAT>  
 F:160-217/Domain: immunoglobulin homology <IMM1>  
 F:252-301/Domain: immunoglobulin homology <IMM2>  
 F:341-398/Domain: immunoglobulin homology <IMM3>  
 F:424-455/Domain: transmembrane #status predicted <TM>  
 F:104, 111, 115, 152, 182, 197, 208, 224, 232, 254, 274, 288, 292, 302, 309, 345, 351, 363, 378, 405/Bindin

Query Match 7.1%; Score 125.5; DB 2; Length 464;  
 Best Local Similarity 25.1%; Pred. No. 0.016;  
 Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;  
 Qy 68 GTTIVTQ-----NRNRERDFPDGYSILKSKKNDSGIYVGISSSL-QQPSIQE 119  
 Db 81 GYAIGTQATGPGPANSGRETI-YFNA--SLIQTONTQDTPGYTLQVTKSDLVMEARQ 137  
 Qy 120 YLVHYEHLSPKPYTMGLQSNNGGTCVNTLTCCMEHGEBDVTYTKALGOANESHNSI 179  
 Db 138 F-HVPELPKPKSSISNNSNPVEDKDAVAFTC--EPETQDTTYLWMT-----NNOS 184  
 Qy 180 LPISMRW---GESDMPTICVAR-----NPVSRRNPSSPILAKLCEG-----A 218  
 Db 185 LPVSPRLQLSGNRRNLTLTSLVRNDTGPCEBICQNPVANSNDPV-TLNVVYGPPTPTIS 243  
 Qy 219 ADD-----PDSSMWLLCLLL--VPLLSLFVLGLFLMFLKREKQOEYIEKKRVDCRETP 272  
 Db 244 PSDTYRRGANVLISCYAASNPAPYSWLNGTF---QOSTQELFI-----P 287  
 Qy 273 NI-CPHSGENTREY--DTIPHTNRITLK 296  
 Db 288 NITVNNSSGYTCNANNSTYGCNRTTVK 314

RESULT 13  
 A32164  
 biliary glycoprotein 1 precursor, splice form a - human  
 N:Alternate names: transmembrane carcinoembryonic antigen 1 (TM1-CEA); transmembrane car  
 N:Contents: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice form x  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
 C:Accession: A32164; B30127; A48078; S45664; S65939; A30847; G44476  
 R:Hindoda, Y.; Neumaier, M.; Hefter, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefter,  
 Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989  
 A:Reference number: A32164  
 A:Contents: erratum  
 A:Accession: A32164  
 A:Molecule type: mRNA  
 A:Residues: 1-526 <HIN>  
 A:Cross-references: UNIPROT:P13688; UNIPARC:UPI0000127483; GB:J03858; NID:9179439; PIDN:  
 R:Hindoda, Y.; Neumaier, M.; Hefter, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefter,  
 Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988  
 A>Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure of  
 A:Reference number: A94206; MUID:88320555; PMID:2457922  
 A:Contents: annotation  
 A>Note: the sequence shown in this reference has been completely corrected in reference  
 R:Barnett, T.R.; Kreischer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; K  
 U. Cell Biol. 108, 267-276, 1989  
 A>Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs  
 A:Reference number: A92752; MUID:89139550; PMID:2537311  
 A:Accession: A30127  
 A:Molecule type: mRNA  
 A:Residues: 1-526 <BAR1>  
 A:Cross-references: UNIPARC:UPI0000127483; EMBL:X16354; NID:937197; PIDN:CAA34404.1; PID  
 A:Experimental source: splice form a  
 A:Accession: B30127  
 A:Molecule type: mRNA  
 A:Residues: 1-319, 'D', 417-526 <BAR2>  
 A:Cross-references: UNIPARC:UPI0000079D2E; EMBL:X14831; NID:937199; PIDN:CAA32940.1; PID  
 A:Experimental source: splice form b  
 R:Barnett, T.R.; Drake, L.; Pickle II, W.  
 Mol. Cell. Biol. 13, 1273-1282, 1993  
 A>Title: Human biliary glycoprotein gene: characterization of a family of novel alternat  
 A:Reference number: A48078; MUID:93140765; PMID:8423792  
 A:Accession: A48078  
 A:Molecule type: mRNA  
 A:Residues: 124-141, 'H', 417-526 <BAR3>  
 A:Cross-references: UNIPARC:UPI0000173868; GB:M76742; NID:9179480; PIDN:AA57142.1; PID:  
 A:Experimental source: splice form x  
 A>Note: sequence extracted from NCBI backbone (NCBI:123602, NCBI:P.123606)  
 A>Note: neither the complete nucleic acid sequence nor the complete translation are show  
 R:Hauck, W.; Nedellec, P.; Turbide, C.; Scannery, C.P.; Barnett, T.R.; Beauchemin, N.  
 Eur. J. Biochem. 223, 529-541, 1994  
 A>Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene faml  
 A:Reference number: S45664; MUID:94333343; PMID:8055923  
 A:Accession: S45664  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-21 <HAU>  
 A:Cross-references: UNIPARC:UPI000006B9AC; EMBL:X67277; NID:929447; PIDN:CAA47694.1; PID  
 R:Nedellec, P.; Turbide, C.; Beauchemin, N.  
 Eur. J. Biochem. 231, 104-114, 1995  
 A>Title: Characterization and transcriptional activity of the mouse biliary glycoprotein  
 A:Reference number: S65939; MUID:95354678; PMID:7628460  
 A:Accession: S65939  
 A:Status: preliminary; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-21 <NED>  
 A:Cross-references: UNIPARC:UPI000006B9AC; EMBL:X67277; NID:929447; PIDN:CAA47694.1; PID  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992  
 R:Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.  
 Genomics 14, 384-390, 1992  
 A>Title: Identification of three new genes and estimation of the size of the carcinoembri  
 A:Reference number: A44476; MUID:93052339; PMID:1427854  
 A:Contents: annotation; alignment of related sequences  
 C:Genetics:



A:Gene: GDB:BCP  
 A:Cross-references: GDB:127992; OMIM:109770  
 A:Map position: 19q13.2-19q13.2  
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin  
 C:Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein  
 F:1-138/Domain: signal sequence #status predicted <SIG>  
 F:1-34/Domain: biliary glycoprotein 1, splice form a #status predicted <MAT>  
 F:35-526/Domain: extracellular #status predicted <EXT>  
 F:35-319,'D',417-526/Product: biliary glycoprotein 1, splice form b #status predicted <M  
 F:35-141,'H',417-526/Product: biliary glycoprotein 1, splice form x #status predicted <M  
 F:160-217/Domain: immunoglobulin homology <IMM1>  
 F:252-301/Domain: immunoglobulin homology <IMM2>  
 F:341-398/Domain: immunoglobulin homology <IMM3>  
 F:425-454/Domain: transmembrane #status predicted <TM>  
 F:455-526/Domain: intracellular #status predicted <INT>  
 F:104,111,115,152,182,197,208,224,232,254,274,286,292,302,309,345,351,363,378,405,475/BI

Query Match 7.1%; Score 125.5; DB 1; Length 526;  
 Best Local Similarity 25.1%; Pred. No. 0.018;  
 Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

Qy 68 GTIIVTQ-----NRNERVDFPDGYSLSKSKKNDGIIYVGIYSSSL-QQPSFOE 119  
 Db 81 GYALIGTQATPGPANSGRETT-YFNA--SLIIQNTQNDTGFYTLQVTKSDLVNKEATGQ 137  
 Qy 120 YLVHYEHLSKPKYTMGLQSNKNGCVNLTCCMHGSEDDVLYTMKALGQANESHNSI 179  
 Db 138 F--HYPELPKPSISSSNSNPVEDKDAVAFTC--EPETQDTTYLWMT-----NNQS 184  
 Qy 180 LPISRW-----GESDMEFICVAR-----NPVSRNFSSPIARKLCEG-----A 218  
 Db 185 LPVSPRLQLSNKNRITLTILSTRNDTGYECEIQNPVANSNDPV-TLNTVYGGPTPTIS 243  
 Qy 219 ADD---PDSSMWLLCLLL--VPLLLSLFVLGLFWLTKRRQOEYIEKKRVDCRETP 272  
 Db 244 PSDTYRPGANILSLSCVAASNPDAQYSLINGTF---QGSTQELFI-----P 287  
 Qy 273 NI-CPHSGENTY--DTIPHNRTILK 296  
 Db 288 NITVNSGSYTCVHANSVTCGNKRTIVK 314

RESULT 14  
 A27681  
 nonpecific cross-reacting antigen precursor - human  
 N:Alternate names: NCA; TEX/NCA  
 C:Species: Homo sapiens (man)  
 C>Date: 31-Mar-1989 #sequence revision 16-Sep-1992 #text change 09-Jul-2004  
 C:Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; B44476; F44  
 R:Oikawa, S.; Kosaki, G.; Nakazato, H.  
 Biochem. Biophys. Res. Commun. 146, 464-469, 1987  
 A:Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene  
 A:Reference number: A26902; MUID:87298464; PMID:3618991  
 A:Accession: A26902  
 A:Molecule type: DNA  
 A:Residues: 1-141 <OIK>  
 A:Cross-references: UNIPROT:Q13774; UNIPARC:UPI000072416; GB:M17082; NID:G180230; PIDN:  
 R:Thompson, J.A.; Pandey, H.; Paxton, R.J.; Shively, L.; Padma, A.; Stimmer, R.L.; Todd, C  
 Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987  
 A:Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene faml  
 A:Reference number: A29875; MUID:87204248; PMID:3033672  
 A:Accession: A29875  
 A:Molecule type: DNA  
 A:Residues: 23-141 <THO>  
 A:Cross-references: UNIPARC:UPI0000177070; GB:M16337  
 A>Note: the authors translated the codon ACT for residue 64 as Tyr  
 R:Ikemargi, Y.; Oikawa, S.; Matsuo, Y.; Kosaki, G.; Nakazato, H.  
 Biochem. Biophys. Res. Commun. 150, 89-96, 1988  
 A:Title: Primary structure of non-specific cross-reacting antigen (NCA), a member of carc  
 A:Reference number: A27681; MUID:88106638; PMID:3337731  
 A:Accession: A27681  
 A:Molecule type: mRNA

A:Residues: 1-238,'V',240-344 <TAN>  
 A:Cross-references: UNIPARC:UPI000012748C; GB:M18728; NID:G189084; PIDN:AAA5907.1; PID:  
 R:Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Eiting, J.J.  
 Genome 3, 59-66, 1988  
 A:Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C  
 A:Reference number: A31037; MUID:89122014; PMID:3220478  
 A:Accession: B31037  
 A:Molecule type: mRNA  
 A:Residues: 1-137,'L',139-344 <BAR>  
 A:Cross-references: UNIPARC:UPI000016AD6C; GB:M29541; NID:G189103; PIDN:AAA59915.1; PID:  
 A>Note: the authors translated the codon TTG for residue 138 as Phe  
 R:Riemann, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Rieger, A.D.; Shively, J.E.  
 J. Biol. Chem. 263, 3202-3207, 1988  
 A:Title: Characterization of a cDNA clone for the non-specific cross-reacting antigen (NC  
 A:Reference number: A29918; MUID:88139389; PMID:2830274  
 A:Accession: A29918  
 A:Molecule type: mRNA  
 A:Residues: 1-344 <NEU>  
 A:Cross-references: UNIPARC:UPI000006DF42; GB:M18216; GB:J03550; NID:G178690; PIDN:AAA51  
 R:Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwalb, H.; von Kleist, S.  
 Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988  
 A:Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and ind  
 A:Reference number: A27709; MUID:88268882; PMID:3390172  
 A:Accession: A27709  
 A:Molecule type: protein  
 A:Residues: 35-95;99-120,123-138;149-151,'X',153-162;166,'X',168-172,'X',174-193;231-235  
 A:Cross-references: UNIPARC:UPI0000177071; UNIPARC:UPI0000177072; UNIPARC:UPI0000177073;  
 078; UNIPARC:UPI0000177079; UNIPARC:UPI000017707A  
 R:Hefta, S.A.; Paxton, R.J.; Shively, J.E.  
 J. Biol. Chem. 265, 8618-8626, 1990  
 A:Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspeci  
 A:Reference number: A36271; MUID:90256782; PMID:2341397  
 A:Accession: A36271  
 A:Molecule type: protein  
 A:Residues: 35-42;44-53;55-80;83-134;139-160;166-172;174-180;191-194;204-224;233-308;310  
 A:Cross-references: UNIPARC:UPI000017707B; UNIPARC:UPI000017707C; UNIPARC:UPI000017707D;  
 082; UNIPARC:UPI0000177083; UNIPARC:UPI0000177084  
 R:Paxton, R.J.; Mosser, G.; Pandey, H.; Lee, T.D.; Shively, J.E.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987  
 A:Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation  
 A:Reference number: A26414; MUID:87147209; PMID:3469650  
 A:Accession: C26414  
 A:Molecule type: protein  
 A:Residues: 35-69 <PAX>  
 A:Cross-references: UNIPARC:UPI0000177085  
 R:Khan, W.N.; Fraengely, L.; Teglund, S.; Israelson, A.; Bremer, K.; Hammastreem, S.  
 Genome 14, 384-390, 1992  
 A:Title: Identification of three new genes and estimation of the size of the carcinoemb  
 A:Reference number: A44476; MUID:93052339; PMID:1427854  
 A:Accession: B44476  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 35-141 <KHA>  
 A:Cross-references: UNIPARC:UPI0000177086  
 A:Accession: P44476  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 35-137,'L',139-141 <KH2>  
 A:Cross-references: UNIPARC:UPI0000177086  
 C:Comment: This protein appears to be processed at the carboxyl terminus and anchored th  
 C:Genetics:  
 A:Gene: GDB:NCA  
 A:Cross-references: GDB:120221; OMIM:163980  
 A:Map position: 19q13.2-19q13.2  
 A:Introns: 22/1  
 A>Note: the list of introns may be incomplete  
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin  
 C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphati  
 F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>  
 F:1-34/Domain: signal sequence #status predicted <SIG>  
 F:35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>  
 F:160-217/Domain: immunoglobulin homology <IMM1>  
 F:252-301/Domain: immunoglobulin homology <IMM2>







## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rnp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 16, 2005, 10:34:22 ; Search time 229 Seconds  
(without alignments)  
1032.105 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 1772  
Sequence: 1 MAGSPCTCLTIYIMQLTGS.....PHSLTMPDPRLPAYENVI 335

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : UniProt\_05.80:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	335	1	SLAF7_HUMAN
2	815	46.0	333	1	SLAF7_MOUSE
3	362.5	20.5	328	2	015430_HUMAN
4	362.5	20.5	329	2	092178_MOUSE
5	359	20.3	339	2	08W18_HUMAN
6	358.5	20.2	645	2	06NZB6_MOUSE
7	358	20.2	345	2	09V1B8_HUMAN
8	354.5	20.0	328	2	06FHA8_HUMAN
9	354.5	20.0	649	2	07TMP7_MOUSE
10	354.5	20.0	654	1	L19_MOUSE
11	353.5	19.9	544	2	08C2D4_MOUSE
12	353.5	19.9	654	2	04VBG4_MOUSE
13	330.5	18.7	289	2	096A28_HUMAN
14	329	18.6	538	2	08C9E4_MOUSE
15	328.5	18.5	289	2	05TRR0_HUMAN
16	318	17.9	655	1	L19_HUMAN
17	315.5	17.8	331	2	05TAT3_HUMAN
18	311.5	17.6	285	2	08BTK0_MOUSE
19	311	17.6	332	1	SLAF6_HUMAN
20	311	17.6	332	2	05TAS4_HUMAN
21	311	17.6	602	2	05VYH7_HUMAN
22	308.5	17.4	285	2	08VE93_MOUSE
23	308	17.4	280	2	095660_HUMAN
24	307.5	17.4	285	2	09D780_MOUSE
25	304	17.2	272	2	09U1B7_HUMAN
26	290.5	16.4	241	2	09U1B6_HUMAN
27	283.5	15.9	526	2	05VYH8_HUMAN
28	281	15.9	197	2	09UIT7_HUMAN
29	260	14.7	177	2	05BKU7_HUMAN
30	250.5	14.1	214	2	05H9R1_HUMAN
31	238.5	13.5	424	2	05VYH8_HUMAN

32	225.5	12.7	351	1	SLAF6_MOUSE	09et39 mus musculus
33	214	12.1	167	2	05RB10_PONPY	09et39 mus musculus
34	213.5	12.0	270	2	05VY11_HUMAN	09et39 mus musculus
35	204.5	11.5	338	2	095MM6_BOVIN	09et39 mus musculus
36	199.5	11.3	221	2	05TAS6_HUMAN	09et39 mus musculus
37	187.5	10.6	336	2	09GJ73_SAGO	09et39 mus musculus
38	186	10.5	343	1	SLAF1_MOUSE	09et39 mus musculus
39	186	10.5	343	2	0544K1_MOUSE	09et39 mus musculus
40	183.5	10.4	335	2	096OR3_HUMAN	09et39 mus musculus
41	183	10.3	266	2	09CUC8_MOUSE	09et39 mus musculus
42	182.5	10.3	335	2	SLAF1_HUMAN	09et39 mus musculus
43	182.5	10.3	335	2	05W172_HUMAN	09et39 mus musculus
44	178	10.0	278	1	SLAF8_MOUSE	09et39 mus musculus
45	177	9.7	329	2	05VY15_HUMAN	09et39 mus musculus
46	170	9.6	365	2	05VY12_HUMAN	09et39 mus musculus
47	167.5	9.5	342	1	SLAF1_CANFA	09et39 mus musculus
48	163.5	9.2	370	1	CD244_HUMAN	09et39 mus musculus
49	163.5	9.2	370	2	05VY17_HUMAN	09et39 mus musculus
50	160.5	9.1	338	2	05MB93_BOVIN	09et39 mus musculus
51	159.5	9.0	329	2	05W7A8_XENLA	09et39 mus musculus
52	158.5	8.9	326	2	08CAU4_MOUSE	09et39 mus musculus
53	150.5	8.5	285	1	SLAF8_HUMAN	09et39 mus musculus
54	145.5	8.2	416	2	08N713_HUMAN	09et39 mus musculus
55	145.5	8.2	416	2	0671P8_HUMAN	09et39 mus musculus
56	145	8.2	211	2	06ZRL7_HUMAN	09et39 mus musculus
57	144	8.1	344	1	CD2_MOUSE	09et39 mus musculus
58	144	8.1	344	2	09R201_MOUSE	09et39 mus musculus
59	144	8.1	344	2	05SRG1_MOUSE	09et39 mus musculus
60	142	8.0	307	2	09HBR9_HUMAN	09et39 mus musculus
61	142	8.0	367	2	06ZML4_HUMAN	09et39 mus musculus
62	141	8.0	291	2	05BKJ7_XENTR	09et39 mus musculus
63	139	7.8	347	2	04SQO1_TETNG	09et39 mus musculus
64	138.5	7.8	340	2	0764N3_PIG	09et39 mus musculus
65	138.5	7.8	413	2	064OR3_MOUSE	09et39 mus musculus
66	137.5	7.8	345	2	06SZG3_PANTR	09et39 mus musculus
67	136.5	7.7	351	2	063P96_HUMAN	09et39 mus musculus
68	135.5	7.6	289	2	06QX36_MOUSE	09et39 mus musculus
69	135	7.6	302	2	04SOP0_TETNG	09et39 mus musculus
70	134.5	7.6	198	2	06UWG1_HUMAN	09et39 mus musculus
71	134	7.6	240	1	CD48_RAT	09et39 mus musculus
72	133.5	7.5	351	2	CD2_HUMAN	09et39 mus musculus
73	133.5	7.5	394	2	09EOK9_RAT	09et39 mus musculus
74	133	7.5	422	2	0502A9_BRARE	09et39 mus musculus
75	132.5	7.5	198	2	05JRO9_HUMAN	09et39 mus musculus
76	132.5	7.5	372	1	CAR_BRARE	09et39 mus musculus
77	131	7.4	344	2	0510M6_RAT	09et39 mus musculus
78	131	7.4	525	2	05R9N6_PONPY	09et39 mus musculus
79	130	7.3	249	2	05BD93_BOVIN	09et39 mus musculus
80	130	7.3	344	1	CD2_RAT	09et39 mus musculus
81	128.5	7.2	253	2	028753_GCETA	09et39 mus musculus
82	128	7.2	193	2	06P2J4_HUMAN	09et39 mus musculus
83	126.5	7.1	240	1	CD48_MOUSE	09et39 mus musculus
84	126.5	7.1	240	2	0545F2_MOUSE	09et39 mus musculus
85	126.5	7.1	240	2	06P905_MOUSE	09et39 mus musculus
86	126	7.1	318	2	04T2U2_TETNG	09et39 mus musculus
87	125.5	7.1	368	2	05UB49_HUMAN	09et39 mus musculus
88	125.5	7.1	464	2	016170_HUMAN	09et39 mus musculus
89	125.5	7.1	468	2	096CA7_HUMAN	09et39 mus musculus
90	125.5	7.1	526	1	CEAM1_HUMAN	09et39 mus musculus
91	125	7.1	344	2	06S262_PAPAN	09et39 mus musculus
92	125	7.1	373	2	07KPY5_HUMAN	09et39 mus musculus
93	124.5	7.0	344	1	CEAM6_HUMAN	09et39 mus musculus
94	124.5	7.0	344	2	053XP7_HUMAN	09et39 mus musculus
95	124.5	7.0	344	2	013774_HUMAN	09et39 mus musculus
96	124.5	7.0	461	2	013854_HUMAN	09et39 mus musculus
97	124	7.0	445	2	06S258_MACAS	09et39 mus musculus
98	123.5	7.0	227	2	028754_GCETA	09et39 mus musculus
99	123	6.9	140	2	08BFV0_MOUSE	09et39 mus musculus
100	123	6.9	311	1	CD244_RAT	09et39 mus musculus
101	122.5	6.9	458	2	061351_MOUSE	09et39 mus musculus
102	122.5	6.9	521	2	061352_MOUSE	09et39 mus musculus
103	122	6.9	326	2	09N166_PAPHA	09et39 mus musculus
104	122	6.9	334	2	06S256_MACNE	09et39 mus musculus



105	122	6.9	341	2	Q6SZ57_MACAR	Q6SZ57 macaca arct	178	101	5.7	432	2	Q6DD57_XENIA	Q6dd57 xenopus lae
106	121.5	6.9	377	2	Q80V04_MOUSE	Q80v04 mus musculu	179	101	5.7	436	2	Q6VAN8_BOVIN	Q6van8 bos taurus
107	121.5	6.9	536	2	Q8BJ62_MOUSE	Q8bj62 mus musculu	180	101	5.7	588	1	Q6166_CHICK	P42292 gallus gall
108	121	6.8	351	1	CD2_MACPA	Q6SZ61 spheroide fasc	181	101	5.7	1637	2	Q610Y1_PICTO	Q610y1 pictophilus
109	119.5	6.7	332	2	Q91B08_SPERC	Q91b08 spheroide fasc	182	100.5	5.7	259	2	Q9CF44_LACLA	Q9cf44 lactococcus
110	119.5	6.7	365	1	Q91B08_SPERC	P78310 homo sapien	183	100.5	5.7	280	2	Q8DWM2_ICTPU	Q8dwm2 ictalurus p
111	119.5	6.7	365	1	Q91B08_SPERC	Q91b08 spheroide fasc	184	100.5	5.7	323	2	Q9BDM2_CBRAR	Q9bdm2 cercopithec
112	118.5	6.7	320	2	Q925P2_MOUSE	Q925p2 mus musculu	185	100.5	5.7	340	2	Q4RR79_TETNG	Q4rr79 tetradon n
113	118	6.7	347	2	Q5XG04_XENYR	Q5xg04 xenopus tro	186	100.5	5.7	555	1	Q6166_CARAU	Q61304 carassius a
114	116.5	6.6	319	2	Q9PA33_HUMAN	Q9p9795 homo sapien	187	100	5.6	324	2	Q6JHT1_ASP	Q6jht1 african swi
115	116.5	6.6	319	2	Q5VZP6_HUMAN	Q5vzp6 homo sapien	188	99.5	5.6	318	2	Q5SNB8_BRARE	Q5snb8 brachydiano
116	116.5	6.6	350	2	Q6SZ59_CERTO	Q6sz59 cercocebus	189	99.5	5.6	323	2	Q9BDM9_MACNE	Q9bdm9 macaca neme
117	115	6.5	351	2	Q6SZ60_MACMU	Q6sz60 macaca mula	190	99.5	5.6	335	2	Q9YGV5_CHICK	Q9ygv5 gallus gall
118	115	6.5	357	2	Q90ZU5_ANAPL	Q90z15 anas platyr	191	99.5	5.6	658	2	Q75UX6_DICDI	Q75ux6 dictyosteli
119	114.5	6.5	430	2	Q8N4F1_HUMAN	Q8n4f1 homo sapien	192	99.5	5.6	693	2	Q559P5_DICDI	Q559p5 dictyosteli
120	114.5	6.5	702	1	Q925P3_MOUSE	Q925p3 mus musculu	193	99.5	5.6	3493	2	Q4RJ20_TETNG	Q4rj20 tetradon n
121	114.5	6.5	702	2	Q53G30_HUMAN	Q53g30 homo sapien	194	99	5.6	417	1	PVR_CERAR	P32506 cercopithec
122	114.5	6.5	702	2	Q8N4D0_HUMAN	Q8n4d0 homo sapien	195	98.5	5.6	229	2	Q8BNV8_MOUSE	Q8bnv8 mus musculu
123	114	6.4	239	2	Q4SPD7_TETNG	Q4spd7 tetradon n	196	98.5	5.6	348	2	Q96SRT1_HUMAN	Q96srt1 homo sapien
124	113.5	6.4	454	2	Q91W54_MOUSE	Q91w54 mus musculu	197	98.5	5.6	404	2	Q9GZZ9_HUMAN	Q9gzz9 homo sapien
125	113.5	6.4	454	2	Q91W54_MOUSE	P31809 mus musculu	198	98.5	5.6	526	1	BT1AL_BOVIN	P18892 bos taurus
126	113.5	6.4	521	2	Q925P3_MOUSE	Q925p3 mus musculu	199	98.5	5.6	733	2	Q8S0B3_TRIVU	Q8sqb3 trichosurus
127	113	6.4	373	2	Q9H6B4_HUMAN	Q9h6b4 homo sapien	200	98.5	5.6	1227	2	Q21038_CAEEL	Q21038 caenorhabdi
128	113	6.4	621	2	Q811T7_MOUSE	Q811t7 mus musculu	201	98.5	5.6	16215	2	Q9NFS3_DROME	Q9nfs3 drosophila
129	112.5	6.3	328	1	VSIG2_MOUSE	Q94109 mus musculu	202	98	5.5	347	2	CD2_HORSE	P37998 equus cabal
130	111.5	6.3	431	2	Q5DX21_HUMAN	Q5dx21 homo sapien	203	98	5.5	484	2	Q6BE00_XENIA	Q6be00 xenopus lae
131	111	6.3	372	2	Q8K1G0_RAT	Q8k1g0 rattus norv	204	98	5.5	503	1	SHPS1_HUMAN	P78324 h tyrosine
132	110.5	6.2	463	1	CD4_CANPA	P33705 canis famli	205	98	5.5	581	2	Q4SPF6_TETNG	Q4spf6 tetradon n
133	110.5	6.2	466	2	Q4WT2_P9PIPI	Q4wt2 xenopus gp.	206	98	5.5	1209	2	Q4SPF8_TETNG	Q4spf8 tetradon n
134	110	6.2	539	2	Q8HX06_PIG	Q8hx06 sus scrofa	207	98	5.5	1382	1	MET_RAT	P57522 rattus norv
135	109.5	6.2	432	2	Q61BR1_CANPA	Q61br1 canis famli	208	97.5	5.5	428	2	Q5U2P2_RAT	Q5u2p2 rattus norv
136	109	6.2	316	2	Q8VBE8_MOUSE	Q8vbe8 mus musculu	209	97.5	5.5	474	2	Q7Q815_ANOGA	Q7q815 anogea
137	108.5	6.1	365	1	Q7TPB4_RAT	Q7tpb4 rattus norv	210	97.5	5.5	562	2	Q6YNR7_BRARE	Q6ynr7 brachydiano
138	108	6.1	316	2	Q7TPB4_RAT	Q7tpb4 rattus norv	211	97.5	5.5	591	2	Q6NP04_DROME	Q6np04 drosophila
139	107	6.0	349	2	Q7QJG3_ANOGA	Q7qjg3 anopheles g	212	97.5	5.5	2772	2	Q9VAV4_DROME	Q9vav4 drosophila
140	107	6.0	399	2	Q9ESSE_MOUSE	Q9esse mus musculu	213	97.5	5.5	2776	2	Q869A0_DROME	Q869a0 drosophila
141	106.5	6.0	752	2	Q8YX64_HYDAT	Q8yx64 hydra atten	214	97.5	5.5	2894	2	Q7KRX2_DROME	Q7kxr2 drosophila
142	106.5	6.0	4138	2	Q811Y3_PLAF7	Q811y3 plasmodium	215	97.5	5.5	2898	2	Q668Z9_DROME	Q668z9 drosophila
143	106	6.0	897	2	Q8J1Y3_ARATH	Q8j1y2 arabidopsis	216	97	5.5	452	2	Q5N0Y6_SYNPE	Q5n0y6 synecococc
144	105.5	6.0	323	2	Q6FHB1_HUMAN	Q6fth1 homo sapien	217	97	5.5	484	2	Q64475_SCHAM	Q64475 schistocerc
145	105.5	6.0	329	1	CD86_HUMAN	P42081 homo sapien	218	97	5.5	773	1	Q60HT1_EPTBU	P01832 oryctolagus
146	105.5	6.0	329	2	Q6GTE4_HUMAN	Q6gte4 homo sapien	219	96.5	5.4	347	2	Q6RWT3_BOVIN	Q6rwt3 bos taurus
147	105.5	6.0	335	2	Q9PWR4_CHICK	Q9pwr4 gallus gall	220	96.5	5.4	368	2	Q6RWT4_BOVIN	Q6rwt4 bos taurus
148	105.5	6.0	398	2	Q9J1EI_MOUSE	Q9j1ei mus musculu	221	96.5	5.4	375	2	Q6RWT4_BOVIN	Q6rwt4 bos taurus
149	105	5.9	245	2	Q566N1_BRARE	Q566n1 brachydiano	222	96.5	5.4	402	2	Q4TZL0_ASP	Q4tzl0 african swi
150	105	5.9	397	1	CD244_MOUSE	Q07763 mus musculu	223	96.5	5.4	402	2	Q89501_ASP	Q89501 african swi
151	104.5	5.9	319	2	Q9UTU5_PIG	Q9utu5 sus scrofa	224	96.5	5.4	432	2	Q6RWT5_BOVIN	Q6rwt5 bos taurus
152	104.5	5.9	1271	2	Q8A321_BACTN	Q8a321 bacteroides	225	96.5	5.4	439	2	Q6RWT6_BOVIN	Q6rwt6 bos taurus
153	104.5	5.9	1656	2	Q50S87_ENTHI	Q50s87 entamoeba h	226	96.5	5.4	493	2	Q6PSY4_HUMAN	Q6psy4 homo sapien
154	104	5.9	555	2	Q92018_MOUSE	Q92018 mus musculu	227	96.5	5.4	533	2	Q8NCB6_HUMAN	Q8ncb6 homo sapien
155	104	5.9	435	2	Q9EQCT_MOUSE	Q9eqct mus musculu	228	96.5	5.4	534	2	Q8NB18_HUMAN	Q8nb18 homo sapien
156	104	5.9	1220	2	Q94191_PABAR	Q94191 paracoccidi	229	96.5	5.4	534	2	Q5ZPR3_HUMAN	Q5zpr3 homo sapien
157	103.5	5.8	319	2	Q9UTU0_CANPA	Q9utu0 canis famli	230	96.5	5.4	1896	2	Q91AJ1_XENIA	Q91aj1 xenopus lae
158	103.5	5.8	323	2	Q9BDB8_CERTO	Q9bdb8 cercocebus	231	96	5.4	339	2	Q91A57_SPERC	Q91a57 spheroide fasc
159	103.5	5.8	373	2	Q8R373_MOUSE	Q8r373 mus musculu	232	96	5.4	341	2	Q61354_MOUSE	Q61354 mus musculu
160	103.5	5.8	406	2	Q8N7T8_HUMAN	Q8n7t8 homo sapien	233	96	5.4	359	1	LACH_DROME	Q24372 drosophila
161	103	5.8	1062	2	Q8AXC7_FUGRU	Q8axc7 fuqu rubrip	234	96	5.4	484	2	Q5QSL1_XENYR	Q5qsl1 xenopus tro
162	103	5.8	1078	2	Q8AXC8_FUGRU	Q8axc8 fuqu rubrip	235	96	5.4	494	2	Q4VAN1_HUMAN	Q4van1 homo sapien
163	103	5.8	1479	2	Q7K0T5_DROME	Q7k0t5 drosophila	236	96	5.4	526	1	BT1AL_HUMAN	Q1410 homo sapien
164	102.5	5.8	304	2	Q8USP1_ASP	Q8usp1 african swi	237	96	5.4	526	2	Q4VAN4_HUMAN	Q4van4 homo sapien
165	102.5	5.8	323	2	Q9BDM4_MACMU	Q9bdm4 macaca mula	238	96	5.4	526	2	Q4VAN3_HUMAN	Q4van3 homo sapien
166	102.5	5.8	335	2	Q9YGH1_CHICK	Q9ygh1 gallus gall	239	96	5.4	526	2	Q4VAN2_HUMAN	Q4van2 homo sapien
167	102.5	5.8	359	2	Q4KLE4_XENIA	Q4kle4 xenopus lae	240	96	5.4	1087	1	PEGRA_XENIA	P262179 xenopus lae
168	102.5	5.8	373	2	Q92085_MOUSE	Q92085 mus musculu	241	96	5.4	1451	2	MYOM1_HUMAN	P52179 homo sapien
169	102.5	5.8	519	1	Q94YV0_RAT	P16573 rattus norv	242	96	5.4	1685	2	Q6ZU00_HUMAN	Q6zu00 homo sapien
170	102	5.8	1482	2	Q94YV0_DROME	Q94y40 drosophila	243	96	5.4	1685	2	Q6H969_HUMAN	Q6h969 homo sapien
171	101.5	5.7	761	2	Q22271_ARATH	Q22271 arabidopsis	244	95.5	5.4	304	2	Q6UTH7_ASP	Q6uth7 african swi
172	101	5.7	324	2	Q4SQP3_TETNG	Q4sqp3 tetradon n	245	95.5	5.4	340	2	Q61349_MOUSE	Q61349 mus musculu
173	101	5.7	349	1	Q94YV0_HUMAN	Q94y97 mus musculu	246	95.5	5.4	365	1	Q9JHL7_RAT	P97792 mus musculu
174	101	5.7	349	1	LACH_SCHAM	Q26474 schistocerc	247	95.5	5.4	448	2	Q9JHL7_RAT	Q9jhl7 rattus norv
175	101	5.7	365	2	Q6VAN5_BOVIN	Q6van5 bos taurus	248	95.5	5.4	458	2	Q63093_RAT	Q63093 rattus norv
176	101	5.7	372	2	Q6VAN6_BOVIN	Q6van6 bos taurus	249	95.5	5.4	459	2	Q9JHL6_RAT	Q9jhl6 rattus norv
177	101	5.7	429	2	Q6VAN7_BOVIN	Q6van7 bos taurus	250	95.5	5.4	463	2	Q4VAH7_MOUSE	Q4vah7 mus musculu



251	95.5	5.4	463	2	Q66U72_XENIA	Q66I72_xenopus lae	324	92	5.2	2828	2	Q9NR99_HUMAN	Q9NR99 homo sapien
252	95.5	5.4	628	1	Q7S409_NEUCR	Q7S409 neurospora	325	91.5	5.2	160	2	Q8C254_MOUSE	Q8C254 mus musculus
253	95.5	5.4	700	1	P2PRE_HUMAN	P23469 homo sapien	326	91.5	5.2	226	2	Q8NH11_HUMAN	Q8NH11 homo sapien
254	95.5	5.4	700	2	Q5VMH4_HUMAN	Q5VMH4 homo sapien	327	91.5	5.2	230	2	Q8UV30_BRARE	Q8UV30 brachydanto
255	95.5	5.4	771	1	P1GR_MOUSE	Q70570 mus musculus	328	91.5	5.2	230	2	Q90266_BRARE	Q90266 brachydanto
256	95.5	5.4	822	1	CAN3_SHERP	Q9ctb8 ovys aries	329	91.5	5.2	306	1	B7LA_MOUSE	Q7ceat3 mus musculus
257	95.5	5.4	1684	2	Q7RIAS_PLAYO	Q7RIAS plasmodium	330	91.5	5.2	527	2	Q4SZU1_TETNG	Q4SZU1 tetradodon n
258	95	5.4	316	2	Q6UX12_HUMAN	Q6UX12 homo sapien	331	91.5	5.2	725	2	Q4VWT3_9PIPI	Q4VWT3 xenopus sp.
259	95	5.4	577	2	Q5REH9_PONPY	Q5REH9 pongo pygma	332	91.5	5.2	943	2	Q7PRK4_ANOGA	Q7PRK4 anophelis g
260	95	5.4	589	2	Q5R770_PONPY	Q5R770 pongo pygma	333	91.5	5.2	1079	2	Q9YWS6_MSEPV	Q9YWS6 melanoplus
261	95	5.4	772	2	Q5U495_XENIA	Q5U495 xenopus lae	334	91.5	5.2	3005	2	Q5OLG3_ALTAL	Q5OLG3 alternaria
262	95	5.4	814	1	P1UNC_HUMAN	Q8Iv11 homo sapien	335	91	5.1	308	2	Q6BEV1_XENIA	Q6BEV1 xenopus lae
263	95	5.4	1237	1	Q610C8_CABER	Q610C8 caenothabdi	336	91	5.1	388	2	Q8NC34_HUMAN	Q8NC34 homo sapien
264	94.5	5.3	280	2	Q8UWK3_ICTPU	Q8UWK3 ictalurus p	337	91	5.1	467	2	Q91VT9_MOUSE	Q91VT9 mus musculus
265	94.5	5.3	379	2	Q8BLX5_MOUSE	Q8BLX5 mus musculus	338	91	5.1	467	2	Q8CFP2_MOUSE	Q8CFP2 mus musculus
266	94.5	5.3	397	2	Q8BFX8_MOUSE	Q8BFX8 m mus muscu	339	91	5.1	491	1	KCN33_RABIT	Q9ct17 oryctolagus
267	94.5	5.3	404	2	Q5R8X4_PONPY	Q5R8X4 pongo pygma	340	91	5.1	510	2	Q9BGV6_MACPA	Q9BGV6 macaca fasc
268	94.5	5.3	588	2	Q6MG92_RAT	Q6MG92 rattus norv	341	91	5.1	722	2	Q4KMG2_HUMAN	Q4KMG2 homo sapien
269	94	5.3	233	1	GP42_RAT	P23505 rattus norv	342	91	5.1	822	1	CAN3_BOVIN	Q6PCX3_MOUSE
270	94	5.3	269	2	Q5C8P0_GADEN	Q5C8P0 simlan aden	343	91	5.1	1150	2	Q6PCX3_MOUSE	Q6PCX3_MOUSE
271	94	5.3	336	2	Q8WNV8_FELICA	Q8WNV8 felis silve	344	91	5.1	1379	2	Q4SMF3_TETNG	Q4SMF3_TETNG
272	94	5.3	419	2	Q96GL5_HUMAN	Q96GL5 homo sapien	345	91	5.1	1496	2	Q92626_HUMAN	Q92626_HUMAN
273	94	5.3	828	2	Q8C8T7_MOUSE	Q8C8T7 mus musculus	346	91	5.1	1548	1	JADID_MOUSE	Q9J103_RAT
274	94	5.3	1088	1	NCA11_XENIA	P16170 xenopus lae	347	91	5.1	1840	2	Q9J103_RAT	Q9J103_RAT
275	93.5	5.3	365	1	CXAR_RAT	Q9I066 rattus norv	348	91	5.1	2053	1	DECL1_HUMAN	Q6PCX3_MOUSE
276	93.5	5.3	403	2	Q5W7A4_RAT	Q5W7A4 rattus norv	349	90.5	5.1	230	2	Q801W9_BRARE	Q801W9 brachydanto
277	93.5	5.3	491	2	Q5BLW6_BOVIN	Q5BLW6 bos taurus	350	90.5	5.1	243	2	Q6IAZ2_HUMAN	Q6IAZ2_HUMAN
278	93.5	5.3	572	2	Q4T854_TETNG	Q4T854 tetradodon n	351	90.5	5.1	325	2	Q5PSW9_PIG	Q5PSW9 pig
279	93.5	5.3	840	2	Q4VYD6_SPICT	Q4VYD6 tetradodon n	352	90.5	5.1	391	2	Q76CT6_MOUSE	Q76CT6 mus musculus
280	93.5	5.3	1039	2	Q5T377_HUMAN	Q5T377 homo sapien	353	90.5	5.1	412	2	Q5U334_RAT	Q5U334_RAT
281	93.5	5.3	1098	2	Q4ARR1_TETNG	Q4ARR1 tetradodon n	354	90.5	5.1	412	2	Q63611_RAT	Q63611_RAT
282	93	5.2	316	2	Q6XJY4_MOUSE	Q6XJY4 mus musculus	355	90.5	5.1	417	1	Q9R1B1_RAT	PVR_HUMAN
283	93	5.2	339	2	Q7KR15_DROME	Q7KR15 drosophila	356	90.5	5.1	474	2	Q5FV48_FUGRU	Q5FV48 fugu rubrip
284	93	5.2	342	2	Q91B00_9PERC	Q91B00 epinoeroides	357	90.5	5.1	483	2	Q7SX76_BRARE	Q7SX76 brachydanto
285	93	5.2	419	1	PSG4_HUMAN	Q00888 homo sapien	358	90.5	5.1	795	2	Q5ONW7_ENTHI	Q5ONW7 entameba n
286	93	5.2	419	1	PSG7_HUMAN	Q13046 homo sapien	359	90.5	5.1	901	2	Q6IR38_MOUSE	Q6IR38 mus musculus
287	93	5.2	535	1	PSYR3_SPICT	P52200 spiroplasma	361	90.5	5.1	922	2	Q9LTU7_ARATH	Q9LTU7 arabidopsis
288	93	5.2	661	2	Q5R1W1_MOUSE	Q5R1W1 mus musculus	362	90.5	5.1	1012	1	ROBO4_MOUSE	ROBO4_MOUSE
289	93	5.2	752	2	Q9DGN6_CHICK	Q9DGN6 gallus gall	363	90.5	5.1	1596	2	Q5CPM9_CRYPV	Q5CPM9 cryptospori
290	93	5.2	813	1	P1UNC_MOUSE	Q8BDC3 mus musculus	364	90.5	5.1	1905	1	Y659_PASMU	Q5CMZ1 pasteurella
291	93	5.2	939	2	Q6FKB0_CANGA	Q6FKB0 candida gla	365	90	5.1	240	2	Q5T325_HUMAN	Q5T325_HUMAN
292	93	5.2	1780	2	Q91AJ0_XENIA	Q91AJ0 xenopus lae	366	90	5.1	250	1	Q5U053_HUMAN	Q5U053 homo sapien
293	93	5.2	160	2	Q8C239_MOUSE	Q8C239 mus musculus	367	90	5.1	309	2	Q91YV7_MOUSE	Q91YV7 mus musculus
294	92.5	5.2	299	1	JAM1_HUMAN	Q9V624 homo sapien	368	90	5.1	348	1	MBGR1_MOUSE	Q91YV7 mus musculus
295	92.5	5.2	299	2	Q6TIB4_HUMAN	Q6TIB4 homo sapien	369	90	5.1	419	1	PGS1_HUMAN	PGS1_HUMAN
296	92.5	5.2	330	1	CD86_RABIT	P42071 oryctolagus	370	90	5.1	419	1	Q6ICR4_HUMAN	Q6ICR4_HUMAN
297	92.5	5.2	491	2	Q5B9J9_BOVIN	Q5B9J9 bos taurus	371	90	5.1	515	2	Q4RP84_TETNG	Q4RP84_TETNG
298	92.5	5.2	733	2	Q5QNS6_BRARE	Q5QNS6 brachydanto	372	90	5.1	541	2	IL1BR_HUMAN	IL1BR_HUMAN
299	92.5	5.2	535	1	BTNL9_HUMAN	Q6UXQ8 homo sapien	373	90	5.1	541	2	Q52LIC9_HUMAN	Q52LIC9_HUMAN
300	92.5	5.2	544	2	Q7Z2B5_BRARE	Q7Z2B5 brachydanto	374	90	5.1	609	2	Q9WHY7_9PARA	Q9WHY7_9PARA
301	92.5	5.2	564	1	CD166_BRARE	Q90460 brachydanto	375	90	5.1	771	2	Q4KMG7_HUMAN	Q4KMG7_HUMAN
302	92.5	5.2	564	2	Q610X4_BRARE	Q610X4 brachydanto	376	90	5.1	1179	2	Q7QXR2_GIALA	Q7QXR2 giardia lam
303	92.5	5.2	760	2	Q8EBB5_SHEON	Q8EBB5 shewanella	377	90	5.1	1290	2	Q6WLBS_9DIPT	Q6WLBS chaetopsis
304	92.5	5.2	777	2	Q9C9S3_ARATH	Q9C9S3 arabidopsis	378	90	5.1	1297	2	Q4RVK8_TETNG	Q4RVK8_TETNG
305	92.5	5.2	782	2	Q8B3U9_9GAMA	Q8B3U9 porcine lym	379	90	5.1	1431	2	Q80U60_MOUSE	Q80U60 mus musculus
306	92.5	5.2	777	2	Q7RAO7_PLAYO	Q7RAO7 plasmodium	380	90	5.1	1495	2	Q4RB92_TETNG	Q4RB92_TETNG
307	92.5	5.2	782	2	Q8B3U9_9GAMA	Q8B3U9 porcine lym	381	90	5.1	243	1	CD48_HUMAN	CD48_HUMAN
308	92.5	5.2	782	2	Q80YB8_9GAMA	Q80YB8 porcine lym	382	89.5	5.1	243	1	Q5U055_HUMAN	Q5U055_HUMAN
309	92.5	5.2	829	2	Q5R1P6_BRARE	Q5R1P6 brachydanto	383	89.5	5.1	339	2	Q4T512_TETNG	Q4T512_TETNG
310	92	5.2	297	2	Q63476_RAT	Q63476 rattus norv	384	89.5	5.1	349	2	Q4T512_TETNG	Q4T512_TETNG
311	92	5.2	419	2	Q68CR6_HUMAN	Q68CR6 homo sapien	385	89.5	5.1	349	1	QMPA_BUCAL	QMPA_BUCAL
312	92	5.2	426	1	PSG8_HUMAN	Q9UG74 homo sapien	386	89.5	5.1	508	2	Q5KUB8_GROKA	Q5KUB8 grobaciillus
313	92	5.2	491	2	Q4ZPT1_HUMAN	Q4ZPT1 homo sapien	387	89.5	5.1	570	2	Q5R640_PONPY	Q5R640_PONPY
314	92	5.2	609	2	Q9YKDT_9PARA	Q9YKDT rinderpest	388	89.5	5.1	756	2	Q8CUM2_STRCO	Q8CUM2 streptococ
315	92	5.2	700	1	K1RR2_MOUSE	Q7EUT7 mus musculus	389	89.5	5.1	770	2	Q8CUM2_STRCO	Q8CUM2_STRCO
316	92	5.2	743	1	Q6P1W7_HUMAN	Q6P1W7 homo sapien	390	89.5	5.1	821	2	CAN3_PIG	CAN3_PIG
317	92	5.2	789	2	Q71512_BACTO	Q71512 bacillus th	391	89.5	5.1	833	2	Q9BPQ7_HALRO	Q9BPQ7 halocynthia
318	92	5.2	822	2	Q9ZOX3_ARATH	Q9ZOX3 arabidopsis	392	89.5	5.1	845	1	SLIK2_HUMAN	SLIK2_HUMAN
319	92	5.2	1020	1	FRM4A_MOUSE	Q8BIE6 mus musculus	393	89.5	5.1	845	2	Q6AL13_HUMAN	Q6AL13_HUMAN
320	92	5.2	1025	2	Q7XTP6_OYRSA	Q7XTP6 oyryza sativ	394	89.5	5.1	1024	1	PRM4A_HUMAN	PRM4A_HUMAN
321	92	5.2	1031	2	Q6PDU4_MOUSE	Q6PDU4 mus musculus	395	89.5	5.1	1170	2	Q4YR55_PLABE	Q4YR55 plasmodium
322	92	5.2	1087	2	Q7ZY71_XENIA	Q7ZY71 xenopus lae	396	89.5	5.1	1644	2	Q9W3D2_DROME	Q9W3D2 drosophilla
323	92	5.2	2008	2	Q4SRX6_TETNG	Q4SRX6 tetradodon n							



397	89.5	5.1	1671	2	Q9W3D3_DROME	Q9w3d3_drosophila	470	87.5	4.9	302	2	Q4JX57_CORJX	Q4jx57_corynebacte
398	89.5	5.1	1716	2	Q61ZV2_CABBR	Q61z2v2_caenothabdi	471	87.5	4.9	325	2	Q0Z838_PIG	Q0z838_sus scrofa
399	89.5	5.1	2214	1	SVIL_HUMAN	Q95425 homo sapien	472	87.5	4.9	332	2	Q64U03_XENTR	Q64u03_xenopus tro
400	89.5	5.1	3193	2	Q7RL38_PLAYO	Q7rl38_plasmodium	473	87.5	4.9	403	2	Q8VE47_MOUSE	Q8ve47_mus muscullu
401	89	5.0	240	2	Q9BRW0_HUMAN	Q9brw0_homo sapien	474	87.5	4.9	416	2	Q5E4A5_BRARE	Q5e4a5_brachydanio
402	89	5.0	262	2	Q8OT70_MOUSE	Q8ot70_mus muscullu	475	87.5	4.9	422	1	KI3L1_RAT	P83556 rattus norv
403	89	5.0	309	1	CD86_MOUSE	P43082 mus muscullu	476	87.5	4.9	464	2	Q6GL25_XENTR	Q6gl25_xenopus tro
404	89	5.0	309	2	Q549Q9_MOUSE	Q549q9_mus muscullu	477	87.5	4.9	487	1	PERL1_CHICK	Q722h2 gallus gall
405	89	5.0	314	2	Q61238_MOUSE	Q61238_mus muscullu	478	87.5	4.9	547	2	Q6M933_RAT	Q6m933_rattus norv
406	89	5.0	322	2	Q9PT88_SPERC	Q9pt88_sphaerooides	479	87.5	4.9	581	2	Q6BN45_DEBHA	Q6bn45_debaryomyce
407	89	5.0	323	2	Q8MKZ7_DROME	Q8mkz7_drosophila	480	87.5	4.9	583	1	CD166_MOUSE	Q61490 mus muscullu
408	89	5.0	356	2	Q64381_MOUSE	Q64381_mus muscullu	481	87.5	4.9	583	1	CD166_RAT	Q35112 rattus norv
409	89	5.0	368	2	Q5BI25_DROME	Q5bi25_drosophila	482	87.5	4.9	652	2	Q54AJ5_MOUSE	Q54aj5_mus muscullu
410	89	5.0	434	2	Q6DN72_HUMAN	Q6dn72_homo sapien	483	87.5	4.9	652	2	Q89703_YITRU	Q89703_yeast
411	89	5.0	438	2	Q5C724_SCHJA	Q5c724_schistosoma	484	87.5	4.9	699	2	Q61V11_CABBR	Q61v11_caenothabdi
412	89	5.0	466	2	Q551Y7_CRYNE	Q551y7_cryptococcu	485	87.5	4.9	723	1	Q5HZP8_XENLA	Q5hzp8_xenopus lae
413	89	5.0	506	2	Q6MG91_RAT	Q6mg91_rattus norv	486	87.5	4.9	769	2	PIGR_RAT	P15083 rattus norv
414	89	5.0	821	1	CAN3_HUMAN	P20807 homo sapien	487	87.5	4.9	1087	2	Q9PUF6_CHICK	Q9puf6_gallus gall
415	89	5.0	1803	2	Q5CMK4_CRYHO	Q5cmk4_cryptospori	488	87.5	4.9	2307	2	Q801V2_PETCO	Q801v2_thelater's-l
416	89	5.0	5175	2	Q810I3_CABEL	Q810i3_caenothabdi	489	87.5	4.9	2340	2	Q78DX7_MOUSE	Q78dx7_mus muscullu
417	89	5.0	5198	2	Q76518_CABEL	Q76518_caenothabdi	490	87.5	4.9	4162	2	Q98918_CHICK	Q98918_gallus gall
418	88.5	5.0	271	1	OX2V_HHVB	P88963 human herpe	491	87.5	4.9	4283	2	Q9ERV0_RAT	Q9erv0_rattus norv
419	88.5	5.0	271	2	Q40948_HHVB	Q40948 human herpe	492	87.5	4.9	17903	2	Q7RTL4_DROME	Q7rtl4_drosophila
420	88.5	5.0	271	2	Q4S7L7_TETNG	Q4s7l7_tetradon n	493	87.5	4.9	18074	2	Q917U4_DROME	Q917u4_drosophila
421	88.5	5.0	315	2	Q9DGT5_CHICK	Q9dgt5_gallus gall	494	87.5	4.9	156	2	Q5APG8_CANAL	Q5apf8_candida alb
422	88.5	5.0	316	2	Q5F3J1_CHICK	Q5f3j1_gallus gall	495	87.5	4.9	225	2	Q5NHZ7_PRAIT	Q5nhz7_franciella
423	88.5	5.0	325	2	Q8UWL3_ICTPU	Q8uwl3_ictalurus p	496	87.5	4.9	229	2	Q9R121_RAT	Q9r121_rattus norv
424	88.5	5.0	327	1	MOX2R_RAT	Q96858 rattus norv	497	87.5	4.9	291	1	KO152_MOUSE	Q6zq13 mus muscullu
425	88.5	5.0	344	2	Q93242_CHICK	Q93242_gallus gall	498	87.5	4.9	337	2	Q5Z8W6_ORYSA	Q5z8w6_oryza sativ
426	88.5	5.0	532	2	Q8WVW6_HUMAN	Q8wvw6_homo sapien	499	87.5	4.9	341	2	Q61353_MOUSE	Q61353_mus muscullu
427	88.5	5.0	534	2	Q96SAA_HUMAN	Q96saa_homo sapien	500	87.5	4.9	344	2	Q568F7_BRARE	Q568f7_brachydanio
428	88.5	5.0	534	2	Q9W4R3_DROME	Q9w4r3_drosophila	501	87.5	4.9	403	2	Q9CYD6_MOUSE	Q9cyd6_mus muscullu
429	88.5	5.0	620	2	Q61G13_DROME	Q61g13_drosophila	502	87.5	4.9	415	2	Q8C6X8_MOUSE	Q8c6x8_mus muscullu
430	88.5	5.0	782	2	Q4S143_TETNG	Q4s143_tetradon n	503	87.5	4.9	457	1	CD4_MOUSE	P06332 mus muscullu
431	88.5	5.0	1081	2	Q8T4N8_PENRS	Q8t4n8_pennaeus sem	504	87.5	4.9	491	1	KCN53_HUMAN	Q9qgqz8 homo sapien
432	88.5	5.0	1283	2	Q7R0P8_PLAYO	Q7r0p8_plasmodium	505	87.5	4.9	491	2	Q8B0Z8_MOUSE	Q8b0z8_mus muscullu
433	88.5	5.0	1390	1	MET_HUMAN	P05581 homo sapien	506	87.5	4.9	514	2	Q8BH18_MOUSE	Q8bh18_m mus muscu
434	88.5	5.0	1769	2	Q4YQ03_PLABE	Q4yq03_plasmodium	507	87.5	4.9	521	1	CD166_FABIT	Q46651 oryctolagus
435	88	5.0	320	2	Q737C6_BACCI	Q737c6_bacillus ce	508	87.5	4.9	522	1	Q8F7F1_LEPIN	Q8f7f1_leptospira
436	88	5.0	324	2	Q7TMA2_MOUSE	Q7tma2_mus muscullu	509	87.5	4.9	543	2	Q4R603_MACPA	Q4r603_macaca fasc
437	88	5.0	329	2	Q9TTP2_CANPA	Q9ttp2_canis famli	510	87.5	4.9	551	2	Q4QOZ7_SCMA	Q4qoz7_schistosoma
438	88	5.0	337	2	Q91AZ4_SPERC	Q91az4_sphaerooides	511	87.5	4.9	583	1	CD166_HUMAN	Q51673 brachydanio
439	88	5.0	339	2	Q91B09_SPERC	Q91b09_sphaerooides	512	87.5	4.9	609	2	Q7EYK0_ORYSA	Q7eyk0_oryza sativ
440	88	5.0	343	2	Q8R4Y0_MOUSE	Q8r4y0_mus muscullu	513	87.5	4.9	1272	2	Q4UDS5_BRARE	Q4uds5_brachydanio
441	88	5.0	363	1	MURG_BORBU	Q51708 borrelia bu	514	87.5	4.9	1284	2	Q5G1V6_CRYNE	Q5g1v6_brachydanio
442	88	5.0	419	2	Q6P520_HUMAN	Q6p520_homo sapien	515	87.5	4.9	1284	2	Q5KLV6_CRYNE	Q5k1v6_cryptococcu
443	88	5.0	422	2	Q58124_PYRHO	Q58124_pyrococcus	516	87.5	4.9	1403	2	Q6DCY7_XENLA	Q6dcy7_xenopus lae
444	88	5.0	457	2	Q61396_MOUSE	Q61396_mus muscullu	517	87.5	4.9	1451	2	Q55Y32_CRYNE	Q55y32_cryptococcu
445	88	5.0	508	1	CP6D5_DROME	Q9yfp1_drosophila	518	87.5	4.9	1497	2	Q5XJY4_MOUSE	Q5xjy4_mus muscullu
446	88	5.0	509	1	SHPS1_RAT	P97710 r tyrosine-	519	87.5	4.9	1501	2	Q7TIT7_MOUSE	Q7t1t7_mus muscullu
447	88	5.0	530	1	PVR2_MOUSE	P32507 mus muscullu	520	87.5	4.9	1569	2	Q6PAC0_MOUSE	Q6pac0_mus muscullu
448	88	5.0	530	2	Q80XJ5_MOUSE	Q80xj5_mus muscullu	521	87.5	4.9	1666	1	MYOM1_MOUSE	Q62234 mus muscullu
449	88	5.0	607	2	Q4LPC1_9BURK	Q4lpc1_burkholderi	522	87.5	4.9	1666	2	Q546T8_MOUSE	Q546t8_mus muscullu
450	88	5.0	623	2	Q7PUCT_ANOGA	Q7puct_anopheles g	523	87.5	4.9	1904	2	Q64699_MOUSE	Q64699_mus muscullu
451	88	5.0	639	2	Q6PAZ7_XENLA	Q6paz7_xenopus lae	524	87.5	4.9	1907	2	Q4JBC7_MOUSE	Q4jbc7_mus muscullu
452	88	5.0	699	1	PTPRB_MOUSE	P49446 mus muscullu	525	87.5	4.9	2673	2	Q96SC3_HUMAN	Q96sc3_homo sapien
453	88	5.0	699	2	Q61042_MOUSE	Q61042_mus muscullu	526	87.5	4.9	3160	1	FREM2_MOUSE	Q05793 mus muscullu
454	88	5.0	821	1	CAN3_RAT	P16259 rattus norv	527	87.5	4.9	3707	1	PCBM_MOUSE	Q05793 mus muscullu
455	88	5.0	837	2	Q8G518_BIFLO	Q8g518_bifidobacte	528	87.5	4.9	5635	2	Q4STR7_HUMAN	Q4str7_homo sapien
456	88	5.0	865	2	Q8UTV9_RIFRU	Q8utv9_fugu rubrip	529	87.5	4.9	210	2	Q4RTW7_MACPA	Q4rtw7_macaca fasc
457	88	5.0	1092	1	NCA12_XENLA	P36335 xenopus lae	530	87.5	4.9	237	2	Q61B65_HUMAN	Q61b65_homo sapien
458	88	5.0	1112	2	Q60U10_CABBR	Q60u10_caenothabdi	531	87.5	4.9	240	2	Q6MG36_RAT	Q6mg36_rattus norv
459	88	5.0	1337	2	Q4RKW0_TETNG	Q4rkwo_tetradon n	532	87.5	4.9	293	2	Q8AXN8_CYPCA	Q8axn8_cypripus cro
460	88	5.0	1379	2	Q813S7_PLAF7	Q813s7_plasmodium	533	87.5	4.9	313	2	Q35531_RAT	Q35531_rattus norv
461	88	5.0	1925	1	PLXDI_HUMAN	Q944d7_homo sapien	534	87.5	4.9	324	2	Q91AY9_SPERC	Q91ay9_sphaerooides
462	88	5.0	1946	2	Q4S290_TETNG	Q4s290_tetradon n	535	87.5	4.9	354	2	Q5RA12_PONPY	Q5ra12_pongo pygma
463	88	5.0	2802	2	Q53T68_HUMAN	Q53t68_homo sapien	536	87.5	4.9	354	2	Q5R645_PONPY	Q5r645_pongo pygma
464	88	5.0	3007	2	Q14215_HUMAN	Q14215_homo sapien	537	87.5	4.9	384	2	Q4SY83_TETNG	Q4sy83_tetradon n
465	88	5.0	6669	1	NEBU_HUMAN	P20929 homo sapien	538	87.5	4.9	443	1	EX7L_VIBVU	Q7fme3_vibrio vuln
466	88	5.0	11696	2	Q5CV09_CRYPV	Q5cv09_cryptospori	539	87.5	4.9	443	1	EX7L_VIBVU	Q7fme3_vibrio vuln
467	87.5	4.9	265	1	CEAM7_HUMAN	Q14002 homo sapien	540	87.5	4.9	474	2	P79355_DEIRA	P79355_felis silve
468	87.5	4.9	276	2	Q98822_ADB41	Q98822 human adeno	541	87.5	4.9	528	2	Q9RTP5_PDIRA	Q9rtp5_delinococcus
469	87.5	4.9	276	2	Q64861_YADEN	Q64861 human adeno	542	87.5	4.9	530	2	Q5FVCS_RAT	Q5fvc5_rattus norv



543	86.5	4.9	626	2	04SM66_TETNG	04sm66_tetradon n	616	85.5	4.8	1587	2	0705D1_ANOGA	0755d1_anopheles g
544	86.5	4.9	650	2	088BN9_PRESM	088bn9_pseudomonas	617	85.5	4.8	1947	2	07ROO4_PIAVO	075r4 plasmidium
545	86.5	4.9	711	2	06LJAI_PHOPR	06ljai_photobacter	618	85.5	4.8	2115	2	08IB55_PIAF7	08ib55 plasmidium
546	86.5	4.9	846	1	SLIK21_MOUSE	0810c0 mus musculu	619	85.5	4.8	2129	2	06FUN0_CANGA	06fun0 candida gla
547	86.5	4.9	1028	2	06INB5_XENTIA	06ibns xenopus lae	620	85.5	4.8	2225	2	05C6G8_DICDI	05c6g8 dictyosteli
548	86.5	4.9	1029	2	04Y4R9_PLACH	04y4r9 plasmidium	621	85.5	4.8	2414	1	059EB23_HUMAN	059eb23 homo sapien
549	86.5	4.9	2752	2	07OKD0_ANOGA	07okd0 anopheles g	622	85.5	4.8	2491	1	MPRI_HUMAN	MPRI1717 homo sapien
550	86	4.9	235	2	04SO01_TETNG	04sg01 tetradon n	623	85.5	4.8	2491	1	096PT5_HUMAN	096pt5 homo sapien
551	86	4.9	259	2	09Y5B2_HUMAN	09y5b2 homo sapien	624	85.5	4.8	2588	1	NSDI_MOUSE	NSDI491 mus musculu
552	86	4.9	265	2	0695R3_YADEN	0695r3 simian aden	625	85.5	4.8	2623	2	06WRIO_HUMAN	06wr10 homo sapien
553	86	4.9	280	2	08UMK1_ICTPU	08umk1 ictalurus p	626	85	4.8	224	2	0870G0_PODAN	0870g0 podospora a
554	86	4.9	330	2	06PEU7_MOUSE	06peu7 mus musculu	627	85	4.8	280	2	08UML1_ICTPU	08uml1 ictalurus p
555	86	4.9	339	2	09IAZI_9PERC	09iazi spheroeoides	628	85	4.8	293	2	06MG56_RAT	06mg56 leptospira
556	86	4.9	348	1	NEGR1_RAT	0920j8 rattus norv	629	85	4.8	332	2	07F52_TEPIC	07f52 leptospira
557	86	4.9	354	1	VGLI_VZVD	P09258 varicella-z	630	85	4.8	332	2	08BX51_LEPIN	08bx51 leptospira
558	86	4.9	354	2	0775H3_HHV3	0775h3 human heppe	631	85	4.8	375	2	093GD6_DESAP	093gd6 deulfovibr
559	86	4.9	354	2	077JF6_HHV3	077jf6 human heppe	632	85	4.8	379	1	JAML1_MOUSE	08u19 mus musculu
560	86	4.9	354	2	098VN1_HHV3	098vn1 human heppe	633	85	4.8	402	1	RAGR_RAT	063495 rattus norv
561	86	4.9	354	2	077NN4_HHV3	077nn4 human heppe	634	85	4.8	402	2	06MG66_RAT	06mg66 rattus norv
562	86	4.9	413	2	06ZNI1_HUMAN	06zni1 homo sapien	635	85	4.8	428	1	PEG3_HUMAN	06557 homo sapien
563	86	4.9	428	2	09BRW2_HUMAN	09brw2 homo sapien	636	85	4.8	475	2	06NZH8_XENTR	06nz8 xenopus tro
564	86	4.9	471	2	06IKI8_CABBR	06iki8 caenorhabdi	637	85	4.8	570	2	06GLY1_XENTIA	06gly1 xenopus lae
565	86	4.9	486	2	082N16_STPMW	082n16 streptomyce	638	85	4.8	583	1	CD166_BOVIN	09bh13 bos taurus
566	86	4.9	487	2	082M13_STPMW	082m13 streptomyce	639	85	4.8	684	2	0211J8_CAEEL	0211j8 caenorhabdi
567	86	4.9	545	2	09VCT4_DROME	09vct4 drosophila	640	85	4.8	709	2	09XSJ2_PIG	09xsj2 sus scrofa
568	86	4.9	556	2	058BO1_BRARE	058bo1 brachydanio	641	85	4.8	712	2	09EB31_HUMAN	09eb31 homo sapien
569	86	4.9	646	2	06DJ24_XENTR	06dj24 xenopus tro	642	85	4.8	821	1	CAN3_MOUSE	064691 mus musculu
570	86	4.9	687	2	09MAJ5_ARATH	09maj5 arabidopsis	643	85	4.8	880	2	091ZV7_MOUSE	091zv7 mus musculu
571	86	4.9	728	2	0762C8_HUMAN	0762c8 homo sapien	644	85	4.8	875	2	06A7L8_PROAC	06a7l8 propionibac
572	86	4.9	731	2	08SP16_MACEU	08sp16 macropus eu	645	85	4.8	976	2	05BN28_9CAUD	05bn28 cyanophaga
573	86	4.9	885	1	RFL1_ARATH	0813r3 arabidopsis	646	85	4.8	1168	2	04UBH6_THBAN	04ubh6 thelieria a
574	86	4.9	1070	2	04S2F2_TETNG	04s2f2 tetradon n	647	85	4.8	1376	2	08AZ23_9GAMA	08az23 porcine lym
575	86	4.9	1187	2	098TF0_CYPCA	098tf0 cyprinus ca	648	85	4.8	1384	2	076915_BOVIN	076915 bos taurus
576	86	4.9	1252	2	06CUN6_KULIA	06cun6 kluyveromyc	649	85	4.8	1389	2	04VA61_MOUSE	04va61 mus musculu
577	86	4.9	1337	2	01S070_HUMAN	01s070 homo sapien	650	85	4.8	1598	2	09P214_HUMAN	09p214 homo sapien
578	86	4.9	18412	2	07Z261_BRARE	07z261 brachydanio	651	85	4.8	1723	2	08CHB2_MOUSE	08chb2 mus musculu
579	85.5	4.8	230	2	05SNP6_BRARE	05snp6 brachydanio	652	85	4.8	1805	2	058EX2_HUMAN	058ex2 homo sapien
580	85.5	4.8	235	2	06GMW6_HUMAN	06gmw6 mus musculu	653	85	4.8	2487	2	09N1T0_ORNAN	09n1t0 ornithorhyn
581	85.5	4.8	249	2	06XJY6_MOUSE	06xjy6 mus musculu	654	85	4.8	210	2	07PVM1_ANOGA	07pvm1 anopheles g
582	85.5	4.8	266	2	04NVB3_GDELT	04nvb3 anemomyxob	655	84.5	4.8	238	2	0749M2_GEOSL	0749m2 geobacter s
583	85.5	4.8	324	2	09UPK5_HUMAN	09upk5 homo sapien	656	84.5	4.8	241	2	04T4Z6_TETNG	04t4z6 tetradon n
584	85.5	4.8	326	2	09UPK8_HUMAN	09upk8 homo sapien	657	84.5	4.8	263	2	04SQO2_TETNG	04sqo2 tetradon n
585	85.5	4.8	332	2	04RFH3_TETNG	04rfh3 tetradon n	658	84.5	4.8	280	2	0899D0_CLOTE	0899d0 clostridium
586	85.5	4.8	333	2	0752J3_HUMAN	0752j3 homo sapien	659	84.5	4.8	289	2	05HZV8_XENTR	05hzv8 xenopus tro
587	85.5	4.8	335	2	075237_HUMAN	075237 homo sapien	660	84.5	4.8	292	1	KO152_HUMAN	041465 homo sapien
588	85.5	4.8	347	2	04R908_MACEA	04r908 macaca fasc	661	84.5	4.8	303	2	09UKJ1_HUMAN	09ukj1 homo sapien
589	85.5	4.8	393	2	07TNZ6_RAT	07tnz6 rattus norv	662	84.5	4.8	308	2	04YCN2_PLABE	04ycn2 plasmidium
590	85.5	4.8	418	2	05FYV4_SPHBL	05fyv4 sphingomona	663	84.5	4.8	337	2	06SU07_MOUSE	06su07 mus musculu
591	85.5	4.8	510	2	05U557_XENTIA	05u557 xenopus lae	664	84.5	4.8	352	1	NEGR1_HUMAN	0753b1 homo sapien
592	85.5	4.8	527	2	06YW20_ORYSA	06yw20 oryza sativ	665	84.5	4.8	354	2	05VT21_HUMAN	05vt21 homo sapien
593	85.5	4.8	620	2	0481C0_TETNG	0481c0 tetradon n	666	84.5	4.8	394	2	09D0G8_MOUSE	09d0g8 m mus muscu
594	85.5	4.8	622	2	05OXJ4_ENTHI	05oxj4 entamoeba h	667	84.5	4.8	397	2	06XRC3_HUMAN	06xrc3 homo sapien
595	85.5	4.8	650	2	08NA84_HUMAN	08na84 homo sapien	668	84.5	4.8	533	2	04IND9_GIBBE	04ind9 gibberella
596	85.5	4.8	657	2	093D79_BACTU	093d79 bacillus th	669	84.5	4.8	605	2	04UG78_THBAN	04ug78 thelieria a
597	85.5	4.8	767	2	05LKB5_BACER	05lkb5 bacteroides	670	84.5	4.8	756	2	004533_ARATH	004533 arabidopsis
598	85.5	4.8	767	2	064SY4_BACFN	064sy4 bacillus th	671	84.5	4.8	798	2	086K66_DICDI	086k66 dictyosteli
599	85.5	4.8	788	2	05JZ20_BACTU	05jz20 bacillus th	672	84.5	4.8	840	2	07Y012_CANBP	07y012 candidatus
600	85.5	4.8	789	2	069270_BACTU	069270 bacillus th	673	84.5	4.8	1164	2	08PX58_METMA	08px58 methanosarc
601	85.5	4.8	789	2	045792_BACTU	045792 bacillus th	674	84.5	4.8	1211	1	M1OL1_HUMAN	09pxc6 homo sapien
602	85.5	4.8	789	2	045793_BACTU	045793 bacillus th	675	84.5	4.8	1485	2	04RH47_TETNG	04rh47 tetradon n
603	85.5	4.8	789	2	05XKPS_BACTU	05xkps bacillus th	676	84.5	4.8	1608	2	08PVI0_METMA	08pvi0 methanosarc
604	85.5	4.8	789	2	079SG2_BACTU	079sg2 bacillus th	677	84.5	4.8	237	2	07YOK5_CANFA	07yok5 canis famli
605	85.5	4.8	789	2	058I33_BACTU	058i33 bacillus th	678	84	4.7	237	2	05VSN2_BRARE	05vsn2 brachydanio
606	85.5	4.8	789	2	058X12_BACTU	058x12 bacillus th	679	84	4.7	262	2	09PTR_9PERC	09ptr7 spheroeoides
607	85.5	4.8	789	2	0938Z1_BACTU	0938z1 bacillus th	680	84	4.7	333	2	091B04_9PERC	091b04 spheroeoides
608	85.5	4.8	789	2	04VYTO_BACTU	04vyto bacillus th	681	84	4.7	343	2	08BY54_MOUSE	08by54 mus musculu
609	85.5	4.8	789	2	04UF54_BACTU	04uf54 bacillus th	682	84	4.7	363	2	0660A8_BORGA	0660a8 botreilla ga
610	85.5	4.8	789	1	KPWS_P5VMD	P00545 feline sarc	683	84	4.7	381	2	05V6F5_HALMA	05v6f5 halocaula
611	85.5	4.8	1101	2	07XJDS_ORYSA	07xjds oryza sativ	684	84	4.7	418	2	08ENX5_OCRH	08enx5 oceanobactio
612	85.5	4.8	1101	2	09FMU8_ORYSA	09fmu8 oryza sativ	685	84	4.7	403	2	0501T5_BRARE	0501t5 brachydanio
613	85.5	4.8	1354	2	09VIC7_DROME	09vic7 drosophila	686	84	4.7	453	2	05KCR5_CRYNE	05kcr5 crytococcu
614	85.5	4.8	1363	2	053P57_ORYSA	053p57 oryza sativ	687	84	4.7	457	2	06FAG8_ACTIAD	06fag8 actinobact
615	85.5	4.8	1416	2	04PZB6_USITWA	04pzb6 usitlago ma	688	84	4.7	464	2	04KFA6_PSEF5	04kfa6 pseudomonas



689	84	4.7	466	2	Q5KCR4_CRYNE	Q5KCR4_cryptococcu	762	83	4.7	281	2	Q6CJ38_MESAU	Q6CJ38_mesocricetu
690	84	4.7	509	2	Q6P618_MOUSE	Q6P618 mus musculu	763	83	4.7	305	2	Q6ZS95_HUMAN	Q6ZS95 homo sapien
691	84	4.7	556	2	Q7ZZU8_BRARE	Q7ZZU8 brachydanto	764	83	4.7	339	2	Q9IA22_9PERC	Q9IA22 epheorides
692	84	4.7	593	2	Q5AYU9_EMENTI	Q5AYU9 aspergillus	765	83	4.7	369	2	Q9JEW5_DESDE	Q9JEW5 desulfovibr
693	84	4.7	593	2	Q8NKB1_EMENTI	Q8NKB1 emericiella	766	83	4.7	373	2	Q8TU74_METAC	Q8TU74 methanosarc
694	84	4.7	594	2	Q5I8S3_BACFN	Q5I8S3 bacteroides	767	83	4.7	401	2	Q08835_CERAE	Q08835 cercopithec
695	84	4.7	611	2	Q5EDKO_ORYSA	Q5EDKO oryza sativ	768	83	4.7	420	2	Q68DM9_HUMAN	Q68DM9 homo sapien
696	84	4.7	611	2	Q7JTM6_MYCPA	Q7JTM6 mycobacteri	769	83	4.7	424	2	Q6CLX2_KJULA	Q6CLX2 kluyveromyc
697	84	4.7	668	1	P8S2_YEAST	Q7JTM4 saccharomyc	770	83	4.7	437	2	Q9OW14_GALLI	Q9OW14 gallus gall
698	84	4.7	685	1	Q54HG9_DICDI	Q54HG9 dictyostelli	771	83	4.7	438	2	Q4RKP5_THICK	Q4RKP5 tetraodon n
699	84	4.7	775	2	Q97754_RABIT	Q97754 coryctolaqus	772	83	4.7	448	2	Q6LU33_PHOPR	Q6LU33 photobacter
700	84	4.7	800	2	Q8H329_ORYSA	Q8H329 oryza sativ	773	83	4.7	463	1	STHA_P5SERL	Q9H0C3_HUMAN
701	84	4.7	810	2	Q8T3J2_DROME	Q8T3J2 dirosophila	774	83	4.7	514	2	Q9H0C3_HUMAN	Q9H0C3_HUMAN
702	84	4.7	811	2	Q9VX54_DROME	Q9VX54 dirosophila	775	83	4.7	538	2	Q9DFU0_SEPAU	Q9DFU0 sepaau
703	84	4.7	812	2	Q8WZ57_DROME	Q8WZ57 dirosophila	776	83	4.7	545	2	Q5OZ57_ENTHI	Q5OZ57 entameba h
704	84	4.7	851	2	Q9UX76_SUILO	Q9UX76 sulfolobus	777	83	4.7	555	2	Q59HD7_HUMAN	Q59HD7 homo sapien
705	84	4.7	880	2	P91643_DROME	P91643 dirosophila	778	83	4.7	577	2	Q9D221_MOUSE	Q9D221 m mus muscu
706	84	4.7	984	2	Q4IMF4_GIBBE	Q4IMF4 gibbeterella	779	83	4.7	594	2	Q64NY2_BACPR	Q64NY2 bacteroides
707	84	4.7	1028	2	Q7XTP5_ORYSA	Q7XTP5 oryza sativ	780	83	4.7	702	2	Q4S767_TETNG	Q4S767 tetraodon n
708	84	4.7	1062	2	Q997A4_9EROM	Q997A4 american pi	781	83	4.7	757	1	P1GR_BOVIN	P1GR_BOVIN
709	84	4.7	1062	2	Q6FXS8_CANGA	Q6FXS8 candida gl	782	83	4.7	845	1	Q5VVP5_HUMAN	Q5VVP5_HUMAN
710	84	4.7	1115	2	Q5UM15_BRARE	Q5UM15 brachydanto	783	83	4.7	873	1	Q5VDFR_HUMAN	Q5VDFR_HUMAN
711	84	4.7	1193	2	Q9YQW1_DROME	Q9YQW1 dirosophila	784	83	4.7	873	2	Q6S4M1_MACMU	Q6S4M1 macaca mlla
712	84	4.7	1206	2	Q4IIR2_GIBBE	Q4IIR2 gibbeterella	785	83	4.7	873	2	Q9U4E4_CABEL	Q9U4E4 caenorhabdi
713	84	4.7	1300	1	INSRR_MOUSE	Q9WC14 mus musculu	786	83	4.7	925	2	Q9UB94_CABEL	Q9UB94 caenorhabdi
714	84	4.7	1379	1	MER_MOUSE	P16056 mus musculu	787	83	4.7	925	2	Q9UB95_CABEL	Q9UB95 caenorhabdi
715	84	4.7	1499	2	Q90815_CHICK	Q90815 gallus gall	788	83	4.7	925	2	Q9UB95_CABEL	Q9UB95 caenorhabdi
716	84	4.7	1671	2	Q57119_MOUSE	Q57119 mus musculu	789	83	4.7	925	2	Q44191_CABEL	Q44191 caenorhabdi
717	84	4.7	1903	2	Q5SRJ6_MOUSE	Q5SRJ6 mus musculu	790	83	4.7	1099	2	Q61KCI_CABER	Q61KCI caenorhabdi
718	84	4.7	3034	1	CERL1_MOUSE	Q35161 mus musculu	791	83	4.7	1106	1	ACTLY_CABEL	ACTLY_CABEL
719	83.5	4.7	270	2	Q4SM17_TETNG	Q4SM17 tetraodon n	792	83	4.7	1106	2	Q8IBR5_PLAF7	Q8IBR5 plaaf7
720	83.5	4.7	284	2	Q9GLJ3_BOVIN	Q9GLJ3 bos taurus	793	83	4.7	1254	2	Q674V1_PODCA	Q674V1 podocoryne
721	83.5	4.7	289	2	Q8KJ33_MERUN	Q8KJ33 meriones un	794	83	4.7	1382	2	Q64RKP2_TETNG	Q64RKP2 brachydanto
722	83.5	4.7	298	1	JAM2_HUMAN	P57087 homo sapien	795	83	4.7	1419	2	Q4RWP2_TETNG	Q4RWP2 tetraodon n
723	83.5	4.7	306	2	Q6PYW4_SCHJA	Q6PYW4 schistosoma	796	83	4.7	2421	2	Q9SMJ1_LEMCA	Q9SMJ1 lemur catta
724	83.5	4.7	315	2	Q5O082_PYRHO	Q5O082 pyrococcus	797	83	4.7	2489	2	Q06116_YEAST	Q06116 saccharomyc
725	83.5	4.7	391	2	Q6F5F0_MOUSE	Q6F5F0 mus musculu	798	83	4.7	140	2	Q5VMH6_HUMAN	Q5VMH6 homo sapien
726	83.5	4.7	392	2	Q76708_CABEL	Q76708 caenorhabdi	799	83	4.7	154	2	Q5VMH5_HUMAN	Q5VMH5 homo sapien
727	83.5	4.7	408	2	Q8BVF6_MOUSE	Q8BVF6 mus musculu	800	83	4.7	155	2	Q96P81_HUMAN	Q96P81 homo sapien
728	83.5	4.7	408	2	Q8KQ94_MOUSE	Q8KQ94 mus musculu	801	83	4.7	218	2	Q4J114_IACRE	Q4J114 lactobacilli
729	83.5	4.7	408	2	Q91WP1_MOUSE	Q91WP1 m musculu	802	83.5	4.7	230	2	Q8UV76_BRARE	Q8UV76 brachydanto
730	83.5	4.7	429	2	Q5Z4H1_MAGCR	Q5Z4H1 magnaporthe	803	83.5	4.7	239	2	Q618J5_CABER	Q618J5 caenorhabdi
731	83.5	4.7	450	2	Q6UX10_HUMAN	Q6UX10 homo sapien	804	83.5	4.7	319	2	Q7YS40_PIG	Q7YS40 pig
732	83.5	4.7	450	2	Q96RE0_HUMAN	Q96RE0 homo sapien	805	83.5	4.7	344	1	GPA33_MOUSE	GPA33_MOUSE
733	83.5	4.7	515	2	Q96PJ5_HUMAN	Q96PJ5 homo sapien	806	83.5	4.7	330	2	P97269_CAVPO	P97269 cavia porce
734	83.5	4.7	528	2	P91670_DROME	P91670 dirosophila	807	83.5	4.7	332	2	Q566E6_RAT	Q566E6 rattus norv
735	83.5	4.7	570	2	Q8IH34_BACCR	Q8IH34 bacillus ce	808	82.5	4.7	341	1	BTNL1_MOUSE	BTNL1_MOUSE
736	83.5	4.7	580	2	Q6CTP7_YARLI	Q6CTP7 yarrowia li	809	82.5	4.7	347	2	Q529W7_MAGCR	Q529W7 magnaporthe
737	83.5	4.7	646	2	Q899Y4_CLOTE	Q899Y4 clostridium	810	82.5	4.7	364	2	Q4KK51_PSEFS	Q4KK51 pseudomonas
738	83.5	4.7	725	2	Q512D5_CANFA	Q512D5 canis famli	811	82.5	4.7	377	2	Q4R920_MACFA	Q4R920 macaca fasc
739	83.5	4.7	738	2	Q4YB64_PLABE	Q4YB64 plasmodium	812	82.5	4.7	378	1	LEPAT4_ARATH	Q814Y2 arabidopsis
740	83.5	4.7	847	2	Q512D7_CANFA	Q512D7 canis famli	813	82.5	4.7	382	2	Q6VEU7_MOUSE	Q6VEU7 mus musculu
741	83.5	4.7	862	2	Q4SAP3_TETNG	Q4SAP3 tetraodon n	814	82.5	4.7	437	2	Q51ZV9_STRT1	Q51ZV9 streptococc
742	83.5	4.7	1028	2	Q5R6D4_PONPY	Q5R6D4 pongo pygma	815	82.5	4.7	437	2	Q5M4H0_STRT2	Q5M4H0 streptococc
743	83.5	4.7	1059	2	Q9DE49_BRARE	Q9DE49 brachydanto	816	82.5	4.7	446	2	Q5B2Q4_EMENTI	Q5B2Q4 aspergillus
744	83.5	4.7	1101	2	Q5YTB6_BRARE	Q5YTB6 brachydanto	817	82.5	4.7	446	2	Q8NKO3_EMENTI	Q8NKO3 emericiella
745	83.5	4.7	1160	2	Q6G587_BABRE	Q6G587 bartonella	818	82.5	4.7	468	2	Q6PJ50_MOUSE	Q6PJ50 mus musculu
746	83.5	4.7	1273	2	Q4RT51_TETNG	Q4RT51 tetraodon n	819	82.5	4.7	540	2	Q582F7_YRRYP	Q582F7 crypanosoma
747	83.5	4.7	1332	2	Q6PRX7_CANGA	Q6PRX7 candida glia	820	82.5	4.7	576	2	Q8TOKO_METAC	Q8TOKO methanosarc
748	83.5	4.7	1463	2	Q5S124_MOUSE	Q5S124 mus musculu	821	82.5	4.7	676	2	Q4S1P9_TETNG	Q4S1P9 tetraodon n
749	83.5	4.7	1483	2	Q5CYR5_CRYPV	Q5CYR5 cryptospori	822	82.5	4.7	773	1	MS22_CABEL	MS22_CABEL
750	83.5	4.7	1501	2	Q9QW00_9MURI	Q9QW00 rattus sp.	823	82.5	4.7	789	2	Q4U3F5_BACTU	Q4U3F5_BACTU
751	83.5	4.7	1556	2	Q4UJF8_RAT	Q4J118 rattus norv	824	82.5	4.7	833	2	Q9VHG1_DROME	Q9VHG1 dirosophila
752	83.5	4.7	1802	2	Q83NPF_TROW8	Q83NPF triopheryma	825	82.5	4.7	840	2	Q84BZ6_SPIKU	Q84BZ6 spiropasma
753	83.5	4.7	1863	2	Q9J5C2_FOWPV	Q9J5C2 fowlpox vir	826	82.5	4.7	986	2	Q6DG17_BRARE	Q6DG17 brachydanto
754	83.5	4.7	1863	2	Q64605_RAT	Q64605 rattus norv	827	82.5	4.7	986	2	Q96167_PLAF7	Q96167 plasmodium
755	83.5	4.7	3354	2	Q7PL01_ANOGA	Q7PL01 anopheles g	828	82.5	4.7	994	2	Q610Q4_CABER	Q610Q4 caenorhabdi
756	83.5	4.7	4651	2	Q7Y889_PIG	Q7Y889 sus scrofa	829	82.5	4.7	1028	1	CNTN6_HUMAN	Q94952 homo sapien
757	83	4.7	151	2	Q8WY66_HUMAN	Q8WY66 homo sapien	830	82.5	4.7	1209	2	Q7PG72_ANOGA	Q7PG72 anopheles g
758	83	4.7	231	2	Q78T27_MOUSE	Q78T27 mus musculu	831	82.5	4.7	1215	2	Q7OEC1_ANOGA	Q7OEC1 anopheles g
759	83	4.7	234	2	Q6DOK5_RABIT	Q6DOK5 oryctolagus	832	82.5	4.7	1241	2	Q83GG1_TROWT	Q83GG1 triopheryma
760	83	4.7	273	2	Q5VY16_HUMAN	Q5VY16 homo sapien	833	82.5	4.7	1345	2	Q9BUP3_OXYTR	Q9BUP3 oxytricha c
761	83	4.7	273	2	Q5VY16_HUMAN	Q5VY16 homo sapien	834	82.5	4.7	1345	2	Q9BUP3_OXYTR	Q9BUP3 oxytricha c



835	82.5	4.7	1397	2	Q4PEN2	USTMA	Q4pen2	ustilago ma	908	81.5	4.6	352	2	Q15403	HUMAN	Q15403	homo sapien
836	82.5	4.7	1560	2	Q59FX6	HUMAN	Q59fx6	homo sapien	909	81.5	4.6	355	1	KCP1	ARATH	Q64493	arabidopsis
837	82.5	4.7	1567	2	Q6M1AI	BDEBA	Q6m1ai	bdellovibri	910	81.5	4.6	355	1	Q66HD4	RAT	Q66hd4	rattus norv
838	82.5	4.7	1642	2	Q515F7	ENTHI	Q515f7	entamoeba h	911	81.5	4.6	373	1	LEUK	RAT	P13838	rattus norv
839	82.5	4.7	2597	2	Q6MRH9	RAT	Q6mrh9	rattus norv	912	81.5	4.6	390	2	Q55IR6	CRYLE	Q55ir6	cryptococcu
840	82.5	4.7	3100	2	Q7KYN5	HUMAN	Q7kyn5	homo sapien	913	81.5	4.6	402	2	Q6ZG94	ORYSA	Q6z94	oryza sativ
841	82.5	4.7	4034	2	Q6ZXI4	MAGFA	Q6zx14	magnaporthe	914	81.5	4.6	411	2	Q15228	HUMAN	Q15228	homo sapien
842	82.5	4.7	4256	2	Q8MJF3	CANFA	Q8mjf3	canis faml1	915	81.5	4.6	427	2	Q4N212	THEPA	Q4n212	theileria p
843	82.5	4.7	4650	2	Q15598	HUMAN	Q15598	homo sapien	916	81.5	4.6	438	2	Q7T028	XENLA	Q7t028	xenopus lae
844	82.5	4.7	26926	2	Q4UIZ6	HUMAN	Q4liz6	homo sapien	917	81.5	4.6	440	2	Q6ZMD4	HUMAN	Q6zmd4	homo sapien
845	82.5	4.7	26926	2	Q8WZB3	HUMAN	Q8wzb3	homo sapien	918	81.5	4.6	444	2	Q6KX28	ORYSA	Q6kx28	oryza sativ
846	82.5	4.7	34350	2	Q8WZ42	HUMAN	Q8wz42	homo sapien	919	81.5	4.6	473	2	Q57R32	SALIC	Q57r32	salmonella
847	82	4.6	151	2	Q7YS88	PIG	Q7ys88	sus scrofa	920	81.5	4.6	473	2	Q8ZD01	SALTY	Q8zd01	salmonella
848	82	4.6	184	2	Q7VM71	HAEDU	Q7vm71	haemophilus	921	81.5	4.6	478	2	Q4HV02	GIBZE	Q4hv02	gibberella
849	82	4.6	214	2	Q4SX01	TESTNG	Q4sx01	tetradodon n	922	81.5	4.6	478	2	Q4UIZ5	THEAN	Q4uiz5	theileria a
850	82	4.6	308	2	Q9SK99	MACPA	Q9sk99	macaca fasc	923	81.5	4.6	479	2	Q6GN24	XENLA	Q6gn24	xenopus lae
851	82	4.6	324	2	Q8NBY6	HUMAN	Q8nby6	homo sapien	924	81.5	4.6	493	2	Q6CGN7	YARLI	Q6cgn7	varrovia li
852	82	4.6	326	2	Q8NC17	HUMAN	Q8nc17	homo sapien	925	81.5	4.6	497	1	GAUT	CIOAB	Q97ez4	clostridium
853	82	4.6	327	1	VSIG2	HUMAN	Q961q7	homo sapien	926	81.5	4.6	502	2	Q842D1	ECOLI	Q842d1	escherichia
854	82	4.6	331	2	Q9IB01	9PERC	Q9ib01	sphaerooides	927	81.5	4.6	504	1	FGRL1	HUMAN	Q84441	homo sapien
855	82	4.6	386	1	Q5RJS5	RAT	Q5rjs5	rattus norv	928	81.5	4.6	507	2	Q751G2	ASHGO	Q751g2	aeshbya goss
856	82	4.6	386	1	NATR	BACCU	P46904	bacillus su	929	81.5	4.6	522	2	Q64D42	PARCH	Q64dk4	uncultured
857	82	4.6	395	2	Q4SLB1	TESTNG	Q4slb1	tetradodon n	930	81.5	4.6	524	2	Q75SW4	ECOLI	Q75sw4	escherichia
858	82	4.6	409	2	Q814M1	BACCR	Q814m1	bacillus ce	931	81.5	4.6	524	2	Q09012	SHISO	Q09012	shigella so
859	82	4.6	412	2	Q8HY14	RABIT	Q8hy14	oryctolagus	932	81.5	4.6	525	2	Q6VMU4	ECOLI	Q6vmu4	escherichia
860	82	4.6	444	2	Q8S917	ARATH	Q8s917	arabidopsis	933	81.5	4.6	525	2	Q6VMU5	ECOLI	Q6vmu5	escherichia
861	82	4.6	449	2	P78721	OROSP	P78721	orpinomyces	934	81.5	4.6	525	2	Q6VMU6	ECOLI	Q6vmu6	escherichia
862	82	4.6	508	2	Q4SJRE	TESTNG	Q4sjre	tetradodon n	935	81.5	4.6	536	2	Q4VSE0	DROME	Q4vse0	drosophila
863	82	4.6	509	2	Q61YK3	CABBR	Q61yk3	caenorhabdi	936	81.5	4.6	606	2	Q9VMN6	DROME	Q9vmn6	drosophila
864	82	4.6	554	2	Q5BAI9	EEMET	Q5bai9	aspergillus	937	81.5	4.6	610	2	Q4H2Y0	CIOIN	Q4h2y0	clona intes
865	82	4.6	587	1	Q9JAA1	CARAU	Q9jaa1	carassius a	938	81.5	4.6	647	2	Q50317	BRARE	Q50317	brachydanto
866	82	4.6	609	1	HEWA	RINDR	P41355	rinderpest	939	81.5	4.6	677	2	Q8A3O5	BACYN	Q8a3o5	bacteroides
867	82	4.6	609	2	Q6IAC4	9PARA	Q6iac4	rinderpest	940	81.5	4.6	708	1	Q9MIP4	ARATH	Q9mip4	arabidopsis
868	82	4.6	636	2	Q5LH72	BACFN	Q5lht2	bacteroides	941	81.5	4.6	709	1	Y939	SULFO	Y939	sulfolobus
869	82	4.6	636	2	Q64Y74	BACFR	Q64yt4	bacteroides	942	81.5	4.6	727	2	Q5W5X8	XENLA	Q5w5x8	xenopus lae
870	82	4.6	637	1	PLB1	CRYLE	Q98811	cryptococcu	943	81.5	4.6	746	2	Q6DIR2	XENIR	Q6dir2	xenopus tro
871	82	4.6	648	2	Q9EPF1	MOUSE	Q9epf1	mus muscullu	944	81.5	4.6	779	2	Q8AAG1	BACYN	Q8aag1	bacteroides
872	82	4.6	709	2	Q9XSJ1	BOVIN	Q9xsl1	bos taurus	945	81.5	4.6	806	2	Q4S9K9	TESTNG	Q4s9k9	tetradodon n
873	82	4.6	709	2	Q08702	RAT	Q08702	rattus norv	946	81.5	4.6	815	1	CAN3	MACPA	Q94197	macaca fasc
874	82	4.6	737	2	Q70376	RAT	Q70376	rattus norv	947	81.5	4.6	824	2	Q8A3C4	BACFN	Q8a3c4	bacteroides
875	82	4.6	745	2	Q59U26	CANAL	Q59u26	candida alb	948	81.5	4.6	829	2	Q5LGP6	BACFN	Q5lgp6	bacteroides
876	82	4.6	757	2	Q70482	RAT	Q70482	rattus norv	949	81.5	4.6	833	2	Q5RHY1	BRARE	Q5rhy1	brachydanto
877	82	4.6	785	2	Q9QZP9	RAT	Q9qzpf	rattus norv	950	81.5	4.6	854	2	Q61E29	CABBR	Q61e29	caenorhabdi
878	82	4.6	880	1	TYROQ3	MOUSE	P55144	mus muscullu	951	81.5	4.6	857	2	Q512D6	CANFA	Q512d6	canis faml1
879	82	4.6	880	2	Q6WZM6	MOUSE	Q6wzm6	mus muscullu	952	81.5	4.6	925	1	Q42595	XENLA	Q42595	xenopus lae
880	82	4.6	912	2	Q4KKU8	HUMAN	Q4kku8	homo sapien	953	81.5	4.6	925	2	CORO7	HUMAN	Q59e18	homo sapien
881	82	4.6	1007	1	GRID2	HUMAN	Q43424	homo sapien	954	81.5	4.6	944	2	Q59E18	DROME	Q59e18	drosophila
882	82	4.6	1007	2	Q4KKV0	HUMAN	Q4kkv0	homo sapien	955	81.5	4.6	1005	2	Q54YD8	DICD1	Q54yd8	dictyosteli
883	82	4.6	1007	2	Q4KKU9	HUMAN	Q4kku9	homo sapien	956	81.5	4.6	1015	2	Q4YNU8	PLABE	Q4ynu8	plasmodiu
884	82	4.6	1009	2	Q59FZ1	HUMAN	Q59fz1	homo sapien	957	81.5	4.6	1187	2	Q93284	FUGRU	Q93284	figu rubrip
885	82	4.6	1038	2	Q8CHM3	MOUSE	Q8chm3	mus muscullu	958	81.5	4.6	1194	2	Q93962	9TRNG	Q93962	glomus vers
886	82	4.6	1166	2	Q8OVPO	MOUSE	Q8ovpo	mus muscullu	959	81.5	4.6	1194	2	Q7TPV3	MOUSE	Q7tpv3	mus muscullu
887	82	4.6	1303	2	Q6PA47	XENLA	Q6pa47	xenopus lae	960	81.5	4.6	1214	2	Q7S054	HUMAN	Q7s054	homo sapien
888	82	4.6	1858	2	Q5CRN8	CRYPV	Q5c8n8	cryptospori	961	81.5	4.6	1214	2	Q4SCTR	TESTNG	Q4sctr	tetradodon n
889	82	4.6	2036	1	GRIPB	HUMAN	Q6qyq7	homo sapien	962	81.5	4.6	1253	2	Q5HAB5	EBRRW	Q5hab5	ethiopia r
890	82	4.6	2262	2	Q5CID4	CRYHO	Q5cid4	cryptospori	963	81.5	4.6	1304	2	Q5HAB5	EBRRW	Q5hab5	ethiopia r
891	82	4.6	2289	2	Q4S3T6	TESTNG	Q4s3t6	tetradodon n	964	81.5	4.6	1470	2	Q5L503	CHILAB	Q5l503	chlamydomo
892	82	4.6	2289	2	Q4S3T6	TESTNG	Q4s3t6	tetradodon n	965	81.5	4.6	1518	2	Q5B7M8	EBMENT	Q5b7m8	aspergillus
893	82	4.6	2940	2	Q81HP9	PLAF7	Q81hp9	pseudomonas	966	81.5	4.6	1596	2	Q9HC16	HUMAN	Q9hc16	homo sapien
894	82	4.6	3173	2	Q882M6	PEBSM	Q882m6	pseudomonas	967	81.5	4.6	2212	2	Q8NHN3	HUMAN	Q8nhn3	homo sapien
895	82	4.6	3562	1	CSBP2	CHICK	Q90953	gallus galli	968	81.5	4.6	2284	2	Q815Y7	PLAF7	Q815y7	plasmidiu
896	82	4.6	5636	2	Q96RW7	HUMAN	Q96rw7	homo sapien	969	81.5	4.6	6620	2	Q96AA2	HUMAN	Q96aa2	homo sapien
897	82	4.6	5636	2	Q6MY89	ASPFU	Q6my89	aspergillus	970	81.5	4.6	6620	2	Q5VST9	HUMAN	Q5vst9	homo sapien
898	82	4.6	206	2	Q4W846	ASPFU	Q4w846	aspergillus	971	81.5	4.6	1449	2	Q86L22	DICD1	Q86l22	d simlar t
899	82	4.6	206	2	Q4W846	ASPFU	Q4w846	aspergillus	972	81.5	4.6	151	2	Q867B8	PIG	Q867b8	sus scrofa
900	81.5	4.6	211	2	Q7PVK5	ANOGA	Q7pvk5	anopheles g	973	81	4.6	252	2	Q957B1	HUMAN	Q957b1	homo sapien
901	81.5	4.6	236	2	Q6P5S3	ANOGA	Q6p5s3	homo sapien	974	81	4.6	266	2	Q8AYP8	RAT	Q8ayp8	rattus norv
902	81.5	4.6	275	2	Q8AUV1	XENLA	Q8auv1	xenopus lae	975	81	4.6	272	2	Q6A1U5	HORSE	Q6a1u5	equus cabal
903	81.5	4.6	301	2	Q70864	ANOGA	Q70864	anopheles g	976	81	4.6	326	2	Q81AY7	9PERC	Q81ay7	sphaerooides
904	81.5	4.6	329	1	ICOSL1	HUMAN	Q75144	homo sapien	977	81	4.6	330	2	Q87W83	PEBSM	Q87w83	pseudomonas
905	81.5	4.6	336	2	Q91AT6	9PERC	Q91at6	sphaerooides	978	81	4.6	333	2	Q5SNP5	BRARE	Q5snp5	brachydanto
906	81.5	4.6	340	2	Q91AZ6	9PERC	Q91az6	sphaerooides	979	81	4.6	338	1	LSAMP	HUMAN	Q13449	homo sapien
907	81.5	4.6	352	2	Q08266	HUMAN	Q08266	homo sapien	980	81	4.6	374	2	Q43741	BROFI	Q43741	bromelaadla



981	81	4.6	423	2	Q9UAG6_DICDI	Q9uag6 dictyosteli	1054	80.5	4.5	823	2	Q39594_CHIRE	Q39594 chlamydomon
982	81	4.6	423	2	Q54D73_DICDI	Q54d73 dictyosteli	1055	80.5	4.5	932	2	Q7TQ14_PAT	Q7tq14 ratu
983	81	4.6	425	2	Q61FM2_CABRR	Q61fm2 caenorhabdi	1056	80.5	4.5	976	2	Q8IRID5_BRARE	Q8irid5 brachydantio
984	81	4.6	451	2	Q8BD40_VIBVU	Q8bd40 vibrio vuln	1057	80.5	4.5	976	2	Q8JFR5_BRARE	Q8jfr5 brachydantio
985	81	4.6	481	2	Q5K374_BRARE	Q5k374 brachydantio	1058	80.5	4.5	976	2	Q9W755_BRARE	Q9w755 brachydantio
986	81	4.6	489	1	CP3102_DROME	Q9ngx9 drosophilla	1059	80.5	4.5	1079	2	Q5QGS4_MOUSE	Q5qgs4 mus musculu
987	81	4.6	507	2	Q9U315_CABEL	Q9u315 caenorhabdi	1060	80.5	4.5	1114	2	Q5QGS4_MOUSE	Q5qgs4 mus musculu
988	81	4.6	517	2	Q4RFQ2_TETNG	Q4rfq2 tetradon n	1061	80.5	4.5	1293	2	Q6WLN9_9DIPT	Q6wln9 heterostomu
989	81	4.6	521	1	CD166_CANPA	Q46634 canis famli	1062	80.5	4.5	1304	2	Q5A2D6_CANAL	Q5a2d6 candida alb
990	81	4.6	580	2	Q54D58_DICDI	Q54d58 dictyosteli	1063	80.5	4.5	1364	1	Q5F475_CHICK	Q5f475 xenopus lae
991	81	4.6	617	2	Q5MY54_BRARE	Q5my54 brachydantio	1064	80.5	4.5	1389	2	Q7Z3Y2_HUMAN	Q7z3y2 gallus galli
992	81	4.6	624	2	Q94AX9_ARATH	Q94ax9 arabidopsis	1065	80.5	4.5	1465	2	Q6UAG6_CYEID	Q6uag6 cretropharyn
993	81	4.6	643	2	Q7Y231_ARATH	Q7y231 arabidopsis	1066	80.5	4.5	1677	2	Q4R321_TETNG	Q4r321 tetradon n
994	81	4.6	648	2	Q6WTL5_XENLA	Q6wtl5 xenopus lae	1067	80.5	4.5	1702	2	PPERS_HUMAN	Q13132 homo sapien
995	81	4.6	700	2	Q4Q3A0_LEIMA	Q4q3a0 leishmania	1068	80.5	4.5	2170	2	Q5CGS0_CRYPO	Q5cgs0 cryptospori
996	81	4.6	745	2	Q6NNX7_DROME	Q6nnx7 drosophila	1069	80.5	4.5	2253	2	Q5CQ17_CRYPO	Q5cq17 cryptospori
997	81	4.6	760	1	YC85_YEAST	P25574 saccharomyc	1070	80.5	4.5	2253	2	Q8JYV2_PILCO	Q8jyv2 ljunqan vir
998	81	4.6	769	2	Q97I59_CIOAB	Q97i59 clostridium	1071	80.5	4.5	2253	2	Q95MJ2_MACRG	Q95mj2 macropus ru
999	81	4.6	829	1	CADH3_HUMAN	P22223 homo sapien	1072	80.5	4.5	2358	2	Q872P1_NEUCR	Q872p1 neurospora
1000	81	4.6	837	2	Q8G4P3_BIFLO	Q8g4p3 bifidobacte	1073	80.5	4.5	2398	2	Q5DUA4_MOUSE	Q5du44 mus musculu
1001	81	4.6	937	2	Q5RDT8_PONPY	Q5rdt8 pongo pygma	1074	80.5	4.5	3267	2	Q5DUU4_MOUSE	Q5duu4 mus musculu
1002	81	4.6	1079	2	Q6E7G6_CANFA	Q6e7g6 canis famli	1075	80.5	4.5	3283	2	Q5DUU5_MOUSE	Q5duu5 mus musculu
1003	81	4.6	1150	2	Q4SL82_TETNG	Q4sl82 tetradon n	1076	80.5	4.5	3337	2	Q9TWY4_CABEL	Q9twy4 caenorhabdi
1004	81	4.6	1180	2	Q5IS40_PANTR	Q5is40 pan troglod	1077	80.5	4.5	3343	1	CAD3_CABEL	Q5w617 caenorhabdi
1005	81	4.6	1196	2	Q96TF1_CYPCA	Q96tf1 cypinus ca	1078	80.5	4.5	3352	2	Q5DUJ3_MOUSE	Q5duj3 mus musculu
1006	81	4.6	1196	2	Q9P3A8_SCHPO	Q9p3a8 schizosacch	1079	80.5	4.5	3354	1	CAD23_MOUSE	Q9pff4 mus musculu
1007	81	4.6	1204	1	NRCAM_HUMAN	Q92823 homo sapien	1080	80.5	4.5	3358	1	CSRG2_MOUSE	Q62059 mus musculu
1008	81	4.6	1305	2	Q6ZPE0_MOUSE	Q6zpe0 mus musculu	1081	80.5	4.5	5992	1	Q5W615_CABEL	Q5w615 caenorhabdi
1009	81	4.6	1335	2	Q51BY2_ENTHI	Q51by2 entamoeba h	1082	80.5	4.5	6632	2	UNC89_CABEL	Q01761 caenorhabdi
1010	81	4.6	1478	2	Q59H90_HUMAN	Q59h90 homo sapien	1083	80.5	4.5	7122	2	Q5W616_CABEL	Q5w616 caenorhabdi
1011	81	4.6	1488	2	Q64604_RAT	Q64604 rattus norv	1084	80.5	4.5	7441	2	Q7Z120_CABEL	Q7z120 caenorhabdi
1012	81	4.6	1901	2	Q7UI70_RHOBA	Q7ui70 rhodospirell	1085	80.5	4.5	8081	2	Q8WV18_HUMAN	Q8wv18 homo sapien
1013	81	4.6	2219	2	Q88W19_LACPL	Q88w19 lactobacilli	1086	80.5	4.5	184	2	Q9UKJ0_HUMAN	Q9ukj0 homo sapien
1014	81	4.6	2283	2	Q4N557_TBPPA	Q4n557 theileria p	1087	80.5	4.5	227	2	Q9M111_MOUSE	Q9m111 mus musculu
1015	81	4.6	2402	2	Q9AER7_STARP	Q9aer7 staphylococ	1088	80.5	4.5	235	2	Q5VSN6_BRARE	Q5vsn6 brachydantio
1016	81	4.6	2402	2	Q5HKR4_STABO	Q5hkr4 staphylococ	1089	80.5	4.5	276	2	Q640S5_XENTR	Q640s5 xenopus tro
1017	81	4.6	2747	2	Q5GQM9_9CAUD	Q5gqm9 bacteriophia	1090	80.5	4.5	327	2	Q4RTW7_TETNG	Q4rtw7 tetradon n
1018	80.5	4.5	261	2	Q9W6V1_CHICK	Q9w6v1 gallus galli	1091	80.5	4.5	337	2	Q4RTW7_TETNG	Q4rtw7 brachydantio
1019	80.5	4.5	290	2	Q8CR9R_STARP	Q8cr9r staphylococ	1092	80.5	4.5	338	1	LSAMP_RAT	Q8uv29 brachydantio
1020	80.5	4.5	291	2	Q5HNO0_STABO	Q5hno0 staphylococ	1093	80.5	4.5	341	1	KI2L3_HUMAN	Q62813 h killer ce
1021	80.5	4.5	346	1	EPNBI_HUMAN	P98172 homo sapien	1094	80.5	4.5	341	1	LSAMP_MOUSE	Q8b1k3 mus musculu
1022	80.5	4.5	371	2	Q4WVPI_BACCE	Q4wvpi bacillus ce	1095	80.5	4.5	343	2	Q8X5J1_BCO57	Q8x5j1 escherichia
1023	80.5	4.5	371	2	Q633A8_BACCH	Q633a8 bacillus ce	1096	80.5	4.5	343	2	Q5M960_RAT	Q5m960 ratu
1024	80.5	4.5	371	2	Q6HCJ8_BACHK	Q6hcj8 bacillus th	1097	80.5	4.5	361	2	Q6XJ12_BACLD	Q6xj12 brachydantio
1025	80.5	4.5	371	2	Q72249_BACCI	Q72249 bacillus ce	1098	80.5	4.5	365	2	Q66MNA_PETMA	Q66mna oncorhynzon
1026	80.5	4.5	371	2	Q816Y2_BACCR	Q816y2 bacillus ce	1099	80.5	4.5	378	2	Q6XNL6_PETMA	Q6xnl6 pseudomonas
1027	80.5	4.5	376	1	GCPI1_ABATH	Q94d08 arabidopsis	1100	80.5	4.5	436	2	Q9J563_HUMAN	Q9j563 homo sapien
1028	80.5	4.5	382	2	Q5X143_RAT	Q5x143 rattus norv	1101	80.5	4.5	440	2	Q6MK36_MACMU	Q6mk36 macaca mla
1029	80.5	4.5	385	2	Q4SOV8_TETNG	Q4sov8 tetradon n	1102	80.5	4.5	465	2	Q67TB8_STYTH	Q67tb8 symbiodace
1030	80.5	4.5	388	2	Q8R464_MOUSE	Q8r464 mus musculu	1103	80.5	4.5	482	1	ABCD_PSEAE	P16275 pseudomonas
1031	80.5	4.5	462	1	MURD_CIOAB	Q97db9 clostridium	1104	80.5	4.5	492	2	Q6UEG2_ASPPA	Q6ueg2 aspergillus
1032	80.5	4.5	472	2	Q811T8_MOUSE	Q811t8 mus musculu	1105	80.5	4.5	509	2	Q5CUC7_CRYPO	Q5cuc7 cryptospori
1033	80.5	4.5	473	2	Q5RGHS_SALPI	Q5rghs salmoneila	1106	80.5	4.5	529	2	Q81WX2_HUMAN	Q81wx2 homo sapien
1034	80.5	4.5	473	2	Q8Z809_SALPI	Q8z809 salmoneila	1107	80.5	4.5	529	2	Q6SJI2_BACLD	Q6sji2 brachydantio
1035	80.5	4.5	476	1	YCAM_BCOLI	Q62056 mus musculu	1108	80.5	4.5	535	2	Q6SJI2_BACLD	Q6sji2 brachydantio
1036	80.5	4.5	476	1	YCAM_BCOLI	P75835 escherichia	1109	80.5	4.5	574	2	Q58E93_BRARE	Q5e933 brachydantio
1037	80.5	4.5	498	2	Q886D9_PSEBM	Q886d9 pseudomonas	1110	80.5	4.5	609	2	Q6Z911_RINDK	Q6z911 rinderpest
1038	80.5	4.5	507	2	Q5K4Q3_PIG	Q5k4q3 sus scrofa	1111	80.5	4.5	753	2	Q54K07_DICDI	Q54k07 dictyosteli
1039	80.5	4.5	514	2	Q5SQUB_MOUSE	Q5squb mus musculu	1112	80.5	4.5	624	2	Q9VUD0_DROME	Q9vud0 drosophila
1040	80.5	4.5	540	2	Q8XEB5_BCO57	Q8xeb5 escherichia	1113	80.5	4.5	627	2	Q7SXCI_BRARE	Q7sxc1 brachydantio
1041	80.5	4.5	546	2	Q8OX70_MOUSE	Q8ox70 mus musculu	1114	80.5	4.5	633	2	PBL1_CRYNV	Q98p22 cryptococcu
1042	80.5	4.5	548	2	Q99NB3_MOUSE	Q99nb3 mus musculu	1115	80.5	4.5	637	1	Q75JX7_DICDI	Q75jx7 dictyosteli
1043	80.5	4.5	556	2	Q8BDM4_VIBVU	Q8bdm4 vibrio vuln	1116	80.5	4.5	753	2	Q68DA2_HUMAN	Q68da2 homo sapien
1044	80.5	4.5	564	2	Q7ZU00_BRARE	Q7zu00 brachydantio	1117	80.5	4.5	865	2	Q64R21_XENLA	Q64r21 xenopus lae
1045	80.5	4.5	602	2	Q6CYJ9_HUMAN	Q6cyj9 homo sapien	1118	80.5	4.5	902	1	BRCC4_CRIGR	Q94tm7 cretropharyn
1046	80.5	4.5	636	2	Q4FWE0_LEIMA	Q4fwe0 leishmania	1119	80.5	4.5	957	2	Q64IF3_XENLA	Q64if3 xenopus lae
1047	80.5	4.5	662	2	Q6O926_HUMAN	Q6o926 homo sapien	1120	80.5	4.5	960	2	Q6BXD5_DEBHA	Q6bxds debrayomyce
1048	80.5	4.5	683	2	Q5CRD8_CRYPV	Q5cird8 cryptospori	1121	80.5	4.5	1000	2	Q4TBK4_TETNG	Q4tbk4 tetradon n
1049	80.5	4.5	707	1	Q7XNT7_ORYSA	Q7xnt7 oryza sativ	1122	80.5	4.5	1005	2	P79921_XENLA	P79921 xenopus lae
1050	80.5	4.5	721	1	DPD5_ASPPU	Q13479 aspergillus	1123	80.5	4.5	1040	2	CNTN2_HUMAN	Q02246 homo sapien
1051	80.5	4.5	739	2	Q53P17_HUMAN	Q53p17 homo sapien	1124	80.5	4.5	1040	2	Q5T054_HUMAN	Q5t054 homo sapien
1052	80.5	4.5	739	2	Q865F2_RABIT	Q865f2 oryctolagus	1125	80.5	4.5	1170	1	TSP1_MOUSE	P35441 mus musculu
1053	80.5	4.5	789	2	Q8RSZ5_BACTU	Q8rsz5 bacillus th	1126	80.5	4.5				



1127	80	4.5	1192	2	081yz8_BACAN	081yz8 bacillus an	1200	79	4.5	323	2	08ND22_HUMAN	08ndd2 homo sapien
1128	80	4.5	1310	2	081714_CABEL	081714 caenorhabdi	1201	79	4.5	340	2	06PKA9_MOUSE	06pkaa2 mus musculu
1129	80	4.5	1431	2	08EW23_MYCPE	08ew23 mycoplasma	1202	79	4.5	342	2	08MK29_MACMU	08mk29 macaca mula
1130	80	4.5	1925	2	09YRB3_YVIRU	09yrb3 nudaurelia	1203	79	4.5	389	2	05U3R8_BRARR	05u3r8 brachydanio
1131	80	4.5	2195	2	0723M7_LISMF	0723m7 listeria mo	1204	79	4.5	406	2	08BP77_MOUSE	08bp77 mus musculu
1132	80	4.5	2456	2	081715_CABEL	081715 caenorhabdi	1205	79	4.5	410	2	081JPS_BACAN	081jps bacillus an
1133	80	4.5	3064	2	06UDW7_PLAFA	06udw7 plasmodium	1206	79	4.5	412	2	06MZS4_HUMAN	06mzs4 homo sapien
1134	80	4.5	5229	2	07RTF4_PLAYO	07rtf4 plasmodium	1207	79	4.5	429	2	08BES1_MOUSE	08bes1 m mus mucu
1135	79.5	4.5	151	2	08C2T1_MOUSE	08c2t1 mus musculu	1208	79	4.5	438	1	Y3532_METUA	08c289 methanococ
1136	79.5	4.5	236	2	06F1Q7_HUMAN	06f1q7 homo sapien	1209	79	4.5	440	2	08MK37_MACMU	08mk37 macaca mula
1137	79.5	4.5	237	2	06DHM4_HUMAN	06dhm4 homo sapien	1210	79	4.5	446	2	P79762_CHICK	P79762 gallus galli
1138	79.5	4.5	244	2	08S0B6_PIG	08s0b6 sus scrofa	1211	79	4.5	446	2	09WPF8_CHICK	09wpf8 gallus galli
1139	79.5	4.5	249	1	MYP0_CHICK	P37301 gallus galli	1212	79	4.5	446	2	Q4VU46_CHICK	Q4vu46 gallus galli
1140	79.5	4.5	257	1	Q5WPT1_SHEEP	Q5wpt1 ovis aries	1213	79	4.5	446	2	Q4VU49_CHICK	Q4vu49 gallus galli
1141	79.5	4.5	289	2	Q97XZ7_SULISO	Q97xz7 sulfobacill	1214	79	4.5	446	2	Q4VU50_CHICK	Q4vu50 gallus galli
1142	79.5	4.5	321	2	Q5WRG0_SHEEP	Q5wrg0 ovis aries	1215	79	4.5	446	2	Q4VU57_CHICK	Q4vu57 gallus galli
1143	79.5	4.5	328	1	CYSP4_BRANA	P25251 brassica na	1216	79	4.5	446	2	Q4VU66_CHICK	Q4vu66 gallus galli
1144	79.5	4.5	345	2	Q6GM08_XENIA	Q6gm08 xenopus lae	1217	79	4.5	446	2	Q4VU63_CHICK	Q4vu63 gallus galli
1145	79.5	4.5	368	2	Q4VA91_MOUSE	Q4va91 mus musculu	1218	79	4.5	451	2	Q7M0R3_VIBVY	Q7mqr3 vibrio vuln
1146	79.5	4.5	399	2	Q8EMV2_OCEBH	Q8emv2 oceanobacti	1219	79	4.5	461	2	Q4RL18_CABEL	Q4rl18 caenorhabdi
1147	79.5	4.5	400	2	Q8ZHN7_YERPE	Q8zhn7 yerinia pe	1220	79	4.5	463	1	STHA_PSEBK	Q8hkx8 pseudomonas
1148	79.5	4.5	400	2	Q66Z6_YERPS	Q66z6 yerinia ps	1221	79	4.5	474	2	Q4V8B3_RAT	Q4v8b3 rattus norv
1149	79.5	4.5	401	2	Q93534_XENIA	Q93534 xenopus lae	1222	79	4.5	479	2	Q9K6X5_BACHD	Q9k6x5 bacillus ha
1150	79.5	4.5	418	2	Q7RLB8_PLAYO	Q7rlb8 plasmodium	1223	79	4.5	490	1	RLUD1_PONPY	07c021 homo sapien
1151	79.5	4.5	430	1	TPSN_CHICK	Q73895 gallus galli	1224	79	4.5	490	1	RLUD1_PONPY	05c066 pongo pygma
1152	79.5	4.5	430	2	Q761J6_COTJA	Q761j6 streptomyx co	1225	79	4.5	491	2	Q8GZP5_LYCES	Q8gzp5 lycopersico
1153	79.5	4.5	446	2	Q69885_STRCO	Q69885 streptomyc	1226	79	4.5	511	2	Q4IG29_GIBBEZ	Q4ig29 gibberella
1154	79.5	4.5	453	2	Q4SSUT_TETNG	Q4ssut tetraodon n	1227	79	4.5	524	2	Q8LTK1_9CAUD	Q8ltk1 lactococcus
1155	79.5	4.5	474	2	Q7ZUJ9_BRARE	Q7zu93 brachydanio	1228	79	4.5	526	2	Q51SR0_MAGGR	Q51seo magnaporthe
1156	79.5	4.5	490	1	TIME_ECOLI	Q47282 escherichia	1229	79	4.5	526	2	Q8WNA6_MOUSE	Q8wna6 mus musculu
1157	79.5	4.5	510	2	Q5E9Z9_BOVIN	Q5e9z9 bos taurus	1230	79	4.5	571	2	Q5B307_ICTPU	Q5bg07 ictalurus p
1158	79.5	4.5	516	2	Q4L8B1_STAHJ	Q4l8b1 staphylococ	1231	79	4.5	584	2	Q9Y3Y8_HUMAN	Q9y3y8 homo sapien
1159	79.5	4.5	520	2	Q8GDL8_PHOLU	Q8gdl8 haloarchabu	1232	79	4.5	586	2	Q5CFV6_CRYHO	Q5cfv6 cryptospori
1160	79.5	4.5	524	2	Q5V7K4_HALMA	Q5v7k4 haloarchabu	1233	79	4.5	590	2	Q9P4U4_CANTR	Q9p4u4 candida tro
1161	79.5	4.5	524	2	Q7PSJ8_ANOGA	Q7psj8 anopheles g	1234	79	4.5	611	2	Q91BR6_XENIA	Q91br6 xenopus lae
1162	79.5	4.5	524	2	Q86SD2_CIOIN	Q86sd2 clona intes	1235	79	4.5	611	2	Q9PTT0_XENIA	Q9ptt0 xenopus lae
1163	79.5	4.5	641	2	Q75WK5_ORYIA	Q75wk5 oryzias lat	1236	79	4.5	617	2	Q51F12_BRARE	Q51f12 brachydanio
1164	79.5	4.5	729	2	Q4RFH6_TETNG	Q4rfh6 tetraodon n	1237	79	4.5	630	2	Q4WG72_ASPTU	Q4wg72 aspergillus
1165	79.5	4.5	740	1	PECAL_PIG	Q95242 sus scrofa	1238	79	4.5	644	2	Q6GINS_XENIA	Q6gins xenopus lae
1166	79.5	4.5	743	2	Q6P4H5_HUMAN	Q6p4h5 homo sapien	1239	79	4.5	653	2	Q4P819_USITMA	Q4p819 usellago ma
1167	79.5	4.5	821	2	Q8CT56_MOUSE	Q8ct56 mus musculu	1240	79	4.5	657	2	P73359_SYNY3	P73359 synechocyst
1168	79.5	4.5	845	2	Q91YY0_MOUSE	Q91yy0 mus musculu	1241	79	4.5	711	2	Q8YR89_MOUSE	Q8y889 mus musculu
1169	79.5	4.5	859	1	PMS2_MOUSE	P54279 mus musculu	1242	79	4.5	778	2	Q9N4B1_CABEL	Q9n4b1 caenorhabdi
1170	79.5	4.5	873	1	VLDLR_MOUSE	P98156 mus musculu	1243	79	4.5	785	2	Q7TNP4_MOUSE	Q7tnp4 mus musculu
1171	79.5	4.5	875	2	Q4RKX6_TETNG	Q4rkx6 tetraodon n	1244	79	4.5	795	2	Q6O0V2_MYCHY	Q6o0v2 mycoplasma
1172	79.5	4.5	924	2	Q7JL80_TREDE	Q7jl80 treponema d	1245	79	4.5	807	2	Q8PTR2_METMA	Q8ptr2 methanosarc
1173	79.5	4.5	961	1	ROBO4_RAT	Q8W087 rattus norv	1246	79	4.5	853	2	Q19372_CABEL	Q19372 caenorhabdi
1174	79.5	4.5	980	1	CSF1R_FELCA	P13369 felis silve	1247	79	4.5	917	2	Q767W4_PIG	Q767w4 sus scrofa
1175	79.5	4.5	1043	1	CEPA07_XENIA	Q6pa07 xenopus lae	1248	79	4.5	928	2	Q61XY3_CABER	Q61xy3 caenorhabdi
1176	79.5	4.5	1162	1	TRF2_HUMAN	Q9unuy4 homo sapien	1249	79	4.5	977	2	Q8GZAO_ARATH	Q8gzao arabidopsis
1177	79.5	4.5	1171	2	Q8OYQ1_MOUSE	Q8oyq1 mus musculu	1250	79	4.5	996	2	Q8BM64_DEBHA	Q8bm64 debaromyce
1178	79.5	4.5	1171	2	Q8GGB2_MOUSE	Q8ggb2 mus musculu	1251	79	4.5	1017	2	Q4SKJ7_TETNG	Q4skj7 tetraodon n
1179	79.5	4.5	1197	2	Q4LWS3_9BURI	Q4lws3 burkholderi	1252	79	4.5	1030	2	Q7XTP4_ORYSA	Q7xtp4 oryza sativ
1180	79.5	4.5	1262	2	Q5AKK4_EMBNI	Q5akk4 aspergillus	1253	79	4.5	1104	2	Q9FKR7_ARATH	Q9fkr7 arabidopsis
1181	79.5	4.5	1342	2	Q9GPP6_DROME	Q9gpp6 drosophila	1254	79	4.5	1177	2	Q6GGB1_XENIA	Q6ggb1 xenopus lae
1182	79.5	4.5	1342	2	Q9VPT7_DROME	Q9vpt7 drosophila	1255	79	4.5	1218	2	Q4N9H0_THIEPA	Q4n9h0 thelperia p
1183	79.5	4.5	1355	2	Q5TUE1_ANOGA	Q5tue1 anopheles g	1256	79	4.5	1228	1	ALAS_ARATH	Q9agq3 arabidopsis
1184	79.5	4.5	1465	1	MYOM2_HUMAN	P54296 homo sapien	1257	79	4.5	1264	2	P91767_MANSE	P91767 menduca sex
1185	79.5	4.5	1614	1	Q7RMN8_PLAYO	Q7rmn8 plasmodium	1258	79	4.5	1361	1	GLI4_XENIA	Q91661 xenopus lae
1186	79.5	4.5	1670	2	Q7QZP4_GIALA	Q7qzp4 giardia lam	1259	79	4.5	1382	1	MET_CANFA	Q75zy3 canis famli
1187	79.5	4.5	1838	2	Q88Z07_MOUSE	Q88z07 mus musculu	1260	79	4.5	1390	2	Q7RRL3_PLAYO	Q7rrl3 plasmodium
1188	79.5	4.5	2253	2	Q8ATV1_9PICO	Q8atv1 ljunjan vir	1261	79	4.5	1416	2	Q5AS50_EMBNI	Q5as50 aspergillus
1189	79.5	4.5	2256	2	Q8ATV19_9PICO	Q8atv19 ljunjan vir	1262	79	4.5	1465	2	Q6ZOB3_MOUSE	Q6zob3 mus musculu
1190	79.5	4.5	2658	2	Q4QG73_LEIMA	Q4qg73 leishmania	1263	79	4.5	1887	2	Q9W67_9MURI	Q9w67 rattus sp.
1191	79.5	4.5	2706	2	Q97292_PLAV7	Q97292 plasmodium	1264	79	4.5	1905	2	Q5VUJ9_HUMAN	Q5vu19 homo sapien
1192	79	4.5	158	2	Q15225_HUMAN	Q15225 homo sapien	1265	79	4.5	1925	2	Q6BHV1_MOUSE	Q6bhv1 mus musculu
1193	79	4.5	210	2	Q9AKC9_CAUCR	Q9akc9 caulobacter	1266	79	4.5	4010	1	FRSVI_MOUSE	Q8oc14 homo sapien
1194	79	4.5	222	2	Q8BWK8_MACPR	Q8bkw8 macrocephid	1267	79	4.5	173	2	Q5VVF8_HUMAN	Q5vff8 pongo pygma
1195	79	4.5	226	2	Q86P32_DROME	Q86p32 drosophila	1268	79.5	4.4	261	2	Q5R602_PONPY	Q5r602 xenopus lae
1196	79	4.5	244	2	Q927X2_LISIN	Q927x2 listeria in	1269	78.5	4.4	292	2	Q5HZR6_XENIA	Q5hzr6 xenopus lae
1197	79	4.5	260	2	Q53H40_HUMAN	Q53h40 homo sapien	1270	78.5	4.4	300	1	CEAL19_HUMAN	Q7z692 homo sapien
1198	79	4.5	271	2	Q95161_GADMO	Q95161 gadus moriu	1271	78.5	4.4	303	2	Q4X5M9_PLACH	Q4x5m9 placcha
1199	79	4.5	274	2	Q5MD24_PIG	Q5md24 sus scrofa	1272	78.5	4.4	305	1	PEX26_MACFA	Q9p665 macaca fasc



1273	78.5	4.4	305	2	Q4HXQ1_GIBBE	Q4hxq1 gibberella	1346	78	4.4	353	1	CEPU1_CHICK	Q99773 gallus galli
1274	78.5	4.4	308	2	Q5WRG1_SHEEP	Q5wrg1 ovine aries	1347	78	4.4	375	2	Q6S280_ASF	Q6S280 african swi
1275	78.5	4.4	318	2	Q91664_XENLA	Q91664 xenopus lae	1348	78	4.4	399	1	V5IG4_HUMAN	Q9Y279 homo sapien
1276	78.5	4.4	325	2	Q501V7_BRASR	Q501v7 brachydano	1349	78	4.4	402	2	Q35444_MOUSE	Q35444 mus musculu
1277	78.5	4.4	333	2	Q7MR78_WOLSTU	Q7mr78 wolfeila s	1350	78	4.4	412	2	Q8G6P7_BIFLO	Q8G6P7 bifidobacte
1278	78.5	4.4	341	2	Q59EM4_HUMAN	Q59em4 homo sapien	1351	78	4.4	423	2	Q9RB12_ACTIAD	Q9RB12 actinobact
1279	78.5	4.4	381	2	Q753P2_ASHGO	Q753p2 ashbya goes	1352	78	4.4	435	2	Q4TBP7_TERTNG	Q4tbp7 tetradon n
1280	78.5	4.4	388	2	Q8NFZ8_HUMAN	Q8nfz8 homo sapien	1353	78	4.4	446	2	Q4VU54_CHICK	Q4vu54 gallus galli
1281	78.5	4.4	429	1	IGHF_RAT	IGHfz8 homo sapien	1354	78	4.4	446	2	Q4VU62_CHICK	Q4vu62 gallus galli
1282	78.5	4.4	431	2	Q8X022_NEUCR	Q8x022 neuropept	1355	78	4.4	452	2	Q4VU62_CHICK	Q4vu62 gallus galli
1283	78.5	4.4	434	2	Q4RFG0_TETNG	Q4rfg0 tetradon n	1356	78	4.4	452	2	Q4VU62_CHICK	Q4vu62 gallus galli
1284	78.5	4.4	439	2	Q5R615_PONPY	Q5r615 pongo pygma	1357	78	4.4	473	2	Q9VU05_DROME	Q9vu05 drosophila
1285	78.5	4.4	452	2	Q76773_LUCPU	Q76773 lucilla cup	1358	78	4.4	473	2	Q4M019_BACCE	Q4mq19 bacillus ce
1286	78.5	4.4	459	2	Q9ES33_ARATH	Q9es33 arabidopsis	1359	78	4.4	490	2	Q74491_SCHPO	Q74491 schizosacch
1287	78.5	4.4	463	2	Q4ML18_BACCE	Q4ml18 bacillus ce	1360	78	4.4	491	2	Q9VKX6_DROME	Q9vkx6 drosophila
1288	78.5	4.4	467	1	SIGL1_MOUSE	Q91y57 mus musculu	1361	78	4.4	515	2	Q4V518_DROME	Q4v518 drosophila
1289	78.5	4.4	471	2	Q9DAV5_MOUSE	Q9dav5 mus musculu	1362	78	4.4	550	2	Q61CX3_CAEBR	Q61cx3 caenorhabdi
1290	78.5	4.4	497	1	UBRD_ECO57	P58194 escherichia	1363	78	4.4	580	2	Q5A325_CANAL	Q5a325 candida alb
1291	78.5	4.4	537	2	Q93E1T_RHILT	Q93e1t rhizobium l	1364	78	4.4	590	2	Q5TTP5_ANOGA	Q5ttd5 anopheles g
1292	78.5	4.4	539	2	Q04252_ARATH	Q04252 arabidopsis	1365	78	4.4	604	2	Q76PD3_SCHPO	Q76pd3 schizosacch
1293	78.5	4.4	542	2	Q6PAB8_XENLA	Q6pab8 xenopus lae	1366	78	4.4	606	2	Q61RH8_RAT	Q61rh8 rattus norv
1294	78.5	4.4	556	2	Q8L6Z9_ARATH	Q8l6z9 arabidopsis	1367	78	4.4	606	2	Q9ES37_MOUSE	Q9es37 mus musculu
1295	78.5	4.4	591	2	Q6NSU9_MOUSE	Q6nsu9 mus musculu	1368	78	4.4	608	2	Q578Z6_BRUAB	Q578z6 bruceella ab
1296	78.5	4.4	603	2	Q7S314_NEUCR	Q7s314 neuropept	1369	78	4.4	608	2	Q8YCV9_BRUME	Q8ycv9 bruceella su
1297	78.5	4.4	618	2	Q54BQ3_DICDI	Q54bq3 dictyosteli	1370	78	4.4	608	2	Q8FVG6_BRUST	Q8fvg6 bruceella su
1298	78.5	4.4	628	1	LU_HUMAN	Q54bq3 dictyosteli	1371	78	4.4	609	1	H5MA_RINDK	P13567 rinderpest
1299	78.5	4.4	629	2	Q8L444_ARATH	P50895 homo sapien	1372	78	4.4	612	2	Q7RE74_PLAYO	Q7re74 plasmodium
1300	78.5	4.4	638	2	Q9LF84_ARATH	Q8L444 arabidopsis	1373	78	4.4	634	2	Q8X024_SHETE	Q8x024 cryptococcu
1301	78.5	4.4	651	2	Q8BBU0_PSRSM	Q9lf84 arabidopsis	1374	78	4.4	634	2	Q9KXK0_SHETE	Q9kxk0 cryptococcu
1302	78.5	4.4	708	1	KIRP2_HUMAN	Q8bbu0 pseudomonas	1375	78	4.4	648	2	Q8R2Y2_MOUSE	Q8r2y2 mus musculu
1303	78.5	4.4	717	2	Q6C1H6_YARLI	Q6uwl6 homo sapien	1376	78	4.4	653	2	Q762C5_MOUSE	Q762c5 mus musculu
1304	78.5	4.4	721	2	Q4XIR6_ASPFU	Q6c1h6 yarrowia li	1377	78	4.4	690	2	Q5ISU0_MACFA	Q5isl0 macaca fasc
1305	78.5	4.4	751	2	Q6FKY3_CANGA	Q4xir6 aspergillus	1378	78	4.4	706	2	Q6YC14_MOUSE	Q6yc14 mus musculu
1306	78.5	4.4	831	1	SAS3_YEAST	Q6fk37 candida gla	1379	78	4.4	706	2	Q8BM11_MOUSE	Q8bm11 mus musculu
1307	78.5	4.4	844	2	Q59YK6_CANAL	P34218 saccharomyc	1380	78	4.4	761	1	NCA112_HUMAN	NCA112 homo sapien
1308	78.5	4.4	844	2	Q59YK6_CANAL	Q59yk6 candida alb	1381	78	4.4	807	2	Q59FL7_HUMAN	Q59fl7 homo sapien
1309	78.5	4.4	844	2	Q59YK6_CANAL	Q59yk6 candida alb	1382	78	4.4	836	2	Q48483_BPSPP	Q48483 bacterioph
1310	78.5	4.4	847	1	CD22_HUMAN	Q875h9 candida alb	1383	78	4.4	848	1	SEMA1_DROME	P13592 homo sapien
1311	78.5	4.4	888	2	Q7ZWM9_XENLA	P20273 homo sapien	1384	78	4.4	850	2	Q4S3Y6_TETNG	Q4s3y6 tetradon n
1312	78.5	4.4	901	2	Q57V64_9TRYP	Q7zwm9 xenopus lae	1385	78	4.4	852	2	Q8O7H7_9H1V1	Q8o7h7 human immun
1313	78.5	4.4	927	1	PCDDG_HUMAN	Q57v64 trypanosoma	1386	78	4.4	865	2	Q8O7H7_9H1V1	Q8o7h7 human immun
1314	78.5	4.4	938	2	Q64BU3_9ARCH	Q955g3 homo sapien	1387	78	4.4	884	1	CADH8_XENLA	P13552 xenopus lae
1315	78.5	4.4	1018	2	Q65L89_BURPV	Q64bu3 uncultured	1388	78	4.4	884	1	Q6NTM0_XENLA	Q6ntm0 xenopus lae
1316	78.5	4.4	1029	2	Q596X0_CARAV	Q65l89 burkholderi	1389	78	4.4	904	2	Q7QCM9_ANOGA	Q7qcm9 anopheles g
1317	78.5	4.4	1033	2	Q62C67_BURMA	Q596x0 carassius a	1390	78	4.4	905	2	Q13955_SCHPO	Q13955 schizosacch
1318	78.5	4.4	1036	1	CNTN2_CHICK	Q62c67 burkholderi	1391	78	4.4	966	2	Q4RKW2_TETNG	Q4rkw2 tetradon n
1319	78.5	4.4	1038	2	Q8YSN0_ANASP	P26885 gallus galli	1392	78	4.4	976	2	Q6LYF8_METMP	Q6lyf8 methanococc
1320	78.5	4.4	1143	2	Q69Z28_MOUSE	Q8ysn0 anabaena sp	1393	78	4.4	1002	2	Q4SP56_TETNG	Q4sp56 tetradon n
1321	78.5	4.4	1198	2	Q60T65_CAEBR	Q69z28 mus musculu	1394	78	4.4	1009	2	Q93250_XENLA	Q93250 xenopus lae
1322	78.5	4.4	1225	2	Q4WK02_ASPFU	Q60t65 caenorhabdi	1395	78	4.4	1016	2	Q8A4W1_BACCTN	Q8a4w1 bacteroides
1323	78.5	4.4	1341	2	Q4YB10_PLABE	Q4wb02 aspergillus	1396	78	4.4	1040	1	CNTN2_MOUSE	Q61330 mus musculu
1324	78.5	4.4	1465	2	Q8GYU3_ARATH	Q4yb10 plasmodium	1397	78	4.4	1288	2	Q62AK5_CAEBR	Q62aks5 kuuyveromyc
1325	78.5	4.4	1468	2	Q8SVU1_ARATH	Q8gyu3 arabidopsis	1398	78	4.4	1341	2	Q4RWS0_TETNG	Q4rws0 tetradon n
1326	78.5	4.4	1615	2	Q7ROM4_PLAYO	Q8svu1 arabidopsis	1399	78	4.4	1458	2	Q5B164_DROME	Q5b164 drosophila
1327	78.5	4.4	1638	2	Q61WT5_CAEBR	Q7rm4 plasmodium	1400	78	4.4	1503	2	Q7KIT2_DROME	Q7kit2 drosophila
1328	78.5	4.4	1897	2	Q50TXX_ENTHI	Q61wt5 caenorhabdi	1401	78	4.4	1510	2	Q4IMK0_GIBBE	Q4imk0 gibberella
1329	78.5	4.4	1915	2	Q9RPL0_9CIOT	Q50tx5 entamoeba h	1402	78	4.4	1677	2	Q54WH5_DICDI	Q54wh5 dictyosteli
1330	78.5	4.4	1994	2	Q6ZPPL2_MOUSE	Q9rpl0 acetylchro	1403	78	4.4	1924	2	Q7Z8U6_ASPOR	Q7z8u6 aspergillus
1331	78.5	4.4	2053	2	Q4WZ40_THERPA	Q6zpp2 mus musculu	1404	78	4.4	1943	2	Q4RPP4_TETNG	Q4rpp4 tetradon n
1332	78.5	4.4	2176	2	Q6W4S5_MOUSE	Q4wz40 theileria p	1405	78	4.4	3722	2	P94873_LYSIA	P94873 lysobacter
1333	78.5	4.4	257	1	UPPS_CIOAB	Q6w4s5 mus musculu	1406	78	4.4	117	2	Q7Z267_BRARE	Q7z267 brachydano
1336	78.5	4.4	2829	2	Q61VD6_STRPU	Q15027 homo sapien	1407	78	4.4	128	2	Q8BUW2_HUMAN	Q8buw2 homo sapien
1337	78.5	4.4	2829	2	Q6UXN2_HUMAN	Q61vd6 strongyloce	1408	78	4.4	154	2	Q4QLO9_HABE18	Q4ql09 haemophilus
1339	78.5	4.4	287	2	Q13984_HUMAN	Q6uxn2 homo sapien	1413	78	4.4	172	2	Q619B9_CAEBR	Q619b9 caenorhabdi
1341	78.5	4.4	292	2	Q6UY47_HUMAN	Q6uy47 homo sapien	1414	78	4.4	182	2	Q13627_CABEL	Q13627 caenorhabdi
1342	78.5	4.4	299	2	Q5XJ15_HUMAN	Q5xj15 homo sapien	1415	78	4.4	172	2	Q8MV99_TKOSC	Q8mv99 ixodes scap
1343	78.5	4.4	304	2	Q4J754_HUMAN	Q4j754 homo sapien	1416	78	4.4	202	2	Q7N6H1_PHOIL	Q7n6h1 photorhabdu
1344	78.5	4.4	313	2	Q57596_CHICK	Q57596 gallus galli	1417	78	4.4	202	2	Q7N6H1_PHOIL	Q7n6h1 photorhabdu
1345	78.5	4.4	335	1	PSGS_HUMAN	Q15538 homo sapien	1418	78	4.4	202	2	Q7N6H1_PHOIL	Q7n6h1 photorhabdu



1419	77.5	4.4	214	2	099VYI_STRAU	099VYI	stephyloccc
1420	77.5	4.4	214	2	07A716_STRAM	07A716	stephyloccc
1421	77.5	4.4	214	2	07A2T3_STRAM	07A2T3	stephyloccc
1422	77.5	4.4	214	2	07A1M5_STRAW	07A1M5	stephyloccc
1423	77.5	4.4	214	2	06GJ36_STARH	06GJ36	stephyloccc
1424	77.5	4.4	214	2	06GBJ6_STAAS	06GBJ6	stephyloccc
1425	77.5	4.4	214	2	05HI34_STAAC	05HI34	stephyloccc
1426	77.5	4.4	216	1	JULI_SCHPO	07414	echizosacch
1427	77.5	4.4	239	1	CD8A_FOLCA	P41688	Felis silve
1428	77.5	4.4	246	2	058CX4_BOVIN	058CX4	bos taurus
1429	77.5	4.4	276	2	06POR7_BRARE	06POR7	brachydanio
1430	77.5	4.4	290	2	05NTW8_ANOGA	05ntw8	anophelae g
1431	77.5	4.4	294	2	08K1Z5_MOUSE	08K1Z5	mus musculi
1432	77.5	4.4	295	2	061B19_CABER	061B19	caenorhabdi
1433	77.5	4.4	300	1	JAMI_RAT	09Jhy1	rattus norv
1434	77.5	4.4	308	2	05O3N7_BRARE	05O3n7	brachydanio
1435	77.5	4.4	310	2	04VB73_BRARE	04VB73	brachydanio
1436	77.5	4.4	314	2	05EYD8_BRARE	05eyd8	brachydanio
1437	77.5	4.4	324	2	094DM5_ARATH	094dm5	arabidopsis
1438	77.5	4.4	326	2	091AZ3_9PERC	091az3	sphoeotoides
1439	77.5	4.4	331	2	0675Z1_9UNOC	06qzz2	calyptopora
1440	77.5	4.4	333	1	CD1B1_CAVPO	09gzw4	brachyryllu
1441	77.5	4.4	338	2	06DH44_BRARB	06dh44	teleogryllu
1442	77.5	4.4	345	2	09G9W4_9ORTH	09g9w4	teleogryllu
1443	77.5	4.4	345	2	09G9W3_9ORTH	09g9w3	teleogryllu
1444	77.5	4.4	351	2	09ADX7_9RHIZ	09adx7	agrobacteri
1445	77.5	4.4	356	2	08AXL7_ONCMY	08axl7	oncorhynch
1446	77.5	4.4	360	2	07VAZ7_PROMA	07vaz7	prochloroco
1447	77.5	4.4	368	2	06P5F1_MOUSE	06f5f1	mus musculi
1448	77.5	4.4	371	2	081KQ7_BACAN	081kq7	bacillus an
1449	77.5	4.4	376	2	051ON4_ENTHI	051on4	entamoeba h
1450	77.5	4.4	410	2	05AVT0_DICDI	05avt0	dicyostele h
1451	77.5	4.4	410	2	04JOM4_AZOVU	04joh4	azotobacter
1452	77.5	4.4	425	2	096VU0_AMAMU	096vu0	amantia mus
1453	77.5	4.4	428	2	072NX8_LBPIC	072nx8	leptospira
1454	77.5	4.4	428	2	08FJV7_LEPIN	08fvj7	leptospi
1455	77.5	4.4	433	2	05S054_MOUSE	05s054	mus musculi
1456	77.5	4.4	446	2	04VTT4_9GALL	04vtc4	tetraco
1457	77.5	4.4	448	1	EXYL_STRFR	08dm9	streptococ
1458	77.5	4.4	460	2	07YTA8_BOMO	07ya8	bombay mori
1459	77.5	4.4	460	2	09CTU3_MOUSE	09ct34	mus musculi
1460	77.5	4.4	476	2	05K373_BRARE	05K373	brachydanio
1461	77.5	4.4	481	2	CNI08_MOUSE	08bj63	mus musculi
1462	77.5	4.4	490	1	SYN19_HUMAN	08686	homo sapien
1463	77.5	4.4	495	2	04TBUD_TETNG	04tbud	tetradion n
1464	77.5	4.4	510	1	MCO_KITGR	08dlv2	wisglewort
1465	77.5	4.4	513	1	SHEB1_MOUSE	p97797	m tyrosine-
1466	77.5	4.4	516	2	06O5M2_METCA	06o5m2	methyloccc
1467	77.5	4.4	536	2	07UZH7_PROMP	07uzh7	prochloroco
1468	77.5	4.4	539	2	09FX24_ARATH	09fx24	arabidopsis
1469	77.5	4.4	591	2	091IK8_PSEAB	091ik8	pseudomonas
1470	77.5	4.4	593	2	06IMNS_XENLA	06imns	xenopus lae
1471	77.5	4.4	602	2	05VPD3_ORYSA	05vpd3	oryza sativ
1472	77.5	4.4	603	1	MUTL_LISMP	071kr6	listeria mo
1473	77.5	4.4	611	2	07OW32_ONCMY	07ow32	oncorhynch
1474	77.5	4.4	650	1	LIRB1_HUMAN	08nl6	h leukocyte
1475	77.5	4.4	672	2	04Z489_PLABE	04z489	plasmodium
1476	77.5	4.4	687	2	06CTK2_KLUTA	06ck2	kilyvetromyc
1477	77.5	4.4	693	2	04FY44_LEIMA	04fy44	leishmania
1478	77.5	4.4	717	2	08UTP9_AGRIT5	08utp9	agrobacteri
1479	77.5	4.4	725	2	06MQQ9_BDBBA	06mqq9	brachydanio
1480	77.5	4.4	735	2	09FG24_ARATH	09fg24	arabidopsis
1481	77.5	4.4	735	2	08S606_9PLVG	08s606	human t-cel
1482	77.5	4.4	739	1	VCAN1_HUMAN	p19320	homo sapien
1483	77.5	4.4	757	1	DNM1_YEAST	p54661	baccharomyc
1484	77.5	4.4	785	2	06CTN0_KLUTA	06ctn0	kilyvetromyc
1485	77.5	4.4	823	2	0517A3_ENTHI	0517a3	entamoeba h
1486	77.5	4.4	829	2	064XJ3_BACPR	064xj3	bacteroides
1487	77.5	4.4	873	2	04T602_TETNG	04t602	tetradion n
1488	77.5	4.4	898	2	05R6T8_PONDY	05r6t8	oryza pygma
1489	77.5	4.4	912	2	06S1Q0_ORKSA	06s1q0	oryza sativ
1490	77.5	4.4	925	2	05R6W3_PONDY	06s1q0	oryza sativ
1491	77.5	4.4	951	2	P91193_CABEL	p91193	caenorhabdi

RESULT 1

SLAF7\_HUMAN

SLAF7\_HUMAN

STANDARD;

PRT; 335 AA.

AC

Q9N025; O8N6Y8; O8ND32; Q9NY08; Q9NY23;

DT

13-SEP-2005 (Rel. 48, Last sequence update)

DT

13-SEP-2005 (Rel. 48, Last sequence update)

DT

13-SEP-2005 (Rel. 48, Last sequence update)

DE

SLM family member 7 precursor (CD2-like receptor activating cytotoxic cells) (CRACC) (Protein 19A) (Membrane protein FOAP-12) (CD2 subset 1) (Novel Lys9)

DE

(Novel Lys9)

CN

Name=SLAF7; Synonyms=CS1; ORFNames=UNQ576/PR01138;

OS

Homo sapiens (Human)

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC

Homo.

NCBI\_TaxID=9606;

NP

[1]

NP

NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1), AND TISSUE SPECIFICITY.

RX

MEDLINE=21115149; PubMed=11220635; DOI=10.1007/s002510000274;

RA

Bales K.S., Mathew P.A.;

RT

"Molecular cloning of CS1, a novel human natural killer cell receptor belonging to the CD2 subset of the immunoglobulin superfamily.";

RL

Immunogenetics 52:302-307(2001).

NP

[2]

NP

NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.

RX

PubMed=11698418;

RA

Bouchon A., Cella M., Grierson H.L., Cohen J.I., Colonna M.;

RT

"Activation of NK cell-mediated cytotoxicity by a SAP-independent receptor of the CD2 family.";

RT	J. Immunol. 167:5517-5521(2001).
NP	[3]
NP	NUCLEOTIDE SEQUENCE [mRNA] (ISOFORMS 1 AND 3), FUNCTION, AND TISSUE SPECIFICITY.
RX	MEDLINE=21661458; PubMed=11802771; DOI=10.1042/0264-6021.3610431;
RA	Murphy J.J., Hobby P., Villarino-Varela J., Bishop B., Jordanidou P.,
RA	Sutton B.J., Norton J.D.;
RT	"A novel immunoglobulin superfamily receptor (19a) related to CD2 is expressed on activated lymphocytes and promotes homotypic B-cell adhesion.";
RT	Biochem. J. 361:431-436(2002).
NP	[4]
NP	NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).
RC	TISSUE=Macrophage;
RA	Fujii Y., Takayama K., Tsuritani K., Yajima Y., Amemiya T., Ukai Y.,
RA	Naito K., Kawaguchi A.;
RT	"Homo sapiens mRNA for FOAP-12 protein, complete cds.";
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
NP	[5]
NP	NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Bruen J.,
RA	Chen Y., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA	Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Haldens S.,
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA	Lewis L., Liao D., Mark M.R., Robbie B., Sanchez C., Schoenfeld J.,
RA	Seshagiri S., Simons L., Singh V., Smith V., Stinson J., Vagts A.,
RA	Van den R., Watanabe C., Wleand D., Woods K., Xie M.-H.,
RA	Yanura D.G., Yi S., Yu G., Yuan J., Zhang W., Zhang Z., Goddard A.D.,



RA Wood W.I., Godowski P.J., Gray A.M.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RN Genome Res. 13:2265-2270(2003).  
[6]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).  
RC TISSUE=Lymph node;  
RG Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
[7]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RG Human chromosome 1 international sequencing consortium;  
RN Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
[8]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).  
RC TISSUE=Fetal lung, and Fetal spleen;  
RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Tashyuk S., Carrinci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.D., Malek J.A., Gunaratne P.H.,  
RA Richardson S., Morley K.C., Hale S.M., Garcia A.M., Gay L.J., Hultik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Schnerch A., Schin J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[9]  
RN PROTEIN SEQUENCE OF 23-37.  
RX PubMed=15340161; DOI=10.1110/pa.04682504;  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites.";  
RN Protein Sci. 13:2819-2824(2004).  
[10]  
RN ALTERNATIVE SPLICING.  
RX PubMed=15368295; DOI=10.1002/eji.200424917;  
RA Lee J.K., Boles K.S., Mathew P.A.;  
RT "Molecular and functional characterization of a CSI (CRACC) splice  
RT variant expressed in human NK cells that does not contain  
RT immunoreceptor tyrosine-based switch motifs.";  
RN Eur. J. Immunol. 34:2791-2799(2004).  
[11]  
RN TISSUE SPECIFICITY, AND SAP-BINDING.  
RX MEDLINE=2222696; PubMed=12242590; DOI=10.1007/s00251-002-0463-3;  
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Plazuela P.,  
RA Bosch J., Terhorst C., Engel P.;  
RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of  
RT leukocyte cell-surface receptors.";  
RN Immunogenetics 54:394-402(2002).  
[12]  
RN FUNCTION: Isoform 1 mediates NK cell activation through a SAP-  
RN independent extracellular signal-regulated ERK-mediated pathway.  
RN May play a role in lymphocyte adhesion. Isoform 3 does not mediate  
RN any activation. SAP can bind the cytoplasmic tail of isoform 1  
RN when phosphorylated in the presence of Fyn (in vitro).  
[13]  
RN SUBCELLULAR LOCATION: Type I membrane protein.  
[14]  
RN ALTERNATIVE PRODUCTS:  
RN Event=Alternative splicing; Named isoforms=3;  
RN Name=1; Synonyms=19A, CSI-L;  
RN IsoId=G9NQ25-1; Sequence=Displayed;  
RN Name=2;  
RN IsoId=G9NQ25-2; Sequence=VSP\_013781;

CC Note=No experimental confirmation available;  
CC Name=3; Synonyms=19A24, CSI-S;  
CC IsoId=G9NQ25-3; Sequence=VSP\_013782;  
CC TISSUE SPECIFICITY: Expressed in spleen, lymph node, peripheral  
CC blood leukocytes, bone marrow, small intestine, stomach, appendix,  
CC lung and trachea. Expression was detected in NK cells, activated  
CC B-cells, NK-cell line but not in promyelocytic B-, or T-cell  
CC lines. The isoform 3 is expressed at much lower level than isoform  
CC 1.  
CC -1- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)  
CC domain.  
CC -1- CAUTION: Ref.3 (CAB76561) sequence differs from that shown due to  
CC framehifts.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC DR EMBL; AF291815; AAK11549.1; -; mRNA.  
CC DR EMBL; AF390894; AAL26989.1; -; mRNA.  
CC DR EMBL; AJ271869; CAB76561.1; ALT FRAME; mRNA.  
CC DR EMBL; AJ276429; CAB81950.2; -; mRNA.  
CC DR EMBL; AB027233; BAB61022.1; -; mRNA.  
CC DR EMBL; AY358512; AAO88876.1; -; mRNA.  
CC DR EMBL; AL834424; CAD39085.1; -; mRNA.  
CC DR EMBL; AL121985; CAC00579.1; -; Genomic DNA.  
CC DR EMBL; AL121985; CAH73507.1; -; Genomic DNA.  
CC DR EMBL; AL121985; CAH73508.1; -; Genomic DNA.  
CC DR EMBL; BC027867; AAH72867.1; -; mRNA.  
CC DR EMBL; ENSG0000026751; Homo sapiens.  
CC DR HGN; HGNC:21394; SLAMF7.  
CC DR MIM; 606625; -.  
CC DR GO; GO:0016020; C:membrane; NAS.  
CC DR GO; GO:0007155; P:cell adhesion; NAS.  
CC DR GO; GO:0030101; P:natural killer cell activation; NAS.  
CC DR GO; GO:0042267; P:natural killer cell mediated cytotoxicity; NAS.  
CC DR PROSITE; PS50835; IG\_LIKE; 1.  
CC DR InterPro; IPR007110; Ig-Like.  
CC DR KX Alternative splicing; Direct protein sequencing; Glycoprotein;  
CC KW Immunoglobulin domain; Receptor; Signal; Transmembrane.  
CC FT SIGNAL 1 22  
CC FT CHAIN 23 335 SLAM family member 7  
CC FT TOPO\_DOM 23 226 Extracellular (Potential).  
CC FT TRANSMEM 227 247 Potential.  
CC FT TOPO\_DOM 248 335 Cytoplasmic (Potential).  
CC FT DOMAIN 131 206 Ig-like C2-type.  
CC FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 176 176 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).  
CC FT DISULFID 145 215 Potential.  
CC FT DISULFID 151 195 By similarity.  
CC FT DISULFID 151 195 Missing (in isoform 2).  
CC FT VARSPLIC 19 125 /FTId=VSP\_013781.  
CC FT VARSPLIC 258 296 -> NNPGRSKYGLHCGNTEKDGKSPVLTMDADRHTAIC  
CC L (in isoform 3).  
CC FT CONFLICT 135 135 /FTId=VSP\_013782.  
CC FT SEQUENCE 335 AA; 37421 MW; D09ABBCF74B8D4 CRC64;  
SQ  
Query Match 100.0%; Score 1772; DB 1; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.2e-139; Indels 0; Gaps 0;  
Matches 335; Conservative 0; Mismatches 0;  
1 MAGSPTCTLLIYIMQLTGSAAAGPVKELVSGAVTFPLSKSKQYDSIVTFTNTPL 60  
1 MAGSPTCTLLIYIMQLTGSAAAGPVKELVSGAVTFPLSKSKQYDSIVTFTNTPL 60



Qy 61 VTIOPEGGTTIYTONRNRERVDPPGGYSLKSLKLNKNDGGIYGYIGSSSLQGPSTQY 120  
 Db 61 VTIOPEGGTTIYTONRNRERVDPPGGYSLKSLKLNKNDGGIYGYIGSSSLQGPSTQY 120  
 Qy 121 VLHYEHHSKRPMYMGLOSNNGTCVTNLTCCMEHGEEDVYTWKALGOANESHSIL 180  
 Db 121 VLHYEHHSKRPMYMGLOSNNGTCVTNLTCCMEHGEEDVYTWKALGOANESHSIL 180  
 Qy 181 PISMRGSDMTFTICVARNPVRNRPSSPILARKLCEGAADPDSSMVLCLLVLPLLSL 240  
 Db 181 PISMRGSDMTFTICVARNPVRNRPSSPILARKLCEGAADPDSSMVLCLLVLPLLSL 240  
 Qy 241 FVLGLFLMFLKRGQREYIEKKRVDICRETPNICEHSGENTYDTPIHNTKTIKEDPA 300  
 Db 241 FVLGLFLMFLKRGQREYIEKKRVDICRETPNICEHSGENTYDTPIHNTKTIKEDPA 300  
 Qy 301 NTYVSTVIEPKKMEPHSLTTPDPRLFAVENVI 335  
 Db 301 NTYVSTVIEPKKMEPHSLTTPDPRLFAVENVI 335

RESULT 2  
 SLAF7\_MOUSE STANDARD: PR7, 333 AA.  
 ID SLAF7\_MOUSE Q8BHK6; Q8BTL2; Q8CJ63; Q8CJ64; Q8CJ65; Q91XA0;  
 AC Q8BHK6; Q8BTL2; Q8CJ63; Q8CJ64; Q8CJ65; Q91XA0;  
 DT 13-SEP-2005 (Rel. 48, Created)  
 DT 13-SEP-2005 (Rel. 48, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE SLAM family member 7 precursor (leukocyte cell-surface antigen) (Novel  
 Ly9).  
 GN Name=Slamf7;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 CC Muridea; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 2 AND 3).  
 RC STRAIN=BA1B/C; and C57BL/6; TISSUE=Thymus;  
 RX MEDLINE=22226966; PubMed=12242590; DOI=10.1007/s00251-002-0483-3;  
 RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Flizcucta P.,  
 RA Bosch J., Terhorst C., Engel P.;  
 RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of  
 leukocyte cell-surface receptors.";  
 RL Immunogenetics 54:394-402(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).  
 RC STRAIN=C57BL/6J; TISSUE=Aorta, Testis, and Vein;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kiyosawa H.,  
 RA Nikiado I., Oosato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,  
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schmitt L.M., Karpman A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusci V., Chochia C., Corbani L.E., Cousins S.,  
 RA Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Guelinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Klotzsch A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagaishima T., Numa K., Okido T., Pavan W.J., Petrea G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed D.U., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shinada K.,  
 RA Sultana R., Takekura Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang L., Yang L.,  
 RA Yuan Z., Zavanian M., Zhu Y., Zimmer A., Carrinci P., Hayatsu N.,  
 RA Hitozane-Kishikawa T., Kono H., Nakamura N., Sakazume N., Seto K.,  
 RA Shitaki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 4).  
 RC STRAIN=FVB/N; TISSUE=Salivary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uddin T.B., Toshilyak S., Carrinci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Mediates NK cell activation through a SAP-independent  
 extracellular signal-regulated BRK-mediated pathway. May play a  
 role in lymphocyte adhesion (By similarity). Isoform 1 does not  
 bind SAP (in vitro).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: Type I membrane protein.  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1;  
 CC IsoId=Q8BHK6-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q8BHK6-2; Sequence=VSP\_013784;  
 CC Name=3;  
 CC IsoId=Q8BHK6-3; Sequence=VSP\_013783, VSP\_013784;  
 CC Name=4;  
 CC IsoId=Q8BHK6-4; Sequence=VSP\_013783;  
 CC Note=No experimental confirmation available;  
 CC -1- TISSUE SPECIFICITY: Expressed in spleen, lymph node, bone marrow  
 and testis. Lower levels detected in thymus. Expressed in NK cells  
 and B-cells.  
 CC -1- SIMILARITY: Contains 1 Ig-1-like C2-type (immunoglobulin-like)  
 domain.  
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to a  
 frameshift in position 255.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 CC EMBL; AF467909; AAN63158.1; -; mRNA.  
 CC EMBL; AF467910; AAN63159.1; -; mRNA.  
 CC EMBL; AF467911; AAN63160.1; -; mRNA.  
 CC EMBL; AK030135; AAC68801.1; -; mRNA.  
 CC EMBL; AK030148; BAC26810.1; -; mRNA.  
 CC EMBL; AK040678; BAC30665.1; -; mRNA.  
 CC EMBL; AK049525; BAC40914.1; -; mRNA.  
 CC EMBL; BC011154; AAH1154.1; ALT FRAMES; mRNA.  
 CC EMBL; ENSMUSG0000038179; Mus musculus.  
 CC MGI; MGI.1922595; Slamf7.  
 CC GO; GO:0016021; C:integral to membrane; TAS.  
 CC InterPro; IPR007110; Ig-1-like.  
 CC PROSITE; PS50835; Ig\_LIKE; 1.  
 CC Alternative splicing; Glycoprotein; Immunoglobulin domain; Receptor;



KW Signal; Transmembrane.  
 FT SIGNAL 1 22 By similarity.  
 FT CHAIN 23 333 SLAM family member 7.  
 FT TOPO DOM 23 224 Extracellular (Potential).  
 FT TRANSMEM 225 245 Potential.  
 FT TOPO DOM 246 333 Cytoplasmic (Potential).  
 FT DOMAIN 128 203 Ig-like C2-type.  
 FT CARBOHYD 42 42 N-linked (GlcNAc . . .) (Potential).  
 FT CARBOHYD 95 95 N-linked (GlcNAc . . .) (Potential).  
 FT CARBOHYD 139 139 N-linked (GlcNAc . . .) (Potential).  
 FT CARBOHYD 145 145 N-linked (GlcNAc . . .) (Potential).  
 FT CARBOHYD 156 156 N-linked (GlcNAc . . .) (Potential).  
 FT DISULFID 142 212 Potential.  
 FT DISULFID 148 192 By similarity.  
 FT VARSPLIC 255 289 Missing (in isoform 3 and isoform 4).  
 FT VARSPLIC 312 333 /FTID=VSP\_013783.  
 FT VARSPLIC /FTID=VSP\_013784.  
 FT CONFLICT 118 118 V -> A (in Ref. 1; AAN63158).  
 FT CONFLICT 248 248 T -> M (in Ref. 1; AAN63158 and 2).  
 FT CONFLICT 253 253 G -> R (in Ref. 1; AAN63159 and 3).  
 SQ SEQUENCE 333 AA; 37187 MW; 8040823FEBB7129 CRC64;  
 Query Match 46.0%; Score 815; DB 1; Length 333;  
 Best Local Similarity 49.3%; Pred. No. 1.7e-59;  
 Matches 167; Conservative 58; Mismatches 104; Indels 10; Gaps 3;  
 QY 1 MAGSTCTLLTLYIIMQLGSAAGSPVKELVSGAVFPELTKSKVKQVDYIWTFTPL 60  
 DB 1 MARSTYIIFTSVLCQLYTATASGTUKKAGALDSDSFTTLTITRKDYVWMTNPTPL 60  
 QY 61 VTIOEGGTLITVONRNRERVDPDGYSYLSKLKSKLKDSDGIIYVSSSLQDPSTOY 120  
 DB 61 AMVKDQ---VTSQSNKERIVFPDGLYSKMLQKDKDSGAYRAEIVTSQSALIDEX 117  
 QY 121 VLAHYEHLSKPYNTMGLQSNKNGTCVTNITCMEHGESEVYITWKLQGAANESHGSL 180  
 DB 118 VLAHYKHLSRPKYITIDROSNGKTCVINTCTDDGENVYTSWRAVGGDQFHDGATL 177  
 QY 181 PISWWSGSDMTFICVARNPVRNFSPIARLCEGAADDDSSMWLCLLVLPLLSL 240  
 DB 178 SIAMSGEKDQALTCARNPVNSSTFPFQKLCEDATDITLSLGLIYILCFSAVLIL 237  
 QY 241 FVLGLFL----WFLKREROEYIEBKRYVICRETPNICPHSGENTYDITPHTRITIK 296  
 DB 238 FAVLLTTHITMTWKKGCE---EDKKRYDRHQEMDLCPHLENADVDTIYTEKRRP 294  
 QY 297 EDPANTVSTVEIPKCMENPHSLTMPDTPRLFAVENVI 335  
 DB 295 EDAPTFYSTVQIPKVVSPSSLPKFLVPRSLSPENVI 333  
 RESULT 3  
 O15430\_HUMAN PRELIMINARY; PRF; 328 AA.  
 ID O15430\_HUMAN PRELIMINARY; PRF; 328 AA.  
 AC O15430; O8WLP1;  
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
 DT 13-SEP-2005 (TREMBLrel. 31, last annotation update)  
 DE Leukocyte antigen CD84 (leukocyte differentiation antigen CD84 isoform CD84c) (MAX.3 cell surface antigen precursor) (CD84 antigen).  
 GN CD84; ORFNames=RP11-528G1.3-001;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 OX NCBI\_TaxID=9606;  
 RN NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=97454416; PubMed=9310491;  
 RA de la Fuente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.,  
 RT "CD84 leukocyte antigen is a new member of the Ig superfamily.";

RL Blood 90:2398-2405(1997).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RA Palou E., Sole J., Piroto F., Gaya A.;  
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RN NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=86188202; PubMed=3008886;  
 RA Andreesen R., Bros K.J., Osterholz J., Emmrich F.;  
 RT "Human macrophage maturation and heterogeneity: analysis with a newly  
 RL Blood 67:1257-1264(1986).  
 RN [4]  
 RN NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20164057; PubMed=10698700; DOI=10.1042/0264-6021.3460729;  
 RA Krause S.W., Rehl M., Heinz S., Ebner S., Andreesen R.;  
 RT "Characterization of Mx3 antigen, a glycoprotein expressed on mature  
 RL macrophages, dendritic cells and blood platelets: identity with  
 RL CD84.";  
 RL Biochem. J. 346:729-736(2000).  
 RN [5]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marzula K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Kane S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lymph;  
 RA Director MGC Project;  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 RN [7]  
 RN NUCLEOTIDE SEQUENCE.  
 RA Lad H.;  
 RL Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U82988; AAB84364.1; -, mRNA.  
 DR EMBL; AF054815; AAF21721.1; -, mRNA.  
 DR EMBL; AJ223324; CAA11264.1; -, mRNA.  
 DR EMBL; BC020063; AAH20063.1; -, mRNA.  
 DR EMBL; AL138930; CAI1518.1; -, Genomic DNA.  
 DR Ensemble; ENSG0000066294; Homo sapiens.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005886; C:plasma membrane; TAS.  
 DR GO; GO:0006952; P:defense response; TAS.  
 DR GO; GO:0007156; P:homophilic cell adhesion; TAS.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR SMART; SM00409; IG\_1; IG-like.  
 DR PROSITE; PS50835; IG\_LINK; 1.  
 DR Immunoglobulin domain; Signal.  
 FT SIGNAL 1 21 Potential.  
 FT CHAIN 22 328 MAX.3 cell surface antigen.  
 SQ SEQUENCE 328 AA; 36871 MW; 6C9A92066AD0344 CRC64;  
 Query Match 20.5%; Score 362.5; DB 2; Length 328;



Best Local Similarity 31.5%; Pred. No. 1e-21;  
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

QY 14 LMOL-----TGSAAAGPYKELV---GSVGAATPPLK-SKYKQVDSIWTNTPTPLVLIQ 64  
DB 6 LMIILLCLQIQTPEAKGKSEIFVTNGILGESVTFPVNIQEPKQVITAMTSKTSVAAYTP 65  
QY 65 PEGGT---IITYONRRERVDPPDGYSIKLSKLNKNSGIYVIGYSSSLQQPSTOEYV 121  
DB 66 GDSERAPVYVYTHRYRHYRIHALGPNVNLVSDLMEDAGDKADINQADPYTTTKRYN 125  
QY 122 LHYEHLKPYVTMGLQSNKNGTCVTNLTCCMEHGBEDVITYWKALGOANESHGSLTP 181  
DB 126 LQIYRLKPKITQSLMASVNSTCVTLTCSVEKEKRYTNWMSPLGE-----EGNVLIQ 179  
QY 182 ISMRGSDMTFICVARRPVSRNFPSSPIARLTCGADDPPS-----SMVLLCLLIVP 235  
DB 180 IFQPEDELITYTCTAQNPSNN-SDSISARQLCADIAMGFTHTHTGLSLVLAFFLLVLT 238  
QY 236 LLSLFLVGLFLMFLKRRQREYIEKKRVDCRETPNICPHSGENTEXTDTPHTNRTL 295  
DB 239 ILSVFLRLP-----KRRQDAASKTITYYIMASRTQF--ASRIYDELIGSKVLPS 290  
QY 296 KEDPANTYSTVEIPKKNENPHSLTMDPTPLFAYENVY 335  
DB 291 KEEPVNTYSEVQFADKKMGKASTQDSKP--PQTSSEYELVY 328

## RESULT 4

Q9Z178 MOUSE PRELIMINARY; PRT; 329 AA.

AC Q9Z178  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE CD84 leukocyte antigen.  
GN Name=CD84; Synonyms=CD84;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Peritoneum;  
RX MEDLINE=99180614; PubMed=10079287; DOI=10.1007/s002510050490;  
RA de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,  
RA Engel P.;  
RT "Molecular cloning, characterization, and chromosomal localization of  
the mouse homologue of CD84, a member of the CD2 family of cell  
surface molecules.";  
RL Immunogenetics 49:249-255(1999).  
DR EMBL; AF043445; AAD02273.1; -; mRNA.  
DR Ensembl; ENSMUSG0000038147; Mus musculus.  
DR MGI; MGI:1336885; CD84.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR SMART; SM00409; IG, 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain.  
SQ SEQUENCE 329 AA; 37345 MW; 43BBIAA5AF1989B0 CRC64;

Query Match 20.5%; Score 362.5; DB 2; Length 329;  
Best Local Similarity 30.5%; Pred. No. 1e-21;  
Matches 105; Conservative 62; Mismatches 136; Indels 41; Gaps 14;

QY 11 IYIILQIAGSAGPYKELV---GSVGAATPPLK-SKYKQVDSIWTNTPTPLVLIQ 65  
DB 8 IWFLLCLQIQTPEAKGKADADPVVWNGILGESVTFPLNIQEPKIKIDNIAWT-SQSSVAFIRG 66  
QY 66 -EGGTIITYONRRERVDPPDGYSIKLSKLNKNSGIYVIGYSSSLQQPSTOEYVLIH 124  
DB 67 VKAKAVTITQGYKRIEIIIDQKYDLVIRDLMEDAGTYKADINEN-EEYTKIYIYLIH 125

QY 125 YEHLKPYVTMGLQSNKNGTCVTNLTCCMEHGBEDVITYWKALGOANESHGSLTPISW 184  
DB 126 YRLKPKITQSLSLNNTCNITLTCSVEKEKQVTSWSPFGKSN-----VLQIVH 179  
QY 185 RWGSDMTFICVARRPVSRNFPSSPIARLTCGAE-----ADDPSSMVLCLLIVPLL 237  
DB 180 SPMQCKLTYTCTAQNPSV-NSSDSVTYVQCPCTDPSPFPHRAVLPGGLAVFLILLIPL 238  
QY 238 LSLFLVGLFLMFLKRRQREYIEKKRVDCRETPNICPHSGENTE---YDTIPTHNRT 293  
DB 239 AFLRL-----YKRRDRIVLEAD--DVSKTYAVAVSKNAQFTSERITDELPQSM 289  
QY 294 ILKEDPANTYSTVEIPKKNENPHSLTMDP--TPRLFAYENVY 335  
DB 290 SKCKDPVTTIYSSVQLSEKMEKTN---MKDRSLPKALGNELIV 329

## RESULT 5

Q8WW18 HUMAN PRELIMINARY; PRT; 339 AA.

AC Q8WW18  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Leukocyte differentiation antigen CD84 precursor (CD84 antigen)  
DE (Leukocyte antigen).  
GN Name=CD84; ORFNames=RP11-528G1.3-002;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Gaye A.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Lad H.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y12632; CAA73181.1; -; mRNA.  
DR EMBL; AL138930; CA115159.1; -; Genomic\_DNA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR SMART; SM00409; IG, 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 339  
SQ SEQUENCE 339 AA; 38082 MW; E78D6D5CAC8D3604 CRC64;

Query Match 20.3%; Score 359; DB 2; Length 339;  
Best Local Similarity 31.6%; Pred. No. 2.1e-21;  
Matches 111; Conservative 51; Mismatches 143; Indels 46; Gaps 12;

QY 14 LMOL-----TGSAAAGPYKELV---GSVGAATPPLK-SKYKQVDSIWTNTPTPLVLIQ 64  
DB 6 LMIILLCLQIQTPEAKGKSEIFVTNGILGESVTFPVNIQEPKQVITAMTSKTSVAAYTP 65  
QY 65 PEGGT---IITYONRRERVDPPDGYSIKLSKLNKNSGIYVIGYSSSLQQPSTOEYV 121  
DB 66 GDSERAPVYVYTHRYRHYRIHALGPNVNLVSDLMEDAGDKADINQADPYTTTKRYN 125  
QY 122 LHYEHLKPYVTMGLQSNKNGTCVTNLTCCMEHGBEDVITYWKALGOANESHGSLTP 181  
DB 126 LQIYRLKPKITQSLMASVNSTCVTLTCSVEKEKRYTNWMSPLGE-----EGNVLIQ 179  
QY 182 ISMRGSDMTFICVARRPVSRNFPSSPIARLTCGADDPPSSW-----VLLCLLIV 234  
DB 180 IFQPEDELITYTCTAQNPSNN-SDSISARQLC-----ADIAMGFTHTHTGLSLVLA 232  
QY 235 PLLSLFLVGLFLMFLKRRQ-----EYIEKKRV-DICRETPNICPHSGENTEX 284



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Db 223 PFLVLILSSVLEFLFKRQSSCLNTFTKMPYASKTTIYYINASRTOP--AESRIY 290
Qy 285 DTIPHTNRTILKEDPANTVSTVEIPKKNENPHSLTMPDRLPAYENVI 335
Db 221 DELLQSKVLPSKEBPVNTVYSEVQPADKKGKASTQDSKP--PGTSYEYELVI 339

RESULT 6
QENZB6_MOUSE
ID QENZB6_MOUSE PRELIMINARY; PRT; 645 AA.
AC QENZB6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Ly9 protein (fragment).
GN Name=Ly9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stacieleon M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalek U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.L.
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC066212; AAH66212.1; -; mRNA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG.1.
DR SMART; SM00409; IG.2.
DR PROSITE; PS50835; IG_LIKE; 2.
PT NON TER
SQ SEQUENCE 645 AA; 71884 MW; 316EFL183DFD510BB CRC64;

Query Match 20.2%; Score 358.5; DB 2; Length 645;
Best Local Similarity 27.9%; Pred. No. 5.1e-21;
Matches 119; Conservative 51; Mismatches 138; Indels 119; Gaps 16;

Qy 14 LMQL-TGSA-----AGCPVKEIVGSGAVTFPLK-SKVQVDSIWTFTPLVITIQPG 67
Db 229 IWQFCTGASRRRTAAG--KTVVGIIGEPYTLPLEFRATRTATKVVWVFMTS--VISQERR 284
Qy 68 GTIITVQNR-----NRERVPDGDGSLSKLKKNDGIIYVGVISSSLQGPSTQEVYL 122
Db 285 GAATADSRKPKPGSEERRVITSDQDQSLKISQLKKEDAGPHAYVCSASRDPVNHFTL 344
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Qy 123 HYVEHLSKPKVTMGLQSNKNGCTVTNLTCCMEHEGEEDVITYTKALGOAANSHNGSIPI 182
Db 345 LVYKRLERPSVTKSPVNMNNGICEVVLTCSDGGNNVTYTMPLOKRAVMSQGRSHLVN 404
Qy 183 SWRMGESDMTFLCVARNPVSRNFPSPILARKLCEGAADDPSSWVLCLILLVPLLSLFV 242
Db 405 SWSEGEHLPNFTCTAHNPVS--NSSQFSSGTTCSG---PRNRKRFMLLLLVLLMLLI 459

Qy 243 LGLFLMLFKRE-----ROEYIEE-----KKRVDCRETFNICEP- 276
Db 460 GGCFILRRKKQCCSLATRYQAEVPAIIPETPTGHGQFVLSQRYKLDMSAKTRHQPT 519
Qy 277 -----HSGENTR---YDIPHTN----- 291
Db 520 PTDSTSSSSATTEBDEKTRMHSYANRNQVYLDLVTHQDIAHALAYEGVEYEAITEPD 579
Qy 292 -----RTLL--KEDPANTVSTVEIPKK-MENPHSLTMPPTP 326
Db 580 KYDGSMEEDPRAIVQVSLNQGFTLPQKEDSNITTCVQPKKTAQTPOQDASPEPTP 639
Qy 327 RLFAVEN 333
Db 640 ---TYEN 643

RESULT 7
Q9UIB8_HUMAN
ID Q9UIB8_HUMAN PRELIMINARY; PRT; 345 AA.
AC Q9UIB8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Leukocyte differentiation antigen CD84 isoform CD84a (CD84 antigen)
DE (Leukocyte antigen).
GN Name=CD84; ORFNames=RP11-528G1.3-003;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Palou E., Sole J., Pirotto F., Gaya A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lad H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF054816; AAF21722.1; -; mRNA.
DR EMBL, AL138930; CAI15160.1; -; Genomic DNA.
DR Ensembl; ENSG00000066294; Homo sapiens.
DR HGNC; HGNC:1704; CD84.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG.1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 345 AA; 38782 MW; DA06BC5A682E62DE CRC64;

Query Match 20.2%; Score 358; DB 2; Length 345;
Best Local Similarity 30.8%; Pred. No. 2.6e-21;
Matches 110; Conservative 52; Mismatches 143; Indels 52; Gaps 11;

Qy 14 LMQL-----TGSAAAGPVKEIV---GSGVGAATFPLK-SKVQVDSIWTFTPLVITIQ 64
Db 6 LMILLICITQTPKPAAGKSEIFTVNGILIGESVTFPVNIQERQVKIIMTSTISIAVYTP 65
Qy 65 PEGGT---IIVTONRRERVDPPDGYSLSKLKKNDGIIYVGVISSSLQGPSTQEVYL 121
Db 66 GDSERAPAVVTYTHRYRERHALGPNVNLVSLDLMEDAGADVKADINQADPYTTTKRYN 125
Qy 122 LHVYHLSKPKVTMGLQSNKNGCTVTNLTCCMEHEGEEDVITYTKALGOAANSHNGSIPI 181
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Db      126 LQIYRLRCKPKITQSLMASVNSTCVTLTCSVEKEKNVTYNWSPGLG-----EGVLIQ 179
Qy      182 ISWRMGSDMTFICVARNPVSRNFSPIIARKLCEGADDDPSSW-----VLLCLILV 234
Db      180 IFQTEDEDELITTCYANPNVSN--SDSISARQLC-----ADINAGFRTHTGLISVLAM 232
Qy      235 PLLLSLFLVGLFLMFLKREKREBEYIEKKRVDCRETP-----NICPMS 278
Db      233 FFLVLLIISVFLPLFKRQRIPEGSCNLTPTKPNFPAASKTITYYIMASRTQTP-- 290
Qy      279 GENTYDPTIPTNRTILKEDPANTYTYTYEIPKKNENPHSLTMDTRELPAIYEVNI 335
Db      291 AESRIYDEILQSKVLPSEKPEPVNTYSEVOFADKMKKASTODSKP--PQTSSEYEIYI 345

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RESULT 8
Q6FHA8_HUMAN
ID Q6FHA8_HUMAN PRELIMINARY; PRT; 328 AA.
AC Q6FHA8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD84 protein (Fragment).
GN Name=CD84;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mkomdinye M., Schick M., Eisenstein S.,
RA Neubert P., Katriang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labber J.,
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR541847; CAG46645.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; Ig; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 328
SQ SEQUENCE 328 AA; 36861 MW; 6C9A8BDD45BD0344 CRC64;

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Query Match      20.0%; Score 354.5; DB 2; Length 328;
Best Local Similarity 31.2%; Pred. No. 4.8e-21;
Matches 106; Conservative 55; Mismatches 144; Indels 35; Gaps 10;

Qy      14 LMQL-----TGSAAAGPVKELV---GSVCGAVTFPLK-SKVQVDSIYVTFNTPLVITQ 64
Db      6 LWILLICLOTWPEBAAGKQSEITTVNGILGESVTFPNIOEPKQKIANTSKTSVAAYTP 65
Qy      65 PEGGT---IIVTQNNRERVDPPDGYSIKLSKLKNDGSIYVVGYSLSLOQPSIQEVY 121
Db      66 GDSERAPAVTVTHRYNRYRIHALGPVYNLVISDLRNEADGDKADINTQADPYTTTKRYN 125
Qy      122 LHYEHLSPKRYTMGQSNKNGTCTVNTLTCMEHGEEDVITYWKALGQANSHNGSILPI 181
Db      126 LQIYRLRCKPKITQSLMASVNSTCVTLTCSVEKEKNVTYNWSPGLG-----EGVLIQ 179
Qy      182 ISWRMGSDMTFICVARNPVSRNFSPIIARKLCEGADDDPSS-----SWLLCLILV 235
Db      180 IFQTEDEDELITTCYANPNVSN--SDSISARQLCADIANGFRTHTGLISVLAMFFLLV 238
Qy      236 LLLSLFVLGLFLMFLKREKREBEYIEKKRVDCRETPNICPSGENTYDPTIPTNRTIL 295
Db      239 ILSVFLPLF-----KRDQAASKTITYYIMASRTQTP--AESRIYDEILQSKVLP 290
Qy      296 KEDPANTYTYEIPKKNENPHSLTMDTRELPAIYEVNI 335
Db      291 KESVNTVYSEVOFADKMKKASTODSKP--PQTSSEYEIYI 328

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RESULT 9
Q7TMP7_MOUSE
ID Q7TMP7_MOUSE PRELIMINARY; PRT; 649 AA.
AC Q7TMP7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lys protein (Fragment).
GN Name=Lys9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.R.,
RA Brownstein M.J., Usdin T.B., Toshlyuk S., Carrinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullaby S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalske U., Smallus D.B.,
RA Scherch A., Schin J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Straubeberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055380; AAH5380.1; -; mRNA.
DR HSSP; P08921; IHNG.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 1
SQ SEQUENCE 649 AA; 72414 MW; AD6A09381C063B34 CRC64;

```

```

Query Match      20.0%; Score 354.5; DB 2; Length 649;
Best Local Similarity 27.6%; Pred. No. 1.1e-20;
Matches 118; Conservative 52; Mismatches 139; Indels 119; Gaps 16;

Qy      14 LMQL-----ASGPVKELVSGAVTFPLSK-VKQVDSIYVTFNTPLVITQPBG 67
Db      233 IMQFTGASRRKTAAG--KTVVGLIGEPVTLPLEPRATRAKTVAVVENTS--VISQERR 288
Qy      68 GTTIYTQNR-----NRKRVDPDGYSIKLSKLKNDGSIYVVGYSLSLOQPSIQEVY 122
Db      289 GAATDSRRKPKGSEERRVRTSDQSLKIQKEDAGPFAVYCSASRPSVRHFTL 348
Qy      123 HYEHLSPKRYTMGQSNKNGTCTVNTLTCMEHGEEDVITYWKALGQANSHNGSILPI 182
Db      349 LVYKLEKPSYTKSVYHMANNGICVAVLTCSVDGGNNVTYTMPLQNKAAVWSQGSHLNV 408
Qy      183 ISWRMGSDMTFICVARNPVSRNFSPIIARKLCEGADDDPSSWVLLCLILVPLLSLFLV 242

```



```
Db 409 SWESGEHLPNFTCTAHNPVS--NSSQFSSGTCSC---PERNKRFMLLLVLLVLLMLI 463
Qy 243 LGFLPFLKRE-----ROEYIEE-----KKRVDICRETPNICP- 276
Db 464 GGYFLRKKKKCSSLATRYRQAEVPAHLEPPTGHSQSVLSQRREKIDMSAKTTRHQPT 523
Qy 277 -----HSGENTB---YDTIPPTN----- 291
Db 524 PTPSTSSSSATTEBDEKTRAHSTANSRNVYDLVTHQDIHAALAYSGVEYEAITPYD 583
Qy 292 -----RTL--KEBPANTVYSVEIPRK-MENPHSLTMPPTP 326
Db 584 KVDGSMDEBGMAYIOVSLNVCGETPLPQCKEDSNITVCSVQKPKTKTAPOQDAESPETP 643
Qy 327 RLPAVEN 333
Db 644 ---TYEN 647

RESULT 10
LY9_MOUSE STANDARD; PRT; 654 AA.
ID LY9_MOUSE
AC 001365; Q9ES29; Q9ES35; Q9ES36;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE T-Lymphocyte surface antigen Ly-9 precursor (Lymphocyte antigen 9)
GN (Cell-surface molecule Ly-9).
OS Name=Ly9; Synonyms=Ly-9;
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE, AND POLYMORPHISM.
RP STRAIN=129/Sv, BALB/c, and C57BL/6; TISSUE=Spleen;
RX MEDLINE=92373005; PubMed=1506686;
RA Tovar V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;
RT "Gene structure of the mouse leukocyte cell surface molecule Ly9.";
RL Immunogenetics 51:788-793(2000).
[2]
RN NUCLEOTIDE SEQUENCE OF 22-654, AND PROTEIN SEQUENCE OF 48-59.
RX MEDLINE=92373005; PubMed=1506686;
RA Sandrin M.S., Gumley T.P., Henning M.M., Vaughan H.A., Genez L.J.,
RA Tripani J.A., McKenzie I.F.C.;
RT "Isolation and characterization of cDNA clones for mouse Ly-9.";
RL J. Immunol. 149:1636-1641(1992).
CC -1- FUNCTION: May participate in adhesion reactions between T
CC lymphocytes and accessory cells by homophilic interaction.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Lymphocytes.
CC -1- SIMILARITY: Contains 2 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC -1- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like)
CC domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF244131; AAG14997.1; -; mRNA.
CC EMBL; AF244130; AAG14996.1; -; mRNA.
CC EMBL; AF246701; AAG13268.2; -; Genomic_DNA.
CC EMBL; AF245117; AAG13268.2; JOINED; Genomic_DNA.
CC EMBL; AF245506; AAG13268.2; JOINED; Genomic_DNA.
CC EMBL; AF245118; AAG13268.2; JOINED; Genomic_DNA.
CC EMBL; AF245507; AAG13268.2; JOINED; Genomic_DNA.
CC EMBL; AF245508; AAG13268.2; JOINED; Genomic_DNA.
CC EMBL; AF245509; AAG13268.2; JOINED; Genomic_DNA.
CC EMBL; AF245510; AAG13268.2; JOINED; Genomic_DNA.
```

```
DR EMBL; AF246699; AAG13268.2; JOINED; Genomic_DNA.
DR EMBL; AF246700; AAG13268.2; JOINED; Genomic_DNA.
DR HSSP; P08921; IHNG.
DR Ensembl; ENSMUSG0000004707; Mus musculus.
DR MGI; MGI:96885; Ly9.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
KW Antigen; Cell adhesion; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin domain; Polymorphism; Repeat; Signal; Transmembrane.
FT SIGNAL 1
FT CHAIN 47
FT TOPO_DOM 48 654 T-Lymphocyte surface antigen Ly-9.
FT TRANSMEM 48 453 Extracellular (Potential).
FT TOPO_DOM 454 474 Potential.
FT DOMAIN 475 654 Cytoplasmic (Potential).
FT DOMAIN 48 158 Ig-like V-type 1.
FT DOMAIN 159 243 Ig-like C2-type 1.
FT DOMAIN 250 362 Ig-like V-type 2.
FT DOMAIN 353 453 Ig-like C2-type 2.
FT CARBOHYD 68 68 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 120 120 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 231 231 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 284 284 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 390 390 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 412 412 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 423 423 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 434 434 N-linked (GlcNAc... ) (Potential).
FT DISULFID 172 242 Potential.
FT DISULFID 178 222 Potential.
FT DISULFID 376 445 Potential.
FT DISULFID 382 426 Potential.
FT VARIANT 10 10 D -> G (in Ly9-1).
FT VARIANT 14 14 G -> S (in Ly9-1).
FT VARIANT 79 79 I -> T (in Ly9-1).
FT VARIANT 91 91 F -> S (in Ly9-1).
FT VARIANT 130 130 H -> Y (in Ly9-1).
FT VARIANT 139 139 I -> T (in Ly9-1).
FT VARIANT 362 362 P -> S.
FT VARIANT 366 366 K -> N (in Ly9-1).
FT VARIANT 377 377 E -> K (in Ly9-1).
FT VARIANT 550 550 M -> I (in Ly9-1).
FT VARIANT 592 592 G -> E (in Ly9-1).
FT VARIANT 283 283 P -> L (in Ref. 2).
FT CONFLICT 499 499 T -> P (in Ref. 2).
FT CONFLICT 560 560 V -> L (in Ref. 2).
FT CONFLICT 647 654 TPYENFY -> SPYL (in Ref. 2).
SQ SEQUENCE 654 AA; 73143 MW; 1CBEB9708A8EBE7 CRC64;

Query Match 20.0%; Score 354.5; DB 1; Length 654;
Beet Local Similarity 27.6%; Pred. No. 11e-20;
Matches 118; Conservative 52; Mismatches 136; Indels 119; Gaps 16;
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QY 243 LGLFLWFLKRE-----ROEYIEB-----KKRYDICREFPNIGP- 276
DB 469 GGYFLLRRKKCCSSLATRYROAEVPAEIPETPTGHGQPSVISQRYEKLDMSAKTTRHOPT 528
QY 277 -----HSGENTE---YDTIPPTN----- 291
DB 529 PFTSSTSSSSATBERDEKTRMHSNANRNOYDLVTHQDIAHALAYGQVEYEAITPYD 588
QY 292 -----RTIL--KEDPANTVSTVEIPKK-MENPSLLTMPDTP 326
DB 589 KVDSDMEEDMAYIQVSLNVOGEFPLPKCKEDSNITYSVQKPKXTAQTPOGDASPEPTP 648
QY 327 RLFAVEN 333
DB 649 ---TYEN 652

RESULT 11
Q8C2D4 MOUSE
Q8C2D4 MOUSE PRELIMINARY; PRT; 544 AA.
AC 08C2D4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
DE length enriched library, clone: B430026K15 product: lymphocyte antigen
DE 9, full insert sequence.
GN Name: Ly9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eumetazoa; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kaenkawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirini L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Kono H., Balarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guetincin S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombereite P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsunki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
```

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Kitesuna T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiroka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai C., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RX EMBL; AK088815; BAC40591.1; -; mRNA.
DR Ensembl; ENSMUSG0000004707; Mus musculus.
DR MGI; MGI:96885; Ly9.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Immunoglobulin domain.
SQ
SEQUENCE 544 AA; 6161 MW; AAED977F3B25914 CRC64;

Query Match 19.9%; Score 353.5; DB 2; Length 544;
Best Local Similarity 27.6%; Pred. No. 1.1e-20;
Matches 118; Conservative 52; Mismatches 138; Indels 119; Gaps 16;

QY 14 LWOL-TGSA---ASGYKELVSGVAGVFPPLSK-VKQVDSIVYTRNTPTLYTIGDEG 67
DB 128 IWQCTGASRRKTAAG--KTVAGTIGSEVPTPLERARRARAKNVVWNTS--VYSQERR 183
QY 68 GTTIVTQNR-----NREYVDPDGGYSLSKTKKNKNSGIYVGYSSLSQSPQOEYVL 122
DB 184 GAATPDSRRKKGSEBERVTRSDQDSIKTSQLKMEBDGPHAYAVYCSASDPSVRHFTL 243
QY 123 HVEHTLSKPYVTMGLQSNKNGCTVNTLLCCMEHGEEDVITYTKALGQANSHNSILPI 182
DB 244 LVYKRLKESVTYNRPVHMNMGICVYVLTCSDGGNNVTYTMPLQNKAVWSQGSHTLV 303
QY 183 SWRMGESDMTFICVARNPVSNNFSSPIARLCEGADDPSSNWLCLLVPLILSLFV 242
DB 304 SWESGEHLPNFTCAHNPVS--NSSSQFSSGTCG---PRNRKRFWILLVLVLVLLMLI 358
QY 243 LGLFLWFLKRE-----ROEYIEB-----KKRYDICREFPNIGP- 276
DB 359 GGYFLLRRKKCCSSLATRYROAEVPAEIPETPTGHGQPSVISQRYEKLDMSAKTTRHOPT 418
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QY	277	-----HSGENTE-----YDTRIPHN-----	291
Db	419	PTSDTSSSSACTTEEDEXTRJHSTANSNOVVDLPTTHODIALHALAYEQVEYEAITPYD	478
QY	292	-----RTIL--REBANTVYSVEIIPK--MENPHSLTLWPTP	326
Db	479	KYDSEMDBEDMAYIQVSLNVQGETPLPKCKEBSNTITYSVQPKTKTAQIPQDASPERP	538
QY	327	RLFAVEN 333	
Db	539	---TYEN 542	
RESULT 12			
Q4VBQ4_MOUSE			
ID	Q4VBQ4_MOUSE PRELIMINARY;	PRT;	654 AA.
AC	Q4VBQ4;		
DT	13-SEP-2005 (TREMBLrel. 31, Created)		
DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)		
DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)		
DE	Lys protein.		
GN	Name=Lys;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
FN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Sheman G.M., Schlier G.D.,		
RA	Altschul S.F., Zeeberg B., Bucoff K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,		
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,		
RA	Fabry J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,		
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,		
RA	Schuerch A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;		
RG	NIH MGC Project;		
RL	Submitted (May-2005) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; BC095921; AA095921.1; --; mRNA.		
DR	MGI; MGI:96885; Lys.		
DR	InterPro; IPR003599; I9.		
DR	InterPro; IPR007110; I9-like.		
DR	PFam; PF00047; I9; 1.		
DR	SMART; SM00409; I9; 2.		
DR	PROSITE; PS00835; I9-LIKE; 2.		
KM	Immunoglobulin domain.		
SEQUENCE	654 AA; 73154 MW; 8C3ABPF571482B2C CRC64;		
Query Match	19.9%;	Score 353.5;	DB 2; Length 654;
Best Local Similarity	27.6%;	Pred. No. 1.4e-20;	
Matches 118;	Conservative 52;	Mismatches 138;	Indels 119; Gaps 16
14	LMQ-TGSA---	ASGPVKELVSGVAGATVPLKRC-VKQVDSIVTNTTPTLVITIQEG	67

Db	238	1WQFCTGASRRKTAAG--KTIVGILGEPTVLPLEFAATATATKANVWVNTS--VISQER	293
Qy	68	GTIIYTONR-----NRERVDPDGGYSILKSLKKNDSGIYYVGISLSLOPSTQEVYL	122
Db	294	GAATADSRKKPKGSEERRVRTSDPOQSILKISQIKMEDADAPYAAVYCEASRDPSVHFLL	353
Qy	123	HYEHHLSPKTYMGLQSNNGTCVYNLTCCMEHGEEDVITYWKALQQAANESINGSLPI	182
Db	354	LVYKKLEPSTVNSPVMHNNNGICKVVLTCSVDGGGNVITYWMPILONKVMISGKSHLVV	413
Qy	163	SWRMGESDMTFICVARNPVSRRPSSPILARKECEGAADPDSSMVLICLLVLLSLFV	242
Db	414	SWSESEHLPNFICTAHNPVS--NSSQFSSGTCISG----PERKKRWLLLVLLMLI	468
Qy	243	IGLFLFMFKRE-----ROEYITEE-----KKRVDCIETPNICP-	276
Db	469	GGVFILRKKKQSSSLATRYRQAENVPAEIPETPLTGHQGFVLSQRVYKLMMSAKTTHQPL	528
Qy	277	-----HSGENTE---YDITIPHN-----	291
Db	529	PTSDTSBSSSATTEDEDEKTRIHSTANSNNQVYDVLVTHODIALALAYEQVEYEALTTPYD	588
Qy	292	-----RTIL--KEDANTVYSVVEIPIPK--MENPHSLITMPDTP	326
Db	569	KVDESMDEBDMAIYQVLSLVNQGSEPLPQKKEDSNITTCYSVQKPKTKTAQTPQDABSPETP	648
Qy	327	RLFAVEN 333	
Db	649	---TYEN 652	
RESULT 13			
ID	Q96A28	HUMAN PRELIMINARY; PRT; 289 AA.	
AC	Q96A28;		
DT	01-DEC-2001	(TREMBLrel. 19, Created)	
DT	01-DEC-2001	(TREMBLrel. 19, last sequence update)	
DT	10-MAY-2005	(TREMBLrel. 30, last annotation update)	
DE	CD84-H1	(CD2 family 10) (SLAM family member 9).	
GN	Name=SLAMP9;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN			
RP	NUCLEOTIDE SEQUENCE.		
RA	Zhang W., Wan T.T., Li N., He L., Yuan Z., Yu M., Cao X.;		
RL	Submitted (JUN-2000) to the EMBL/Genbank/DBD databases.		
RN			
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=21541411; PubMed=11685473; DOI=10.1007/s002510100364;		
RT	Pennelly J.A., Tiwari B., Davis S.J., Evans E.J.;		
RT	"CD2F-10: a new member of the CD2 subset of the immunoglobulin		
RT	superfamily.";		
RT	Immunogenetics 53:599-602(2001).		
RL			
RN			
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Pooled tissue;		
RX	MEDLINE=23288857; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strunberg R.L., Feingold E.A., Grouse L.H., Derge J.G.;		
RA	Klausner R.D., Collins F.S., Wagner L., Schenem C.M., Schuler G.D.;		
RA	Altshul S.F., Zeeberg B., Buecker K.H., Schenfer C.F., Bhat N.K.;		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.;		
RA	Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.;		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.;		
RA	Brownstein M.J., Uediri T.B., Toshiyuki S., Carninci P., Prange C.;		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.;		
RA	Boesk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.;		
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.;		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.;		
RA	Fahy J., Helton B., Kerteman M., Madan A., Rodriguez S., Sanchez A.;		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.;		



RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,  
 RA Schnerch A., Schin J.B., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE-Pooled tissue;  
 RA Director MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF275725; AAK69052.1; -; mRNA.  
 DR EMBL; AY034613; AAK61389.1; -; mRNA.  
 DR EMBL; BC074754; AAK74754.1; -; mRNA.  
 DR Ensembl; ENSG000016723; Homo sapiens.  
 DR InterPro; IPR003599; 19-like.  
 DR InterPro; IPR007110; 19-like.  
 DR SMART; SM00409; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin domain.  
 SQ SEQUENCE 289 AA; 32436 MW; 2FB67EB8B4D18205 CRC64;  
 Query Match 18.7%; Score 330.5; DB 2; Length 289;  
 Best Local Similarity 30.6%; Pred. No. 4.1e-19;  
 Matches 87; Conservative 60; Mismatches 102; Indels 35; Gaps 10;  
 QY 1 MAGSTCTCTLYI-----LMQLTGSAASGPVKELVSGAVFPPK-SKVKQVDSIV 52  
 DB 1 MCAFFWLLLLLOSGQRRLRMWGS-----EEVAVLQESISLPLEIPPEEVENII 54  
 QY 53 WFTNTPLVITOP--EG--GTTIVQNNRERVDPPDGYSLKSLKKNDSGIYVGIY 108  
 DB 55 WSSHS-LATVPGEGHPATIMVTPHYQGVSLDYSLSHTNLMSWDSGLYQAVN 113  
 QY 109 SSSLOQPSIOEVLVHYEHLSPKVTMGLQSNKNGTCVTNLCCMEHSEBDVIYTKALG 168  
 DB 114 LRTSGISTMQQYNLCVYRWLSPQITVNPESGEGACMSLYCSYKXKGMQMTYEWLSRG 173  
 QY 169 QAANSHNGSITLPISWRGSESDMTPTCVARNPVSNRFPSPILAKLCRG-----AAD 220  
 DB 174 DSTYTFHGSPVLTSTWRPQDSLTSTCRANNDISVSSCP-----PDGPPYADPNVASE 228  
 QY 221 DPDSMVLTC-LVYPLLSTPLVGLPIPLFKRERQETIEKK 263  
 DB 229 KPSTAFCLAKGLIFLLVLAMG--LWVIRVQKHKPRMKK 270  
 RESULT 14  
 ID Q8C9E4\_MOUSE PRELIMINARY; PRT; 538 AA.  
 AC Q8C9E4;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched  
 DE library, clone:A630078M16 product:lymphocyte antigen 9, full insert  
 DE sequence. (fragment).  
 GN Name:Ly9;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44 (1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shitagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Arakawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Stebbins F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
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 DR EMBL; AK042288; BAC1215.1; -; mRNA.  
 DR HSSP; P08921; IHNG.  
 DR MGI; MGI:96885; Ly9.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0016021; C:integral to membrane; TAS.







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OM protein - protein search, using sw model

Run on: December 16, 2005, 10:40:47 (Search time 49 Seconds

(without alignments)  
565.232 Million cell updates/sec

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Perfect score: 1772

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Scoring table:

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Searched: 572060 segs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Issued Patents AA: \*  
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4: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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54	120	6.8	352	2	US-09-990-444-505	Sequence 505, App
55	120	6.8	352	2	US-09-997-333-505	Sequence 505, App
56	120	6.8	352	2	US-09-992-598-505	Sequence 505, App
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81	113	6.4	373	2	US-09-997-333-503	Sequence 503, App
82	113	6.4	373	2	US-09-992-598-503	Sequence 503, App
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88	109.5	6.2	315	2	US-09-620-461-28	Sequence 28, Appl1
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103	105.5	6.0	329	2	US-09-425-762-2	Sequence 2, Appli	176	91	5.1	251	6	5185441-38	Patent No. 5185441
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105	105.5	6.0	329	2	US-09-206-133-2	Sequence 26, Appli	178	90.5	5.1	521	2	US-08-996-338-20	Sequence 20, Appli
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107	105.5	6.0	329	2	US-09-425-516-2	Sequence 2, Appli	180	90	5.1	156	2	US-09-370-838-210	Sequence 210, App
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156	92.5	5.2	299	2	US-09-312-283C-189	Sequence 189, App	229	89	5.0	309	2	US-09-441-411-13	Sequence 13, Appli
157	92.5	5.2	299	2	US-09-912-283C-331	Sequence 331, App	230	89	5.0	309	2	US-09-441-411-18	Sequence 18, Appli
158	92.5	5.2	299	2	US-09-907-794A-119	Sequence 119, App	231	89	5.0	309	2	US-09-441-411-24	Sequence 24, Appli
159	92.5	5.2	299	2	US-09-905-125A-119	Sequence 119, App	232	89	5.0	309	2	US-09-425-516-23	Sequence 23, Appli
160	92.5	5.2	299	2	US-09-902-775A-119	Sequence 119, App	233	89	5.0	309	4	PCT-US95-02576-21	Sequence 21, Appli
161	92.5	5.2	299	2	US-09-397-243D-3	Sequence 3, Appli	234	89	5.0	314	2	US-08-205-697A-13	Sequence 13, Appli
162	92.5	5.2	299	2	US-09-906-700-119	Sequence 119, App	235	89	5.0	314	2	US-08-702-525-13	Sequence 13, Appli
163	92.5	5.2	299	2	US-09-903-603A-119	Sequence 119, App	236	89	5.0	314	2	US-08-837-867A-13	Sequence 13, Appli
164	92.5	5.2	299	2	US-09-904-920A-119	Sequence 119, App	237	89	5.0	314	2	US-09-441-411-14	Sequence 14, Appli
165	92.5	5.2	299	2	US-09-909-064-119	Sequence 119, App	238	89	5.0	314	4	US-09-441-411-19	Sequence 19, Appli
166	92.5	5.2	299	2	US-09-905-381A-119	Sequence 119, App	239	89	5.0	314	4	PCT-US95-02576-13	Sequence 13, Appli
167	92.5	5.2	299	2	US-09-906-618-119	Sequence 119, App	240	89	5.0	356	2	US-09-441-411-11	Sequence 11, Appli
168	92.5	5.2	299	2	US-09-953-499-1	Sequence 1, Appli	241	89	5.0	356	2	US-09-441-411-12	Sequence 12, Appli
169	92.5	5.2	299	2	US-09-906-646-119	Sequence 119, App	242	89	5.0	356	2	US-09-441-411-16	Sequence 16, Appli
170	92.5	5.2	299	2	US-09-904-462-119	Sequence 119, App	243	89	5.0	356	2	US-09-441-411-17	Sequence 17, Appli
171	92.5	5.2	299	2	US-09-902-736A-119	Sequence 119, App	244	89	5.0	821	2	US-09-422-865-24	Sequence 24, Appli
172	92.5	5.2	299	2	US-09-906-722A-119	Sequence 119, App	245	89	5.0	821	2	US-09-538-092-972	Sequence 972, App
173	92	4.91	2	2	US-09-181-339-12	Sequence 12, Appli	246	89	5.0	821	2	US-08-836-734E-6	Sequence 6, Appli



247	88.5	5.0	237	2	US-08-756-416-36	Sequence 36, Appl	320	85.5	4.8	789	2	US-09-233-752A-2	Sequence 2, Appl1
248	88.5	5.0	611	1	US-08-752-307B-10	Sequence 10, Appl	321	85.5	4.8	789	2	US-09-233-752A-4	Sequence 4, Appl1
249	88.5	5.0	611	2	US-09-707-802-10	Sequence 10, Appl	322	85.5	4.8	789	2	US-09-402-036-2	Sequence 2, Appl1
250	88.5	5.0	611	2	US-09-991-326-10	Sequence 10, Appl	323	85.5	4.8	789	2	US-09-402-036-4	Sequence 4, Appl1
251	88	5.0	329	2	US-09-651-200-19	Sequence 19, Appl	324	85.5	4.8	789	2	US-09-002-285-78	Sequence 78, Appl
252	88	5.0	329	2	US-09-646-561-7	Sequence 7, Appl1	325	85.5	4.8	789	2	US-09-002-285-80	Sequence 80, Appl
253	88	5.0	329	2	US-09-487-558B-238	Sequence 238, App	326	85.5	4.8	789	2	US-09-002-285-94	Sequence 94, Appl
254	88	5.0	699	1	US-08-348-006B-7	Sequence 7, Appl1	327	85.5	4.8	789	2	US-09-002-285-100	Sequence 100, App
255	88	5.0	699	1	US-08-800-825A-7	Sequence 7, Appl1	328	85.5	4.8	789	2	US-09-904-226-2	Sequence 2, Appl1
256	88	5.0	699	2	US-09-158-657-7	Sequence 7, Appl1	329	85.5	4.8	789	2	US-09-904-226-4	Sequence 4, Appl1
257	88	5.0	821	2	US-08-836-734B-7	Sequence 7, Appl1	330	85.5	4.8	789	2	US-09-589-477-78	Sequence 78, Appl
258	88	5.0	1023	2	US-09-270-767-43827	Sequence 43827, A	331	85.5	4.8	789	2	US-09-589-477-80	Sequence 80, Appl
259	87.5	4.9	302	2	US-09-789-697A-21	Sequence 21, Appl	332	85.5	4.8	789	2	US-09-589-477-94	Sequence 94, Appl
260	87.5	4.9	325	2	US-09-651-200-20	Sequence 20, Appl	333	85.5	4.8	789	2	US-09-589-477-100	Sequence 100, App
261	87.5	4.9	769	2	US-08-434-000A-10	Sequence 10, Appl	334	85.5	4.8	789	2	US-10-099-285A-78	Sequence 78, Appl
262	87.5	4.9	769	2	US-09-312-157-10	Sequence 10, Appl	335	85.5	4.8	789	2	US-10-099-285A-80	Sequence 80, Appl
263	87.5	4.9	769	2	US-09-717-888-10	Sequence 10, Appl	336	85.5	4.8	789	2	US-10-099-285A-94	Sequence 94, Appl
264	87.5	4.9	769	2	US-09-818-247-3	Sequence 3, Appl1	337	85.5	4.8	789	2	US-10-099-285A-100	Sequence 100, App
265	87	4.9	490	2	US-09-336-643A-6	Sequence 6, Appl1	338	85.5	4.8	790	2	US-08-960-780-8	Sequence 8, Appl1
266	87	4.9	491	2	US-09-181-339-7	Sequence 7, Appl1	339	85.5	4.8	790	2	US-09-073-898-8	Sequence 8, Appl1
267	87	4.9	507	2	US-09-949-016-9860	Sequence 9860, Ap	340	85.5	4.8	790	2	US-09-307-106-2	Sequence 2, Appl1
268	87	4.9	582	2	US-09-702-705-334	Sequence 334, App	341	85.5	4.8	790	2	US-09-850-351A-8	Sequence 8, Appl1
269	87	4.9	582	2	US-09-736-457-334	Sequence 334, App	342	85.5	4.8	2491	2	US-09-207-363-1	Sequence 1, Appl1
270	87	4.9	582	2	US-09-614-124B-334	Sequence 334, App	343	85	4.8	239	2	US-09-828-995B-26	Sequence 26, Appl
271	87	4.9	582	2	US-09-671-325-334	Sequence 334, App	344	85	4.8	512	2	US-08-999-698A-7	Sequence 7, Appl1
272	87	4.9	582	2	US-09-589-184-334	Sequence 334, App	345	85	4.8	757	2	US-08-434-000A-6	Sequence 6, Appl1
273	87	4.9	582	2	US-09-658-824-334	Sequence 334, App	346	85	4.8	757	2	US-09-312-157-6	Sequence 6, Appl1
274	87	4.9	582	2	US-10-017-754-334	Sequence 334, App	347	85	4.8	757	2	US-09-717-888-6	Sequence 6, Appl1
275	87	4.9	582	2	US-09-651-563-334	Sequence 334, App	348	85	4.8	821	2	US-09-622-880B-15	Sequence 15, Appl
276	87	4.9	582	2	US-09-519-642-334	Sequence 334, App	349	84.5	4.8	175	2	US-09-869-388-8	Sequence 8, Appl1
277	87	4.9	583	1	US-08-432-016-2	Sequence 2, Appl1	350	84.5	4.8	303	2	US-08-985-950-2	Sequence 2, Appl1
278	87	4.9	583	1	US-08-684-594-2	Sequence 2, Appl1	351	84.5	4.8	303	2	US-09-546-049-2	Sequence 2, Appl1
279	87	4.9	4126	2	US-09-953-096-4	Sequence 4, Appl1	352	84.5	4.8	303	2	US-09-869-388-2	Sequence 2, Appl1
280	87	4.9	5518	2	US-09-953-096-2	Sequence 2, Appl1	353	84	4.7	218	2	US-09-451-291-12	Sequence 12, Appl
281	86.5	4.9	354	2	US-10-104-047-2965	Sequence 2965, Ap	354	84	4.7	219	2	US-09-915-782A-22	Sequence 22, Appl1
282	86.5	4.9	790	2	US-08-960-780-4	Sequence 4, Appl1	355	84	4.7	339	2	US-09-719-243-2	Sequence 2, Appl1
283	86.5	4.9	790	2	US-09-073-898-4	Sequence 4, Appl1	356	84	4.7	351	2	US-09-756-983-18	Sequence 18, Appl
284	86.5	4.9	902	2	US-09-850-351A-4	Sequence 4, Appl1	357	84	4.7	358	2	US-09-719-243-3	Sequence 3, Appl1
285	86	4.9	302	2	US-09-877-730-14	Sequence 14, Appl	358	84	4.7	668	1	US-08-530-950-13	Sequence 13, Appl
286	86	4.9	380	2	US-09-877-730-4	Sequence 4, Appl1	359	84	4.7	668	2	US-09-149-879-13	Sequence 13, Appl
287	86	4.9	604	2	US-09-949-016-9548	Sequence 9548, Ap	360	84	4.7	668	2	US-09-057-009-13	Sequence 13, Appl
288	86	4.9	826	2	US-09-877-730-16	Sequence 16, Appl	361	83.5	4.7	260	2	US-09-254-465A-23	Sequence 23, Appl
289	86	4.9	904	2	US-09-877-730-6	Sequence 6, Appl1	362	83.5	4.7	260	2	US-09-953-499-23	Sequence 23, Appl
290	86	4.9	907	2	US-09-877-730-20	Sequence 20, Appl	363	83.5	4.7	263	2	US-09-254-465A-25	Sequence 25, Appl
291	86	4.9	985	2	US-09-877-730-10	Sequence 10, Appl	364	83.5	4.7	263	2	US-09-953-499-25	Sequence 25, Appl
292	86	4.9	991	2	US-09-877-730-12	Sequence 12, Appl	365	83.5	4.7	298	2	US-09-152-060-76	Sequence 76, Appl
293	86	4.9	1069	2	US-09-877-730-2	Sequence 2, Appl1	366	83.5	4.7	298	2	US-09-852-797-76	Sequence 76, Appl
294	86	4.9	1072	2	US-09-877-730-18	Sequence 18, Appl	367	83.5	4.7	298	2	US-09-853-161-76	Sequence 76, Appl
295	86	4.9	1150	2	US-09-877-730-8	Sequence 8, Appl1	368	83.5	4.7	298	2	US-10-058-993-76	Sequence 76, Appl
296	85.5	4.8	650	2	US-10-104-047-3355	Sequence 3355, Ap	369	83.5	4.7	312	2	US-09-254-465A-9	Sequence 9, Appl1
297	85.5	4.8	746	2	US-08-838-219B-6	Sequence 6, Appl1	370	83.5	4.7	312	2	US-09-907-794A-94	Sequence 94, Appl
298	85.5	4.8	746	2	US-09-233-336A-6	Sequence 6, Appl1	371	83.5	4.7	312	2	US-09-905-125A-64	Sequence 64, Appl
299	85.5	4.8	746	2	US-09-233-752A-6	Sequence 6, Appl1	372	83.5	4.7	312	2	US-09-905-125A-64	Sequence 64, Appl
300	85.5	4.8	746	2	US-09-402-036-6	Sequence 6, Appl1	373	83.5	4.7	312	2	US-09-902-775A-64	Sequence 64, Appl
301	85.5	4.8	746	2	US-09-904-226-6	Sequence 6, Appl1	374	83.5	4.7	312	2	US-09-906-700-64	Sequence 64, Appl
302	85.5	4.8	789	1	US-08-471-033-29	Sequence 29, Appl	375	83.5	4.7	312	2	US-09-903-603A-64	Sequence 64, Appl
303	85.5	4.8	789	1	US-08-471-033-32	Sequence 32, Appl	376	83.5	4.7	312	2	US-09-909-064-64	Sequence 64, Appl
304	85.5	4.8	789	1	US-08-471-044-32	Sequence 32, Appl	377	83.5	4.7	312	2	US-09-905-381A-64	Sequence 64, Appl
305	85.5	4.8	789	1	US-08-471-044-32	Sequence 32, Appl	378	83.5	4.7	312	2	US-09-906-618-64	Sequence 64, Appl
306	85.5	4.8	789	1	US-08-463-483A-29	Sequence 29, Appl	379	83.5	4.7	312	2	US-09-953-499-9	Sequence 9, Appl1
307	85.5	4.8	789	1	US-08-463-483A-32	Sequence 32, Appl	380	83.5	4.7	312	2	US-09-906-646-64	Sequence 64, Appl
308	85.5	4.8	789	1	US-08-471-046A-29	Sequence 29, Appl	381	83.5	4.7	312	2	US-09-904-462-64	Sequence 64, Appl
309	85.5	4.8	789	1	US-08-471-046A-32	Sequence 32, Appl	382	83.5	4.7	312	2	US-09-902-736A-64	Sequence 64, Appl
310	85.5	4.8	789	1	US-08-470-566B-29	Sequence 29, Appl	383	83.5	4.7	312	2	US-09-906-722A-64	Sequence 64, Appl
311	85.5	4.8	789	1	US-08-470-566B-32	Sequence 32, Appl	384	83.5	4.7	312	2	US-09-066-051A-32	Sequence 32, Appl
312	85.5	4.8	789	1	US-08-838-219B-2	Sequence 2, Appl1	385	83.5	4.7	341	2	US-09-401-636-4	Sequence 4, Appl1
313	85.5	4.8	789	1	US-08-838-219B-4	Sequence 4, Appl1	386	83.5	4.7	391	2	US-08-999-689A-8	Sequence 8, Appl1
314	85.5	4.8	789	1	US-08-469-334-29	Sequence 29, Appl	387	83.5	4.7	408	2	US-09-724-864-62	Sequence 62, Appl
315	85.5	4.8	789	1	US-08-469-334-32	Sequence 32, Appl	388	83.5	4.7	450	2	US-09-907-794A-320	Sequence 320, App
316	85.5	4.8	789	2	US-09-300-529-32	Sequence 29, Appl	389	83.5	4.7	450	2	US-09-905-125A-320	Sequence 320, App
317	85.5	4.8	789	2	US-09-300-529-32	Sequence 32, Appl	390	83.5	4.7	450	2	US-09-902-775A-320	Sequence 320, App
318	85.5	4.8	789	2	US-09-233-336A-2	Sequence 2, Appl1	391	83.5	4.7	450	2	US-09-906-700-320	Sequence 320, App
319	85.5	4.8	789	2	US-09-233-336A-4	Sequence 4, Appl1	392	83.5	4.7	450	2	US-09-903-603A-320	Sequence 320, App



393	83.5	4.7	450	2	US-09-904-920A-320	Sequence 320, App	466	81.5	4.6	846	1	US-08-451-883-4	Sequence 4, Appl1
394	83.5	4.7	450	2	US-09-909-064-320	Sequence 320, App	467	81.5	4.6	1441	6	US-09-949-016-10397	Sequence 10397, A
395	83.5	4.7	450	2	US-09-905-381A-320	Sequence 320, App	468	81	4.6	144	2	5169835-8	Patent No. 5169835
396	83.5	4.7	450	2	US-09-906-618-320	Sequence 320, App	469	81	4.6	252	1	US-08-414-657D-56	Sequence 56, Appl1
397	83.5	4.7	450	2	US-09-906-646-320	Sequence 320, App	470	81	4.6	287	1	US-08-414-657D-44	Sequence 48, Appl1
398	83.5	4.7	450	2	US-09-904-462-320	Sequence 320, App	471	81	4.6	304	1	US-08-414-657D-46	Sequence 46, Appl1
399	83.5	4.7	450	2	US-09-902-736A-320	Sequence 320, App	472	81	4.6	308	1	US-08-414-657D-46	Sequence 2, Appl1
400	83.5	4.7	450	2	US-09-906-722A-320	Sequence 320, App	473	81	4.6	325	1	US-08-414-657D-2	Sequence 2, Appl1
401	83.5	4.7	450	2	US-09-002-285-96	Sequence 96, Appl1	474	81	4.6	325	2	US-08-414-657D-41	Sequence 41, Appl1
402	83.5	4.7	789	2	US-09-589-477-96	Sequence 96, Appl1	475	81	4.6	325	2	US-09-135-080-2	Sequence 2, Appl1
403	83.5	4.7	789	2	US-10-099-285A-96	Sequence 96, Appl1	476	81	4.6	338	2	US-08-414-657D-60	Sequence 60, Appl1
404	83.5	4.7	1501	2	US-08-447-464-3	Sequence 3, Appl1	477	81	4.6	338	2	US-09-135-080-8	Sequence 8, Appl1
405	83.5	4.7	1501	1	US-08-716-679-3	Sequence 3, Appl1	478	81	4.6	338	2	US-09-976-594-404	Sequence 404, App
406	83	4.7	1501	1	US-09-401-636-5	Sequence 5, Appl1	479	80.5	4.5	205	2	US-09-134-001C-4766	Sequence 4766, Ap
407	83	4.7	342	2	US-09-297-468-2	Sequence 2, Appl1	480	80.5	4.5	302	2	US-09-915-789A-18	Sequence 18, Appl1
408	83	4.7	757	2	US-09-818-247-2	Sequence 2, Appl1	481	80.5	4.5	313	2	US-09-701-623C-3	Sequence 3, Appl1
409	83	4.7	846	1	US-08-149-103-3	Sequence 3, Appl1	482	80.5	4.5	346	1	US-08-213-403-2	Sequence 2, Appl1
410	83	4.7	846	1	US-08-451-883-3	Sequence 3, Appl1	483	80.5	4.5	346	1	US-08-458-077-2	Sequence 2, Appl1
411	83	4.7	873	1	US-08-393-734-2	Sequence 2, Appl1	484	80.5	4.5	346	1	US-08-747-240-2	Sequence 2, Appl1
412	83	4.7	873	1	US-08-894-489-2	Sequence 2, Appl1	485	80.5	4.5	346	1	US-08-747-240-2	Sequence 2, Appl1
413	83	4.7	873	1	US-10-167-264-2	Sequence 2, Appl1	486	80.5	4.5	346	1	US-08-299-657-6	Sequence 6, Appl1
414	83	4.7	894	2	US-09-949-016-10605	Sequence 10605, A	487	80.5	4.5	346	2	US-09-039-642B-2	Sequence 2, Appl1
415	83	4.7	904	2	US-09-949-016-9528	Sequence 9528, Ap	488	80.5	4.5	522	2	US-08-635-130A-9	Sequence 9, Appl1
416	82.5	4.7	194	2	US-08-630-172-14	Sequence 14, Appl1	489	80.5	4.5	650	1	US-09-949-016-11189	Sequence 11189, A
417	82.5	4.7	194	2	US-09-375-419-14	Sequence 14, Appl1	490	80.5	4.5	650	1	US-08-121-713D-60	Sequence 60, Appl1
418	82.5	4.7	226	2	US-09-869-388-10	Sequence 10, Appl1	491	80.5	4.5	650	1	US-08-835-268-60	Sequence 60, Appl1
419	82.5	4.7	238	2	US-09-149-476-485	Sequence 485, App	492	80.5	4.5	650	1	US-09-060-632-60	Sequence 60, Appl1
420	82.5	4.7	456	2	US-09-949-016-7564	Sequence 7564, Ap	493	80.5	4.5	650	2	US-08-833-331-60	Sequence 60, Appl1
421	82.5	4.7	456	2	US-09-134-000C-5552	Sequence 5552, Ap	494	80.5	4.5	650	2	US-09-060-610-60	Sequence 60, Appl1
422	82.5	4.7	511	2	US-09-002-285-88	Sequence 88, Appl1	495	80.5	4.5	650	4	PCT-US94-10151A-60	Sequence 60, Appl1
423	82.5	4.7	511	2	US-09-589-477-88	Sequence 88, Appl1	496	80.5	4.5	721	2	US-09-390-234-20	Sequence 20, Appl1
424	82.5	4.7	511	2	US-10-099-285A-88	Sequence 88, Appl1	497	80.5	4.5	721	2	US-09-603-311-20	Sequence 20, Appl1
425	82.5	4.7	789	2	US-09-002-285-82	Sequence 82, Appl1	498	80.5	4.5	789	2	US-09-960-780-6	Sequence 6, Appl1
426	82.5	4.7	789	2	US-09-002-285-84	Sequence 84, Appl1	499	80.5	4.5	789	2	US-09-073-888-6	Sequence 6, Appl1
427	82.5	4.7	789	2	US-09-002-285-92	Sequence 92, Appl1	500	80.5	4.5	789	2	US-09-850-351A-6	Sequence 2, Appl1
428	82.5	4.7	789	2	US-09-589-477-82	Sequence 82, Appl1	501	80.5	4.5	828	1	US-08-261-304-2	Sequence 6, Appl1
429	82.5	4.7	789	2	US-09-589-477-84	Sequence 84, Appl1	502	80	4.5	227	2	US-09-869-388-6	Sequence 6, Appl1
430	82.5	4.7	789	2	US-09-589-477-92	Sequence 84, Appl1	503	80	4.5	252	1	US-08-414-657D-57	Sequence 57, Appl1
431	82.5	4.7	789	2	US-09-589-477-92	Sequence 82, Appl1	504	80	4.5	287	1	US-08-414-657D-49	Sequence 49, Appl1
432	82.5	4.7	789	2	US-10-099-285A-84	Sequence 82, Appl1	505	80	4.5	310	1	US-08-414-657D-45	Sequence 45, Appl1
433	82.5	4.7	789	2	US-10-099-285A-84	Sequence 84, Appl1	506	80	4.5	315	1	US-08-414-657D-47	Sequence 47, Appl1
434	82.5	4.7	790	2	US-09-002-285-102	Sequence 92, Appl1	507	80	4.5	338	1	US-08-414-657D-42	Sequence 42, Appl1
435	82.5	4.7	790	2	US-09-589-477-102	Sequence 102, App	508	80	4.5	338	1	US-08-414-657D-43	Sequence 43, Appl1
436	82.5	4.7	790	2	US-10-099-285A-102	Sequence 102, App	509	80	4.5	338	2	US-09-135-080-4	Sequence 4, Appl1
437	82.5	4.6	82	2	US-09-107-532A-4919	Sequence 4919, Ap	510	80	4.5	499	2	US-09-252-991A-3338	Sequence 20, Appl1
438	82	4.6	370	2	US-09-248-796A-18365	Sequence 18365, A	511	80	4.5	528	2	US-09-010-147B-20	Sequence 20, Appl1
439	82	4.6	449	2	US-09-118-319-7	Sequence 7, Appl1	512	80	4.5	528	2	US-10-188-495-71	Sequence 71, Appl1
440	82	4.6	449	2	US-09-286-691-4	Sequence 4, Appl1	513	80	4.5	529	2	US-09-383-568-31	Sequence 31, Appl1
441	82	4.6	449	2	US-09-687-147-4	Sequence 4, Appl1	514	80	4.5	529	2	US-09-823-038A-31	Sequence 31, Appl1
442	82	4.6	567	2	US-09-773-877B-20	Sequence 20, Appl1	515	80	4.5	607	1	US-08-752-307B-12	Sequence 12, Appl1
443	82	4.6	757	2	US-09-622-880B-1	Sequence 1, Appl1	516	80	4.5	607	2	US-09-707-802-12	Sequence 12, Appl1
444	82	4.6	874	1	US-08-456-647B-6	Sequence 6, Appl1	517	80	4.5	607	2	US-09-991-326-12	Sequence 12, Appl1
445	82	4.6	874	1	US-08-237-401A-6	Sequence 6, Appl1	518	80	4.5	1233	2	US-09-194-613-5	Sequence 5, Appl1
446	82	4.6	880	1	US-08-445-640-10	Sequence 10, Appl1	519	79.5	4.5	202	6	US-09-570-367C-21	Patent No. 5189147
447	82	4.6	880	1	US-08-170-558-10	Sequence 10, Appl1	520	79.5	4.5	278	2	US-09-915-524-21	Sequence 21, Appl1
448	82	4.6	880	2	US-08-447-314-10	Sequence 10, Appl1	521	79.5	4.5	278	2	US-09-934-634-21	Sequence 21, Appl1
449	82	4.6	880	2	US-08-445-461-10	Sequence 10, Appl1	522	79.5	4.5	278	2	US-09-917-278-21	Sequence 21, Appl1
450	82	4.6	880	2	US-09-223-490-10	Sequence 10, Appl1	523	79.5	4.5	278	2	US-09-917-278-21	Sequence 21, Appl1
451	82	4.6	1248	2	US-09-949-016-10595	Sequence 10595, A	524	79.5	4.5	309	2	US-09-248-796A-30432	Sequence 20432, A
452	82	4.6	1248	2	US-09-949-016-10596	Sequence 10596, A	525	79.5	4.5	329	2	US-08-821-994-84	Sequence 84, Appl1
453	81.5	4.6	309	2	US-09-667-135-6	Sequence 6, Appl1	526	79.5	4.5	335	2	US-09-489-038A-11298	Sequence 11298, A
454	81.5	4.6	309	2	US-09-910-174B-7	Sequence 7, Appl1	527	79.5	4.5	374	2	US-08-821-994-68	Sequence 68, Appl1
455	81.5	4.6	352	2	US-09-620-461-7	Sequence 7, Appl1	528	79.5	4.5	402	2	US-09-292-097-16	Sequence 16, Appl1
456	81.5	4.6	352	2	US-09-999-833A-612	Sequence 612, App	529	79.5	4.5	402	2	US-09-933-561-16	Sequence 16, Appl1
457	81.5	4.6	352	2	US-10-020-445A-612	Sequence 612, App	530	79.5	4.5	643	1	US-08-477-570-6	Sequence 6, Appl1
458	81.5	4.6	504	2	US-09-949-016-7020	Sequence 7020, App	531	79.5	4.5	769	1	US-08-477-570-8	Sequence 8, Appl1
459	81.5	4.6	504	2	US-09-991-181-119	Sequence 119, App	532	79.5	4.5	859	2	US-09-708-200-7	Sequence 7, Appl1
460	81.5	4.6	504	2	US-09-990-444-119	Sequence 119, App	533	79.5	4.5	859	2	US-09-788-657-16	Sequence 16, Appl1
461	81.5	4.6	504	2	US-09-992-333-119	Sequence 119, App	534	79.5	4.5	859	2	US-09-712-691-5	Sequence 5, Appl1
462	81.5	4.6	504	2	US-09-997-598-119	Sequence 119, App	535	79.5	4.5	859	2	US-10-641-068-16	Sequence 16, Appl1
463	81.5	4.6	511	2	US-09-949-016-10054	Sequence 10054, A	536	79	4.5	859	2	US-09-707-468C-5	Sequence 5, Appl1
464	81.5	4.6	558	2	US-09-667-135-31	Sequence 31, Appl1	537	78.5	4.4	340	2	US-09-401-636-2	Sequence 2, Appl1
465	81.5	4.6	846	1	US-08-149-103-4	Sequence 4, Appl1	538	78.5	4.4	393	1	US-08-429-742-2	Sequence 2, Appl1



539	78.5	4.4	439	2	US-09-383-586-32	Sequence 32, Appl	612	76.5	4.3	1089	2	US-08-464-436-2	Sequence 2, Appl
540	78.5	4.4	439	2	US-09-823-038A-32	Sequence 32, Appl	613	76.5	4.3	1089	2	US-09-769-987-2	Sequence 2, Appl
541	78.5	4.4	544	2	US-09-999-833A-259	Sequence 259, App	614	76.5	4.3	1089	2	US-09-866-510-2	Sequence 2, Appl
542	78.5	4.4	544	2	US-10-020-445A-259	Sequence 259, App	615	76.5	4.3	1089	2	US-09-866-510-4	Sequence 4, Appl
543	78.5	4.4	831	1	US-09-047-026A-4	Sequence 4, Appl	616	76.5	4.3	1089	2	US-09-866-510-6	Sequence 6, Appl
544	78.5	4.4	847	2	US-09-949-002-338	Sequence 328, App	617	76.5	4.3	1089	2	US-09-866-510-8	Sequence 8, Appl
545	78.5	4.4	857	2	US-09-248-796A-20522	Sequence 20522, A	618	76.5	4.3	1089	2	US-09-866-510-10	Sequence 10, Appl
546	78.5	4.4	862	2	US-09-949-002-427	Sequence 427, App	619	76.5	4.3	1089	2	US-09-919-497-90	Sequence 90, Appl
547	78	4.4	341	1	US-08-248-628A-2	Sequence 2, Appl	620	76.5	4.3	1089	2	US-09-949-016-6703	Sequence 6703, Ap
548	78	4.4	345	2	US-09-214-631-5	Sequence 5, Appl	621	76.5	4.3	1089	4	PCT-US92-00730-4	Sequence 4, Appl
549	78	4.4	588	2	US-09-949-016-10547	Sequence 10547, A	622	76.5	4.3	1089	4	PCT-US92-00862-4	Sequence 4, Appl
550	78	4.4	624	1	US-08-642-406A-22	Sequence 22, Appl	623	76.5	4.3	1125	2	US-09-949-016-10194	Sequence 10194, A
551	78	4.4	624	1	US-09-199-534-22	Sequence 22, Appl	624	76.5	4.3	1328	2	US-08-781-891-76	Sequence 76, Appl
552	78	4.4	624	2	US-09-199-534-22	Sequence 22, Appl	625	76.5	4.3	1328	2	US-09-618-166-76	Sequence 16, Appl
553	78	4.4	624	2	US-09-491-322-22	Sequence 22, Appl	626	76.5	4.3	1617	2	US-09-784-358-16	Sequence 16, Appl
554	78	4.4	655	2	US-09-248-796A-14308	Sequence 14308, A	627	76.5	4.3	1691	2	US-09-784-358-2	Sequence 2, Appl
555	78	4.4	833	2	US-09-949-016-11496	Sequence 11496, A	628	76.5	4.3	1723	2	US-09-194-612A-31	Sequence 31, Appl
556	78	4.4	848	2	US-09-787-443-44	Sequence 44, Appl	629	76.5	4.3	1745	2	US-09-800-729-89	Sequence 89, Appl
557	78	4.4	1180	2	US-09-949-016-6577	Sequence 6577, Ap	630	76	4.3	277	2	US-09-543-681A-4527	Sequence 4527, Ap
558	77.5	4.4	321	2	US-09-254-465A-2	Sequence 2, Appl	631	76	4.3	378	1	US-08-225-477B-9	Sequence 9, Appl
559	77.5	4.4	321	2	US-09-953-499-2	Sequence 2, Appl	632	76	4.3	378	4	PCT-US95-04353-9	Sequence 2, Appl
560	77.5	4.4	321	2	US-09-999-833A-52	Sequence 52, Appl	633	76	4.3	390	2	US-08-961-554A-2	Sequence 2, Appl
561	77.5	4.4	321	2	US-10-020-445A-52	Sequence 52, Appl	634	76	4.3	390	2	US-09-050-861B-2	Sequence 2, Appl
562	77.5	4.4	477	1	US-08-432-016-3	Sequence 3, Appl	635	76	4.3	390	2	US-09-135-228B-2	Sequence 2, Appl
563	77.5	4.4	477	1	US-08-684-594-3	Sequence 3, Appl	636	76	4.3	390	2	US-09-651-150B-2	Sequence 2, Appl
564	77.5	4.4	650	2	US-09-310-463-2	Sequence 2, Appl	637	76	4.3	462	2	US-09-773-877B-18	Sequence 18, Appl
565	77.5	4.4	650	2	US-08-842-248A-2	Sequence 2, Appl	638	76	4.3	463	2	US-09-082-310-1	Sequence 1, Appl
566	77.5	4.4	650	2	US-09-949-002-390	Sequence 390, App	639	76	4.3	463	2	US-09-575-205-1	Sequence 1, Appl
567	77.5	4.4	662	1	US-08-261-304-7	Sequence 7, Appl	640	76	4.3	463	2	US-09-976-594A-721	Sequence 721, App
568	77.5	4.4	677	2	US-09-949-002-416	Sequence 416, App	641	76	4.3	567	2	US-09-773-877B-12	Sequence 12, Appl
569	77.5	4.4	735	4	PCT-US93-00031-13	Sequence 13, Appl	642	76	4.3	599	1	US-08-442-542-18	Sequence 18, Appl
570	77.5	4.4	735	4	PCT-US93-00031-15	Sequence 15, Appl	643	76	4.3	599	2	US-08-765-469-18	Sequence 18, Appl
571	77.5	4.4	739	2	US-08-482-073-6	Sequence 6, Appl	644	76	4.3	759	2	US-09-902-540-16161	Sequence 16161, A
572	77.5	4.4	739	4	PCT-US93-00031-9	Sequence 9, Appl	645	75.5	4.3	446	2	US-09-583-110-4602	Sequence 4602, Ap
573	77.5	4.4	757	2	US-09-538-092-520	Sequence 520, App	646	75.5	4.3	448	2	US-09-107-433-3945	Sequence 3945, Ap
574	77.5	4.4	824	2	US-09-949-002-448	Sequence 448, App	647	75.5	4.3	514	2	US-10-142-231-68	Sequence 68, Appl
575	77.5	4.4	1312	2	US-09-554-572-26	Sequence 26, Appl	648	75.5	4.3	530	2	US-09-949-016-9519	Sequence 9519, Ap
576	77	4.3	278	2	US-09-570-367C-2	Sequence 2, Appl	649	75.5	4.3	648	1	US-08-817-436A-2	Sequence 2, Appl
577	77	4.3	278	2	US-09-915-524-2	Sequence 2, Appl	650	75.5	4.3	1215	2	US-09-949-002-321	Sequence 321, App
578	77	4.3	278	2	US-09-934-634-2	Sequence 2, Appl	651	75	4.2	261	2	US-10-101-464A-691	Sequence 691, App
579	77	4.3	306	2	US-09-917-278-2	Sequence 2, Appl	652	75	4.2	303	2	US-09-509-347-7	Sequence 7, Appl
580	77	4.3	306	2	US-10-191-029-12	Sequence 12, Appl	653	75	4.2	379	2	US-09-605-703B-2418	Sequence 2418, Ap
581	77	4.3	362	2	US-09-291-299A-6	Sequence 6, Appl	654	75	4.2	512	2	US-09-356-818A-2	Sequence 2, Appl
582	77	4.3	458	2	US-09-435-956A-1	Sequence 1, Appl	655	75	4.2	527	2	US-09-910-174B-10	Sequence 10, Appl
583	77	4.3	470	2	US-09-291-299A-1	Sequence 1, Appl	656	75	4.2	527	2	US-09-620-461-10	Sequence 10, Appl
584	77	4.3	476	2	US-09-291-299A-3	Sequence 3, Appl	657	75	4.2	641	2	US-09-422-869-26	Sequence 26, Appl
585	77	4.3	523	2	US-08-948-564-8	Sequence 8, Appl	658	75	4.2	762	2	US-09-949-016-7568	Sequence 7568, Ap
586	77	4.3	581	2	US-09-270-767-42396	Sequence 42396, A	659	75	4.2	855	2	US-09-328-352-6216	Sequence 6216, Ap
587	77	4.3	651	2	US-09-270-767-44877	Sequence 44877, A	660	75	4.2	1729	2	US-09-696-115B-2	Sequence 2, Appl
588	77	4.3	1021	1	US-08-497-025-3	Sequence 3, Appl	661	75	4.2	2137	2	US-09-134-001C-4463	Sequence 4463, Ap
589	77	4.3	1021	2	US-09-949-002-363	Sequence 363, App	662	74.5	4.2	218	2	US-09-068-655-7	Sequence 7, Appl
590	77	4.3	1024	2	US-09-949-002-523	Sequence 523, App	663	74.5	4.2	230	6	5169835-13	Parent No. 5169835
591	77	4.3	1033	2	US-09-252-991A-00611	Sequence 20611, A	664	74.5	4.2	338	2	US-09-688-188B-152	Sequence 152, App
592	77	4.3	4866	2	US-09-424-783-2	Sequence 2, Appl	665	74.5	4.2	373	2	US-09-291-417D-152	Sequence 152, App
593	76.5	4.3	292	2	US-09-800-729-175	Sequence 175, App	666	74.5	4.2	373	2	US-09-688-188B-97	Sequence 97, Appl
594	76.5	4.3	364	2	US-08-896-537A-3	Sequence 3, Appl	667	74.5	4.2	373	2	US-09-291-417D-97	Sequence 97, Appl
595	76.5	4.3	490	2	US-09-667-135-28	Sequence 28, Appl	668	74.5	4.2	374	2	US-08-821-994-69	Sequence 69, Appl
596	76.5	4.3	589	2	US-09-866-510-12	Sequence 12, Appl	669	74.5	4.2	463	1	US-08-853-659A-52	Sequence 52, Appl
597	76.5	4.3	1089	1	US-09-961-403-4	Sequence 4, Appl	670	74.5	4.2	640	2	US-09-949-016-7565	Sequence 7565, Ap
598	76.5	4.3	1089	1	US-08-180-195-36	Sequence 36, Appl	671	74.5	4.2	789	2	US-09-002-285-98	Sequence 98, Appl
599	76.5	4.3	1089	1	US-08-168-917-4	Sequence 4, Appl	672	74.5	4.2	789	2	US-09-589-477-98	Sequence 98, Appl
600	76.5	4.3	1089	1	US-08-477-329-36	Sequence 36, Appl	673	74.5	4.2	789	2	US-10-099-285A-98	Sequence 98, Appl
601	76.5	4.3	1089	1	US-08-475-458-36	Sequence 36, Appl	674	74.5	4.2	789	2	US-08-452-052-2	Sequence 2, Appl
602	76.5	4.3	1089	1	US-08-460-510-4	Sequence 4, Appl	675	74.5	4.2	1018	1	US-10-104-047-2506	Sequence 2506, Ap
603	76.5	4.3	1089	1	US-08-460-490-4	Sequence 4, Appl	676	74.5	4.2	1104	1	US-08-313-165-58	Sequence 58, Appl
604	76.5	4.3	1089	2	US-08-980-400-36	Sequence 36, Appl	677	74.5	4.2	1148	1	US-09-082-614A-58	Sequence 58, Appl
605	76.5	4.3	1089	2	US-08-462-728-2	Sequence 2, Appl	678	74.5	4.2	1571	2	US-08-956-991-11	Sequence 11, Appl
606	76.5	4.3	1089	2	US-09-583-459A-36	Sequence 36, Appl	679	74.5	4.2	1788	1	US-08-963-284-2	Sequence 2, Appl
607	76.5	4.3	1089	2	US-09-583-459A-36	Sequence 36, Appl	680	74.5	4.2	1910	1	US-08-956-991-2	Sequence 2, Appl
608	76.5	4.3	1089	2	US-09-583-459A-36	Sequence 36, Appl	681	74.5	4.2	1911	1	US-08-346-006B-5	Sequence 5, Appl
609	76.5	4.3	1089	2	US-09-435-059-36	Sequence 36, Appl	682	74.5	4.2	1911	1	US-08-800-825A-5	Sequence 5, Appl
610	76.5	4.3	1089	2	US-08-461-917-2	Sequence 2, Appl	683	74.5	4.2	1911	1	US-09-158-657-5	Sequence 5, Appl
611	76.5	4.3	1089	2	US-08-464-436-2	Sequence 2, Appl	684	74.5	4.2	1911	2		



685	74.5	4.2	1911	4	PCT-US94-10166-5	Sequence 5, Appli	758	72.5	4.1	293	6	5189147-3	Patent No. 5189147
686	74.5	4.2	4654	2	US-08-476-515A-84	Sequence 84, Appl	759	72.5	4.1	331	1	US-08-364-081-3	Sequence 3, Appli
687	74.5	4.2	4655	2	US-08-652-877-84	Sequence 86, Appl	760	72.5	4.1	331	1	US-08-630-552-3	Sequence 3, Appli
688	74.5	4.2	4655	2	US-08-652-877-86	Sequence 86, Appl	761	72.5	4.1	331	4	PCT-US95-16558-3	Sequence 3, Appli
689	74.5	4.2	4655	2	US-08-652-877-88	Sequence 89, Appl	762	72.5	4.1	331	4	US-09-667-135-4	Sequence 4, Appli
690	74.5	4.2	4655	2	US-08-652-877-90	Sequence 90, Appl	763	72.5	4.1	354	6	5169835-4	Patent No. 5169835
691	74	4.2	342	2	US-09-401-636-8	Sequence 8, Appli	764	72.5	4.1	374	2	US-08-821-994-70	Sequence 70, Appl
692	74	4.2	343	2	US-09-454-034-8	Sequence 8, Appli	765	72.5	4.1	390	2	US-08-979-424-1	Sequence 1, Appli
693	74	4.2	387	2	US-09-175-928-2	Sequence 2, Appli	766	72.5	4.1	390	2	US-09-907-794A-39	Sequence 39, Appl
694	74	4.2	451	2	US-09-107-532A-6552	Sequence 6552, Ap	767	72.5	4.1	390	2	US-09-905-125A-39	Sequence 39, Appl
695	74	4.2	543	2	US-09-042-709A-18	Sequence 18, Appl	768	72.5	4.1	390	2	US-09-902-775A-39	Sequence 39, Appl
696	74	4.2	548	2	US-08-247-902A-2	Sequence 2, Appli	769	72.5	4.1	390	2	US-09-906-700-39	Sequence 39, Appl
697	74	4.2	548	4	PCT-US93-10541-2	Sequence 2, Appli	770	72.5	4.1	390	2	US-09-903-603A-39	Sequence 39, Appl
698	74	4.2	862	2	US-09-949-016-10140	Sequence 10140, A	771	72.5	4.1	390	2	US-09-904-620A-39	Sequence 39, Appl
699	74	4.2	705	2	US-08-556-422A-2	Sequence 2, Appli	772	72.5	4.1	390	2	US-09-909-064-39	Sequence 39, Appl
700	74	4.2	1027	2	US-09-162-0021B-2	Sequence 2, Appli	773	72.5	4.1	390	2	US-09-905-381A-39	Sequence 39, Appl
701	74	4.2	1027	2	US-10-268-051-8	Sequence 8, Appli	774	72.5	4.1	390	2	US-09-906-618-39	Sequence 39, Appl
702	74	4.2	1027	2	US-10-125-772-2	Sequence 2, Appli	775	72.5	4.1	390	2	US-09-906-646-39	Sequence 39, Appl
703	74	4.2	1165	2	US-09-487-558B-76	Sequence 76, Appl	776	72.5	4.1	390	2	US-09-904-462-39	Sequence 39, Appl
704	74	4.2	1194	2	US-10-191-029-10	Sequence 10, Appl	777	72.5	4.1	390	2	US-09-904-462A-39	Sequence 39, Appl
705	74	4.2	1333	1	US-08-447-411-76	Sequence 76, Appl	778	72.5	4.1	390	2	US-09-907-76A-39	Sequence 39, Appl
706	74	4.2	1333	1	US-08-662-227-34	Sequence 34, Appl	779	72.5	4.1	424	6	US-09-906-722A-39	Sequence 39, Appl
707	74	4.2	1333	2	US-09-017-947-34	Sequence 34, Appl	780	72.5	4.1	489	2	US-09-134-001C-4902	Patent No. 5169835
708	74	4.2	1333	2	US-09-925-442-34	Sequence 34, Appl	781	72.5	4.1	521	1	US-08-504-048-9	Sequence 9, Appli
709	74	4.2	1709	2	US-09-949-016-10503	Sequence 10503, A	782	72.5	4.1	526	1	US-08-471-570-4	Sequence 4, Appli
710	73.5	4.1	217	2	US-09-134-001C-5638	Sequence 5638, Ap	783	72.5	4.1	560	2	US-09-071-025-220	Sequence 220, App
711	73.5	4.1	238	2	US-08-978-289-10	Sequence 10, Appl	784	72.5	4.1	560	2	US-10-206-576-220	Sequence 220, App
712	73.5	4.1	321	2	US-09-171-461-22	Sequence 22, Appl	785	72.5	4.1	605	1	US-08-752-307B-8	Sequence 8, Appli
713	73.5	4.1	321	2	US-09-970-711-22	Sequence 22, Appl	786	72.5	4.1	605	2	US-09-707-802-8	Sequence 8, Appli
714	73.5	4.1	332	2	US-09-248-796A-18143	Sequence 18143, A	787	72.5	4.1	605	2	US-09-991-326-8	Sequence 8, Appli
715	73.5	4.1	344	2	US-09-700-397-3	Sequence 3, Appli	788	72.5	4.1	627	2	US-09-071-025-218	Sequence 218, App
716	73.5	4.1	344	2	US-09-999-833A-523	Sequence 523, App	789	72.5	4.1	627	2	US-10-206-576-218	Sequence 218, App
717	73.5	4.1	344	2	US-10-020-445A-523	Sequence 523, App	790	72.5	4.1	635	2	US-10-101-464A-932	Sequence 93, App
718	73.5	4.1	348	2	US-10-104-047-2468	Sequence 2468, Ap	791	72.5	4.1	652	1	US-08-471-570-10	Sequence 10, Appl
719	73.5	4.1	513	2	US-09-910-174B-18	Sequence 18, Appl	792	72.5	4.1	659	2	US-09-134-000C-6124	Sequence 6124, Ap
720	73.5	4.1	513	2	US-09-620-461-18	Sequence 18, Appl	793	72.5	4.1	759	2	US-09-002-285-86	Sequence 86, Appl
721	73.5	4.1	631	2	US-09-248-796A-19450	Sequence 19450, A	794	72.5	4.1	759	2	US-09-589-477-86	Sequence 86, Appl
722	73.5	4.1	699	2	US-09-134-001C-4054	Sequence 4054, Ap	795	72.5	4.1	759	2	US-10-099-285A-86	Sequence 86, Appl
723	73.5	4.1	716	2	US-09-171-945-125	Sequence 125, App	796	72.5	4.1	768	2	US-09-489-039A-12897	Sequence 12897, A
724	73.5	4.1	716	2	US-09-910-059-125	Sequence 125, App	797	72.5	4.1	790	2	US-09-543-681A-5459	Sequence 5459, Ap
725	73.5	4.1	842	2	US-09-902-540-11810	Sequence 11810, A	798	72.5	4.1	913	2	US-09-140-378A-2	Sequence 2, Appli
726	73.5	4.1	913	1	US-08-445-640-4	Sequence 4, Appli	799	72.5	4.1	919	1	US-08-336-343A-2	Sequence 2, Appli
727	73.5	4.1	913	2	US-08-170-558-4	Sequence 4, Appli	800	72.5	4.1	919	2	US-09-551-188-2	Sequence 2, Appli
728	73.5	4.1	913	2	US-08-447-314-4	Sequence 4, Appli	801	72.5	4.1	937	2	US-09-949-016-8366	Sequence 8366, Ap
729	73.5	4.1	913	2	US-08-445-461-4	Sequence 4, Appli	802	72.5	4.1	937	2	US-09-949-016-8367	Sequence 8367, Ap
730	73.5	4.1	913	2	US-09-223-490-4	Sequence 4, Appli	803	72.5	4.1	937	2	US-09-949-016-8368	Sequence 8368, Ap
731	73.5	4.1	1000	2	US-09-193-562D-30	Sequence 30, Appl	804	72.5	4.1	1434	1	US-08-540-406-10	Sequence 10, Appl
732	73.5	4.1	1000	2	US-10-053-412B-30	Sequence 30, Appl	805	72.5	4.1	1434	2	US-08-656-055-10	Sequence 10, Appl
733	73.5	4.1	1544	1	US-08-469-486-52	Sequence 52, Appl	806	72.5	4.1	1434	2	US-08-954-668-10	Sequence 10, Appl
734	73.5	4.1	4544	1	US-08-469-658-52	Sequence 52, Appl	807	72.5	4.1	1434	2	US-08-918-658-10	Sequence 10, Appl
735	73.5	4.1	1112	2	US-08-545-809A-136	Sequence 136, App	808	72.5	4.1	1434	2	US-09-724-631-10	Sequence 10, Appl
736	73	4.1	112	2	US-09-515-697-136	Sequence 57664, A	809	72.5	4.1	1434	2	US-08-954-701A-10	Sequence 10, Appl
737	73	4.1	155	2	US-09-270-767-57684	Sequence 106, App	810	72.5	4.1	1434	2	US-09-754-032-10	Sequence 10, Appl
738	73	4.1	175	2	US-10-144-929-106	Sequence 106, App	811	72.5	4.1	1434	2	US-08-916-140-10	Sequence 10, Appl
739	73	4.1	250	2	US-09-270-767-42724	Sequence 42724, A	812	72.5	4.1	1434	4	PCT-US95-13223-10	Sequence 20374, A
740	73	4.1	270	2	US-09-569-611C-37	Sequence 37, Appl	813	72	4.1	222	2	US-09-248-796A-10974	Sequence 10974, A
741	73	4.1	308	2	US-09-248-796A-14626	Sequence 14626, A	814	72	4.1	311	2	US-09-252-991A-28792	Sequence 12316, A
742	73	4.1	373	2	US-09-823-038A-60	Sequence 60, Appl	815	72	4.1	328	1	US-09-489-039A-13216	Sequence 13216, A
743	73	4.1	389	2	US-08-724-378D-3	Sequence 3, Appli	816	72	4.1	348	1	US-09-031-485-28	Sequence 28, Appl
744	73	4.1	459	1	US-08-157-101A-7	Sequence 7, Appli	817	72	4.1	348	1	US-08-847-429A-28	Sequence 28, Appl
745	73	4.1	501	1	US-08-408-095-31	Sequence 31, Appl	818	72	4.1	348	2	US-09-065-474-28	Sequence 28, Appl
746	73	4.1	504	2	US-08-868-373-6	Sequence 6, Appli	819	72	4.1	348	2	US-09-557-034-28	Sequence 28, Appl
747	73	4.1	548	2	US-09-398-395A-12	Sequence 12, Appl	820	72	4.1	358	2	US-09-265-585C-118	Sequence 118, App
748	73	4.1	548	2	US-09-887-586A-12	Sequence 12, Appl	821	72	4.1	378	2	US-09-265-585C-109	Sequence 109, App
749	73	4.1	548	2	US-09-895-752-12	Sequence 12, Appl	822	72	4.1	379	2	US-09-186-276B-46	Sequence 46, Appl
750	73	4.1	548	2	US-09-893-820-12	Sequence 12, Appl	823	72	4.1	379	2	US-08-842-445-46	Sequence 46, Appl
751	73	4.1	548	2	US-09-903-012B-12	Sequence 12, Appl	824	72	4.1	379	2	US-09-186-188B-46	Sequence 46, Appl
752	73	4.1	548	2	US-09-900-797-12	Sequence 12, Appl	825	72	4.1	394	2	US-09-265-585C-16	Sequence 46, Appl
753	73	4.1	623	2	US-09-949-016-11206	Sequence 11206, A	826	72	4.1	427	2	US-09-949-016-6716	Sequence 6716, Ap
754	73	4.1	646	2	US-09-653-961-2	Sequence 22, Appli	827	72	4.1	452	2	US-09-949-016-9842	Sequence 9842, Ap
755	73	4.1	651	2	US-08-985-950-22	Sequence 22, Appl	828	72	4.1	456	4	US-09-773-877B-16	Sequence 16, Appli
756	73	4.1	651	2	US-09-546-049-22	Sequence 22, Appl	829	72	4.1	456	1	US-08-435-933-6	Sequence 6, Appli
757	72.5	4.1	283	2	US-09-248-796A-19610	Sequence 19610, A	830	72	4.1	456	1	PCT-US96-06035-6	Sequence 6, Appli



831	72	4.1	497	2	US-08-709-731A-39	Sequence 29, Appl	904	71	4.0	107	1	US-08-425-336-125	Sequence 125, App
832	72	4.1	514	2	US-09-949-016-11380	Sequence 11380, A	905	71	4.0	107	1	US-08-488-113B-125	Sequence 125, App
833	72	4.1	517	2	US-09-723-368-4	Sequence 4, Appl1	906	71	4.0	107	1	US-08-477-448B-125	Sequence 125, App
834	72	4.1	528	2	US-09-710-279-1930	Sequence 1930, Ap	907	71	4.0	107	1	US-08-107-669D-65	Sequence 65, Appl
835	72	4.1	546	2	US-09-303-518D-58	Sequence 58, Appl	908	71	4.0	107	1	US-08-472-788A-87	Sequence 87, Appl
836	72	4.1	548	2	US-09-398-395A-2	Sequence 2, Appl1	909	71	4.0	107	1	US-08-477-531B-65	Sequence 65, Appl
837	72	4.1	548	2	US-09-887-755A-2	Sequence 2, Appl1	910	71	4.0	107	1	US-08-646-360-125	Sequence 125, App
838	72	4.1	548	2	US-09-895-752-2	Sequence 2, Appl1	911	71	4.0	107	1	US-08-082-842A-87	Sequence 87, Appl
839	72	4.1	548	2	US-09-903-012B-2	Sequence 2, Appl1	912	71	4.0	107	2	US-08-839-765-125	Sequence 125, App
840	72	4.1	548	2	US-09-900-797-2	Sequence 2, Appl1	913	71	4.0	107	2	US-09-136-389-125	Sequence 125, App
841	72	4.1	548	2	US-09-893-820-2	Sequence 2, Appl1	914	71	4.0	107	2	US-09-610-838-125	Sequence 125, App
842	72	4.1	557	2	US-09-773-877B-14	Sequence 14, Appl1	915	71	4.0	107	2	US-09-711-485-125	Sequence 125, App
843	72	4.1	633	2	US-09-248-796A-20407	Sequence 20407, A	916	71	4.0	233	2	US-09-198-452A-244	Sequence 244, App
844	72	4.1	646	2	US-09-949-016-6728	Sequence 6728, Ap	917	71	4.0	236	2	US-09-438-155A-236	Sequence 236, App
845	72	4.1	646	2	US-09-653-961-4	Sequence 4, Appl1	918	71	4.0	233	2	US-09-049-672A-7	Sequence 7, Appl1
846	72	4.1	670	2	US-09-575-081B-27	Sequence 27, Appl	919	71	4.0	240	1	US-08-488-113B-147	Sequence 147, App
847	72	4.1	670	2	US-09-949-016-6584	Sequence 6584, Ap	920	71	4.0	240	1	US-08-488-113B-148	Sequence 148, App
848	72	4.1	670	2	US-09-949-016-6590	Sequence 6590, Ap	921	71	4.0	240	1	US-08-477-484B-147	Sequence 147, App
849	72	4.1	679	2	US-09-949-016-8034	Sequence 8034, Ap	922	71	4.0	240	1	US-08-477-484B-148	Sequence 148, App
850	72	4.1	679	2	US-09-949-016-8035	Sequence 8035, Ap	923	71	4.0	240	1	US-08-646-360-147	Sequence 147, App
851	72	4.1	754	1	US-08-525-864A-2	Sequence 2, Appl1	924	71	4.0	240	1	US-08-646-360-148	Sequence 148, App
852	72	4.1	852	2	US-09-319-588C-18	Sequence 18, Appl	925	71	4.0	240	2	US-08-839-765-147	Sequence 147, App
853	72	4.1	1297	2	US-09-540-245A-17	Sequence 17, Appl	926	71	4.0	240	2	US-08-839-765-148	Sequence 148, App
854	72	4.1	1297	2	US-10-289-776-17	Sequence 17, Appl	927	71	4.0	240	2	US-09-136-389-147	Sequence 147, App
855	72	4.1	1456	1	US-08-803-973-2	Sequence 2, Appl1	928	71	4.0	240	2	US-09-136-389-148	Sequence 148, App
856	72	4.1	1456	1	US-08-803-973-2	Sequence 2, Appl1	929	71	4.0	240	2	US-09-610-838-147	Sequence 147, App
857	72	4.1	1745	1	US-09-031-485-33	Sequence 33, Appl	930	71	4.0	240	2	US-09-610-838-148	Sequence 148, App
858	72	4.1	1745	1	US-08-847-429A-33	Sequence 33, Appl	931	71	4.0	240	2	US-09-711-485-147	Sequence 147, App
859	72	4.1	1745	2	US-09-065-474-33	Sequence 33, Appl	932	71	4.0	240	2	US-09-711-485-148	Sequence 148, App
860	72	4.1	1745	2	US-09-557-034-33	Sequence 33, Appl	933	71	4.0	379	2	US-09-543-681A-1089	Sequence 7089, App
861	72	4.1	2383	2	US-09-492-709A-302	Sequence 302, App	934	71	4.0	384	2	US-08-504-617-2	Sequence 2, Appl1
862	72	4.1	2753	2	US-09-949-016-7659	Sequence 7659, Ap	935	71	4.0	475	2	US-08-657-749D-11	Sequence 11, Appl
863	72	4.1	2753	2	US-09-949-016-7660	Sequence 7660, Ap	936	71	4.0	621	2	US-09-297-937C-9	Sequence 9, Appl
864	72	4.1	2780	2	US-10-220-587-2	Sequence 2, Appl1	937	71	4.0	621	2	US-09-248-796A-14463	Sequence 14463, A
865	72	4.1	4872	2	US-09-424-783-3	Sequence 3, Appl1	938	71	4.0	647	2	US-08-753-007A-32	Sequence 32, Appl
866	71.5	4.0	206	2	US-08-821-994-77	Sequence 77, Appl	939	71	4.0	647	2	US-09-398-456-32	Sequence 32, Appl
867	71.5	4.0	241	2	US-09-248-796A-17942	Sequence 17942, A	940	71	4.0	649	2	US-10-188-445-63	Sequence 63, Appl
868	71.5	4.0	248	6	5169835-15	Sequence 375, App	941	71	4.0	661	1	US-08-232-538-12	Sequence 12, Appl
869	71.5	4.0	276	2	US-09-949-002-375	Sequence 5, Appl1	942	71	4.0	661	1	US-08-786-164-12	Sequence 12, Appl
870	71.5	4.0	327	2	US-09-173-581-5	Sequence 5, Appl1	943	71	4.0	671	2	US-10-188-445-61	Sequence 61, Appl
871	71.5	4.0	327	2	US-09-420-915-5	Sequence 5, Appl1	944	71	4.0	687	1	US-08-232-538-6	Sequence 6, Appl1
872	71.5	4.0	333	2	US-09-949-002-502	Sequence 502, App	945	71	4.0	687	1	US-08-786-164-6	Sequence 6, Appl1
873	71.5	4.0	384	2	US-09-552-322-2	Sequence 2, Appl1	946	71	4.0	687	2	US-09-427-353-2	Sequence 2, Appl1
874	71.5	4.0	403	2	US-09-638-649-5	Sequence 5, Appl1	947	71	4.0	687	2	US-10-104-047-2982	Sequence 2982, App
875	71.5	4.0	403	2	US-09-638-648-5	Sequence 5, Appl1	948	71	4.0	731	2	US-09-107-532A-6999	Sequence 6999, App
876	71.5	4.0	456	2	US-09-248-796A-23791	Sequence 23791, A	949	71	4.0	758	1	US-08-874-678-1	Sequence 1, Appl1
877	71.5	4.0	462	2	US-09-166-350-18	Sequence 18, Appl	950	71	4.0	758	1	US-08-643-839-1	Sequence 1, Appl1
878	71.5	4.0	523	2	US-09-910-174B-11	Sequence 11, Appl	951	71	4.0	758	2	US-09-051-363-24	Sequence 24, Appl
879	71.5	4.0	523	2	US-09-620-461-11	Sequence 11, Appl	952	71	4.0	758	2	US-09-348-886-1	Sequence 1, Appl1
880	71.5	4.0	608	2	US-09-095-385-4	Sequence 4, Appl1	953	71	4.0	758	2	US-10-105-901A-1	Sequence 1, Appl
881	71.5	4.0	624	2	US-09-949-016-10587	Sequence 10587, A	954	71	4.0	780	1	US-08-232-538-14	Sequence 14, Appl
882	71.5	4.0	746	2	US-08-434-000A-4	Sequence 4, Appl1	955	71	4.0	780	1	US-08-786-164-14	Sequence 14, Appl
883	71.5	4.0	746	2	US-09-312-157-4	Sequence 4, Appl1	956	71	4.0	821	1	US-08-451-822A-13	Sequence 13, Appl
884	71.5	4.0	746	2	US-09-717-888-4	Sequence 4, Appl1	957	71	4.0	821	2	US-08-323-430-13	Sequence 13, Appl
885	71.5	4.0	764	2	US-09-949-016-6254	Sequence 6254, Ap	958	71	4.0	905	4	PCT-US96-06221-2	Sequence 2, Appl1
886	71.5	4.0	764	2	US-09-818-247-1	Sequence 1, Appl1	959	71	4.0	905	2	US-09-651-656-13	Sequence 13, Appl
887	71.5	4.0	816	2	US-09-949-016-8119	Sequence 8119, Ap	960	71	4.0	906	2	US-09-650-855-13	Sequence 13, Appl
888	71.5	4.0	919	1	US-08-788-674-4	Sequence 4, Appl1	961	71	4.0	916	2	US-09-919-457-64	Sequence 64, Appl
889	71.5	4.0	941	2	US-09-949-016-6062	Sequence 6062, Ap	962	71	4.0	930	2	US-09-134-001C-5314	Sequence 5314, App
890	71.5	4.0	1006	2	US-09-949-016-10730	Sequence 10730, A	963	71	4.0	930	2	US-09-386-962C-10	Sequence 10, Appl
891	71.5	4.0	1115	2	US-10-012-231A-58	Sequence 58, Appl	964	71	4.0	975	2	US-09-695-481-4	Sequence 4, Appl1
892	71.5	4.0	1115	2	US-10-015-389A-58	Sequence 58, Appl	965	71	4.0	1018	1	US-08-408-093-6	Sequence 6, Appl1
893	71.5	4.0	1115	2	US-10-006-768A-58	Sequence 58, Appl	966	71	4.0	1018	1	US-08-408-430A-6	Sequence 6, Appl1
894	71.5	4.0	1115	2	US-10-015-671A-58	Sequence 58, Appl	967	71	4.0	1018	1	US-08-714-901-6	Sequence 6, Appl1
895	71.5	4.0	1115	2	US-10-015-393A-58	Sequence 58, Appl	968	71	4.0	1018	2	US-08-040-741-6	Sequence 6, Appl1
896	71.5	4.0	1115	2	US-10-011-833A-58	Sequence 58, Appl	969	71	4.0	1044	2	US-09-949-016-10321	Sequence 10321, A
897	71.5	4.0	1115	2	US-10-006-041A-58	Sequence 58, Appl	970	71	4.0	1082	2	US-09-538-092-533	Sequence 53, App
898	71.5	4.0	1115	2	US-10-012-064A-58	Sequence 58, Appl	971	71	4.0	1276	2	US-09-297-937C-13	Sequence 13, Appl
899	71.5	4.0	1255	2	US-09-902-540-12628	Sequence 12628, A	972	71	4.0	1338	2	US-08-750-141A-3	Sequence 3, Appl1
900	71.5	4.0	1405	2	US-09-248-796A-18103	Sequence 18103, A	973	71	4.0	1338	2	US-09-119-014D-6	Sequence 6, Appl1
901	71.5	4.0	2468	2	US-09-976-594-726	Sequence 726, App	974	71	4.0	1362	1	US-08-874-678-3	Sequence 33, Appl
902	71.5	4.0	2468	2	US-09-538-092-1135	Sequence 1135, App	975	71	4.0	1362	1	US-08-643-839-33	Sequence 33, Appl
903	71.5	4.0	2522	2	US-09-949-016-10237	Sequence 10237, A	976	71	4.0	1362	2	US-09-348-886-33	Sequence 33, Appl



977	71	4.0	1362	2	US-10-105-901A-33	Sequence 33, Appl	1050	70	4.0	320	2	US-09-370-700-14	Sequence 14, Appl
978	71	4.0	1481	1	US-08-616-844-40	Sequence 40, Appl	1051	70	4.0	320	2	US-09-603-207-14	Sequence 14, Appl
979	71	4.0	1481	1	US-08-599-654-40	Sequence 40, Appl	1051	70	4.0	320	2	US-09-442-043A-17	Sequence 17, Appl
980	71	4.0	1481	2	US-08-944-868A-40	Sequence 40, Appl	1053	70	4.0	338	1	US-08-441-893A-17	Sequence 17, Appl
981	71	4.0	1481	2	US-08-944-423A-40	Sequence 40, Appl	1054	70	4.0	338	1	US-07-940-861-13	Sequence 43, Appl
982	71	4.0	1481	2	US-08-944-496-40	Sequence 40, Appl	1055	70	4.0	347	1	US-08-459-512-43	Sequence 43, Appl
983	71	4.0	4391	2	US-10-006-011A-2	Sequence 2, Appl1	1056	70	4.0	347	1	US-08-459-657-43	Sequence 43, Appl
984	71	4.0	183	2	US-09-621-976-3942	Sequence 3942, Ap	1057	70	4.0	347	1	US-08-460-132-43	Sequence 43, Appl
985	70.5	4.0	184	2	US-09-303-518D-774	Sequence 774, App	1058	70	4.0	347	1	US-08-466-465-8	Sequence 8, Appl1
986	70.5	4.0	223	2	US-09-303-518D-776	Sequence 776, App	1059	70	4.0	347	2	US-09-730-465-8	Sequence 8, Appl1
987	70.5	4.0	223	2	US-09-303-518D-778	Sequence 778, App	1060	70	4.0	347	2	US-09-730-465-8	Sequence 8, Appl1
988	70.5	4.0	241	2	US-09-915-789A-11	Sequence 11, Appl1	1061	70	4.0	412	2	US-09-543-681A-6782	Sequence 6782, Ap
989	70.5	4.0	261	2	US-09-899-634C-2	Sequence 2, Appl1	1062	70	4.0	469	2	US-08-753-007A-8	Sequence 8, Appl1
990	70.5	4.0	314	2	US-09-438-185A-452	Sequence 452, App	1063	70	4.0	469	2	US-09-398-496-8	Sequence 8, Appl1
991	70.5	4.0	334	2	US-09-248-796A-15329	Sequence 15329, A	1064	70	4.0	490	2	US-09-489-039A-9610	Sequence 9610, Ap
992	70.5	4.0	338	2	US-08-922-957-1	Sequence 1, Appl1	1065	70	4.0	523	2	US-09-248-796A-17555	Sequence 17555, A
993	70.5	4.0	338	2	US-08-922-957-3	Sequence 3, Appl1	1066	70	4.0	548	2	US-09-398-395A-4	Sequence 4, Appl1
994	70.5	4.0	343	2	US-09-134-000C-6363	Sequence 6363, Ap	1067	70	4.0	548	2	US-09-398-395A-6	Sequence 6, Appl1
995	70.5	4.0	371	2	US-09-248-796A-16428	Sequence 16428, A	1068	70	4.0	548	2	US-09-398-395A-8	Sequence 8, Appl1
996	70.5	4.0	374	2	US-09-248-796A-15744	Sequence 15744, A	1069	70	4.0	548	2	US-09-398-395A-10	Sequence 10, Appl1
997	70.5	4.0	466	2	US-09-134-001C-3526	Sequence 3526, Ap	1070	70	4.0	548	2	US-09-887-586A-4	Sequence 4, Appl1
998	70.5	4.0	467	2	US-08-821-99A-83	Sequence 83, Appl	1071	70	4.0	548	2	US-09-887-586A-6	Sequence 6, Appl1
999	70.5	4.0	472	2	US-08-821-99A-83	Sequence 83, Ap	1072	70	4.0	548	2	US-09-887-586A-8	Sequence 8, Appl1
1000	70.5	4.0	491	2	US-09-134-001C-4727	Sequence 4727, Ap	1073	70	4.0	548	2	US-09-887-586A-10	Sequence 10, Appl
1001	70.5	4.0	495	2	US-10-154-515A-6	Sequence 6, Appl1	1074	70	4.0	548	2	US-09-895-752-6	Sequence 6, Appl1
1002	70.5	4.0	495	2	US-10-122-706-6	Sequence 2, Appl1	1075	70	4.0	548	2	US-09-895-752-8	Sequence 8, Appl1
1003	70.5	4.0	502	2	US-09-489-039A-8035	Sequence 8035, Ap	1076	70	4.0	548	2	US-09-895-752-10	Sequence 10, Appl1
1004	70.5	4.0	533	1	US-07-820-011A-2	Sequence 2, Appl1	1077	70	4.0	548	2	US-09-903-012B-4	Sequence 4, Appl1
1005	70.5	4.0	533	4	PCT-US93-00445-2	Sequence 3, Appl1	1078	70	4.0	548	2	US-09-903-012B-6	Sequence 6, Appl1
1006	70.5	4.0	533	4	PCT-US93-00445-2	Sequence 2, Appl1	1079	70	4.0	548	2	US-09-903-012B-8	Sequence 8, Appl1
1007	70.5	4.0	579	2	US-09-173-151A-2	Sequence 2, Appl1	1080	70	4.0	548	2	US-09-903-012B-10	Sequence 10, Appl1
1008	70.5	4.0	610	2	US-09-976-594-947	Sequence 947, App	1081	70	4.0	548	2	US-09-903-012B-12	Sequence 12, Appl1
1009	70.5	4.0	617	2	US-09-188-930-303	Sequence 303, App	1082	70	4.0	548	2	US-09-900-797-4	Sequence 4, Appl1
1010	70.5	4.0	617	2	US-09-312-283C-303	Sequence 303, App	1083	70	4.0	548	2	US-09-900-797-6	Sequence 6, Appl1
1011	70.5	4.0	644	2	US-09-949-016-11714	Sequence 11714, A	1084	70	4.0	548	2	US-09-900-797-8	Sequence 8, Appl1
1012	70.5	4.0	668	1	US-08-232-538-13	Sequence 13, Appl	1085	70	4.0	548	2	US-09-900-797-10	Sequence 10, Appl
1013	70.5	4.0	668	1	US-08-786-164-13	Sequence 13, Appl	1086	70	4.0	548	2	US-09-893-820-6	Sequence 6, Appl1
1014	70.5	4.0	686	2	US-09-173-151A-4	Sequence 4, Appl1	1087	70	4.0	548	2	US-09-893-820-8	Sequence 8, Appl1
1015	70.5	4.0	724	2	US-10-104-047-2224	Sequence 2224, Ap	1088	70	4.0	548	2	US-09-893-820-10	Sequence 10, Appl
1016	70.5	4.0	760	2	US-09-248-796A-17568	Sequence 17568, A	1089	70	4.0	548	2	US-09-893-820-12	Sequence 12, Appl
1017	70.5	4.0	764	2	US-09-142-956B-14	Sequence 14, Appl	1090	70	4.0	550	1	US-08-443-639-8	Sequence 8, Appl1
1018	70.5	4.0	767	2	US-08-874-678-2	Sequence 2, Appl1	1091	70	4.0	550	2	US-08-577-483-8	Sequence 8, Appl1
1019	70.5	4.0	767	2	US-08-643-839-2	Sequence 2, Appl1	1092	70	4.0	550	2	US-09-435-380-8	Sequence 8, Appl1
1020	70.5	4.0	767	2	US-09-348-886-2	Sequence 2, Appl1	1093	70	4.0	550	2	US-09-303-064-53	Sequence 53, Appl
1021	70.5	4.0	767	2	US-10-105-901A-2	Sequence 2, Appl1	1094	70	4.0	551	2	US-09-086-503-53	Sequence 53, Appl
1022	70.5	4.0	788	1	US-08-232-538-15	Sequence 15, Appl	1095	70	4.0	576	1	US-07-821-716-4	Sequence 4, Appl1
1023	70.5	4.0	788	1	US-08-786-164-15	Sequence 15, Appl	1096	70	4.0	576	1	US-08-381-603-4	Sequence 4, Appl1
1024	70.5	4.0	915	2	US-10-282-162-52	Sequence 52, Appl	1097	70	4.0	576	2	US-08-924-376-4	Sequence 4, Appl1
1025	70.5	4.0	940	2	US-09-198-452A-500	Sequence 500, App	1098	70	4.0	576	2	US-08-685-212-4	Sequence 2, Appl1
1026	70.5	4.0	940	2	US-09-438-185A-468	Sequence 468, App	1099	70	4.0	576	2	US-09-173-151A-30	Sequence 30, Appl1
1027	70.5	4.0	983	2	US-09-412-554A-2	Sequence 2, Appl1	1100	70	4.0	576	2	US-08-466-932A-4	Sequence 4, Appl1
1028	70.5	4.0	1088	1	US-08-485-588-6	Sequence 6, Appl1	1101	70	4.0	576	2	PCT-US94-02414-4	Sequence 4, Appl1
1029	70.5	4.0	1088	1	US-08-484-565-6	Sequence 6, Appl1	1102	70	4.0	576	4	PCT-US94-02414-4	Sequence 4, Appl1
1030	70.5	4.0	1088	1	US-08-484-751-6	Sequence 6, Appl1	1103	70	4.0	576	4	PCT-US96-08899-4	Sequence 4, Appl1
1031	70.5	4.0	1088	1	US-08-943-986-6	Sequence 6, Appl1	1104	70	4.0	582	2	US-09-147-405B-13	Sequence 13, Appl
1032	70.5	4.0	1088	2	US-08-353-784-6	Sequence 6, Appl1	1105	70	4.0	590	2	US-10-104-047-3415	Sequence 3415, Ap
1033	70.5	4.0	1088	2	US-08-484-719B-6	Sequence 6, Appl1	1106	70	4.0	611	2	US-07-757-342D-8	Sequence 8, Appl1
1034	70.5	4.0	1088	2	US-08-484-159-6	Sequence 6, Appl1	1107	70	4.0	611	2	US-07-757-342D-8	Sequence 8, Appl1
1035	70.5	4.0	1088	2	US-08-810-116-8	Sequence 8, Appl1	1108	70	4.0	625	2	US-09-461-657B-8	Sequence 8, Appl1
1036	70.5	4.0	1088	2	US-07-930-548A-8	Sequence 8, Appl1	1109	70	4.0	625	2	US-09-134-001C-4504	Sequence 4504, Ap
1037	70.5	4.0	1088	2	US-09-098-707A-2	Sequence 2, Appl1	1110	70	4.0	636	2	US-07-757-342D-7	Sequence 7, Appl1
1038	70.5	4.0	1088	2	US-09-483-539-2	Sequence 2, Appl1	1111	70	4.0	636	2	US-09-461-657B-7	Sequence 7, Appl1
1039	70.5	4.0	1088	2	US-09-949-016-6198	Sequence 6198, Ap	1112	70	4.0	637	2	US-09-569-611C-35	Sequence 35, Appl
1040	70.5	4.0	1088	2	US-10-100-405A-2	Sequence 2, Appl1	1113	70	4.0	652	2	US-09-310-463-4	Sequence 4, Appl1
1041	70.5	4.0	1088	2	US-09-949-016-9853	Sequence 9853, Ap	1114	70	4.0	652	2	US-08-842-248A-4	Sequence 4, Appl1
1042	70.5	4.0	1088	2	US-10-022-939-2	Sequence 2, Appl1	1115	70	4.0	652	2	PCT-US91-09784-2	Sequence 2, Appl1
1043	70.5	4.0	1088	2	US-09-240-274-146	Sequence 146, App	1116	70	4.0	687	4	US-08-780-562-7	Sequence 7, Appl1
1044	70.5	4.0	1088	2	US-09-848-798-146	Sequence 146, App	1117	70	4.0	837	1	US-07-923-976-2	Sequence 2, Appl1
1045	70.5	4.0	1088	2	US-08-821-994-43	Sequence 43, Appl	1118	70	4.0	837	1	US-08-599-455B-2	Sequence 2, Appl1
1046	70.5	4.0	1088	2	US-09-602-787A-162	Sequence 162, App	1119	70	4.0	894	2	US-09-069-781B-2	Sequence 2, Appl1
1047	70.5	4.0	1088	2	US-09-602-787A-164	Sequence 164, App	1120	70	4.0	894	2	US-08-618-957A-12	Sequence 12, Appl
1048	70.5	4.0	1088	2	US-09-252-991A-32836	Sequence 32836, A	1121	70	4.0	894	2	US-09-137-132-2	Sequence 2, Appl1
1049	70.5	4.0	1088	2	US-09-036-987A-14	Sequence 14, Appl	1122	70	4.0	894	2		



1123	70	4.0	894	2	US-08-864-564A-2	Sequence 2, Appl1	1196	69	3.9	355	2	US-08-875-811-41	Sequence 41, Appl
1124	70	4.0	894	2	US-09-094-410-2	Sequence 2, Appl1	1197	69	3.9	355	2	US-08-875-811-49	Sequence 49, Appl
1125	70	4.0	894	2	US-08-708-123D-2	Sequence 2, Appl1	1198	69	3.9	355	2	US-08-875-811-64	Sequence 64, Appl
1126	70	4.0	894	2	US-08-583-153A-2	Sequence 2, Appl1	1199	69	3.9	357	2	US-09-949-016-9074	Sequence 9074, Ap
1127	70	4.0	894	2	US-08-570-142D-2	Sequence 2, Appl1	1200	69	3.9	358	2	US-08-875-811-45	Sequence 45, Appl
1128	70	4.0	894	2	US-08-638-524B-2	Sequence 2, Appl1	1201	69	3.9	358	2	US-08-875-811-51	Sequence 51, Appl
1129	70	4.0	894	2	US-10-095-929-12	Sequence 12, Appl	1202	69	3.9	360	2	US-08-875-811-47	Sequence 47, Appl
1130	70	4.0	944	2	US-09-449-285A-2	Sequence 2, Appl1	1203	69	3.9	373	2	US-08-875-811-43	Sequence 43, Appl
1131	70	4.0	944	2	US-09-964-238-2	Sequence 2, Appl1	1204	69	3.9	383	2	US-09-079-030-82	Sequence 82, Appl
1132	70	4.0	950	2	US-09-449-285A-4	Sequence 4, Appl1	1205	69	3.9	408	2	US-09-248-796A-17517	Sequence 17517, A
1133	70	4.0	950	2	US-09-964-238-4	Sequence 4, Appl1	1206	69	3.9	467	2	US-08-030-175-42	Sequence 42, Appl
1134	70	4.0	1092	2	US-09-147-405B-15	Sequence 15, Appl	1207	69	3.9	468	1	US-08-220-151-16	Sequence 16, Appl
1135	70	4.0	1162	1	US-08-599-455B-43	Sequence 43, Appl	1208	69	3.9	468	1	US-08-413-118-16	Sequence 16, Appl
1136	70	4.0	1162	2	US-09-069-781B-43	Sequence 43, Appl	1209	69	3.9	468	2	US-08-473-446-15	Sequence 15, Appl
1137	70	4.0	1162	2	US-09-137-132-43	Sequence 43, Appl	1210	69	3.9	514	2	US-09-800-729-114	Sequence 124, App
1138	70	4.0	1162	2	US-08-864-564A-43	Sequence 43, Appl	1211	69	3.9	519	2	US-08-996-338-21	Sequence 21, Appl
1139	70	4.0	1162	2	US-09-094-410-43	Sequence 43, Appl	1212	69	3.9	519	2	US-09-556-972-21	Sequence 21, Appl
1140	70	4.0	1162	2	US-08-708-123D-43	Sequence 43, Appl	1213	69	3.9	523	2	US-08-606-505B-67	Sequence 67, Appl
1141	70	4.0	1162	2	US-08-638-524B-43	Sequence 43, Appl	1214	69	3.9	523	2	US-09-616-990-67	Sequence 67, Appl
1142	70	4.0	1214	2	US-09-949-016-6885	Sequence 6885, Ap	1215	69	3.9	537	1	US-08-604-333-4	Sequence 4, Appl1
1143	70	4.0	1214	2	US-09-949-016-7130	Sequence 7130, Ap	1216	69	3.9	537	2	US-09-110-618-4	Sequence 4, Appl1
1144	70	4.0	1461	2	US-09-976-594-531	Sequence 531, App	1217	69	3.9	537	2	US-09-173-151A-29	Sequence 29, Appl
1145	70	4.0	2183	2	US-08-746-111-5	Sequence 5, Appl1	1218	69	3.9	537	2	US-09-578-178-4	Sequence 4, Appl1
1146	69.5	3.9	223	2	US-09-303-518D-780	Sequence 780, App	1219	69	3.9	537	2	US-09-577-806-4	Sequence 4, Appl1
1147	69.5	3.9	307	2	US-09-540-236-2790	Sequence 2790, Ap	1220	69	3.9	537	2	US-09-621-502-8	Sequence 8, Appl1
1148	69.5	3.9	314	2	US-08-353-476-71	Sequence 71, App	1221	69	3.9	542	1	US-08-140-729A-5	Sequence 5, Appl1
1149	69.5	3.9	324	1	US-09-328-352-4577	Sequence 4577, Ap	1222	69	3.9	542	1	US-08-546-666-5	Sequence 5, Appl1
1150	69.5	3.9	328	4	US-08-225-477B-5	Sequence 5, Appl1	1223	69	3.9	542	1	US-08-916-745-5	Sequence 5, Appl1
1151	69.5	3.9	332	4	PCT-US95-04353-5	Sequence 5, Appl1	1224	69	3.9	542	1	US-08-663-808-4	Sequence 4, Appl1
1152	69.5	3.9	333	1	US-08-436-463-6	Sequence 6, Appl1	1225	69	3.9	542	1	US-09-042-929-5	Sequence 5, Appl1
1153	69.5	3.9	333	1	US-08-024-253-6	Sequence 6, Appl1	1226	69	3.9	542	1	US-08-546-661-5	Sequence 5, Appl1
1154	69.5	3.9	333	1	US-09-134-000C-5207	Sequence 5207, Ap	1227	69	3.9	542	1	US-09-042-960-5	Sequence 5, Appl1
1155	69.5	3.9	334	1	US-08-646-981-16	Sequence 16, Appl	1228	69	3.9	542	2	US-09-198-650-5	Sequence 5, Appl1
1156	69.5	3.9	447	2	US-09-198-452A-972	Sequence 972, App	1229	69	3.9	542	2	US-09-332-740-4	Sequence 4, Appl1
1157	69.5	3.9	456	2	US-09-438-185A-901	Sequence 901, App	1230	69	3.9	542	2	US-09-042-913-5	Sequence 5, Appl1
1158	69.5	3.9	484	2	US-09-248-796A-15483	Sequence 15483, A	1231	69	3.9	542	2	US-09-188-496-4	Sequence 4, Appl1
1159	69.5	3.9	496	2	US-10-104-047-3006	Sequence 3006, Ap	1232	69	3.9	542	2	US-09-042-937-5	Sequence 4, Appl1
1160	69.5	3.9	499	2	US-09-049-672A-1	Sequence 1, Appl1	1233	69	3.9	542	2	US-09-368-282-4	Sequence 4, Appl1
1161	69.5	3.9	503	2	US-09-487-558B-424	Sequence 424, App	1234	69	3.9	542	2	US-09-566-708A-4	Sequence 4, Appl1
1162	69.5	3.9	506	2	US-08-888-998-2	Sequence 2, Appl1	1235	69	3.9	542	2	US-09-042-709A-5	Sequence 5, Appl1
1163	69.5	3.9	506	2	US-09-362-633-2	Sequence 2, Appl1	1236	69	3.9	542	2	US-09-227-614-5	Sequence 5, Appl1
1164	69.5	3.9	506	2	US-09-877-476-2	Sequence 2, Appl1	1237	69	3.9	542	2	US-09-949-016-6662	Sequence 6662, Ap
1165	69.5	3.9	506	2	US-09-877-476-28	Sequence 28, Appl	1238	69	3.9	543	2	US-09-949-016-10085	Sequence 10085, A
1166	69.5	3.9	506	2	US-09-877-476-36	Sequence 36, Appl	1239	69	3.9	561	2	US-09-198-452A-744	Sequence 744, App
1167	69.5	3.9	512	2	US-09-248-796A-14219	Sequence 14219, A	1240	69	3.9	584	2	US-09-911-909B-14	Sequence 14, Appl
1168	69.5	3.9	548	2	US-09-538-092-1058	Sequence 1058, Ap	1241	69	3.9	627	2	US-09-303-518B-456	Sequence 456, App
1169	69.5	3.9	555	2	US-09-328-352-5873	Sequence 5873, Ap	1242	69	3.9	657	2	US-08-508-761B-2	Sequence 2, Appl1
1170	69.5	3.9	559	2	US-09-949-016-9137	Sequence 9137, Ap	1243	69	3.9	673	2	US-09-196-387-8	Sequence 8, Appl1
1171	69.5	3.9	677	2	US-09-270-767-58094	Sequence 58094, A	1244	69	3.9	673	2	US-09-841-835-8	Sequence 8, Appl1
1172	69.5	3.9	697	2	US-09-486-072-3	Sequence 3, Appl1	1245	69	3.9	688	2	US-09-071-035-464	Sequence 464, App
1173	69.5	3.9	742	2	US-09-494-297A-4	Sequence 4, Appl1	1246	69	3.9	688	2	US-10-206-576-464	Sequence 464, App
1174	69.5	3.9	804	2	US-08-981-446B-3	Sequence 3, Appl1	1247	69	3.9	712	2	US-09-949-016-10600	Sequence 10600, A
1175	69.5	3.9	847	2	US-09-270-767-42783	Sequence 42783, A	1248	69	3.9	745	2	US-09-949-016-9976	Sequence 9976, Ap
1176	69.5	3.9	898	2	US-09-949-016-10987	Sequence 10987, A	1249	69	3.9	821	2	US-09-308-345A-8	Sequence 48, Appl
1177	69.5	3.9	948	2	US-10-363-937-13	Sequence 13, Appl	1250	69	3.9	919	2	US-09-543-681A-7277	Sequence 7277, Ap
1178	69.5	3.9	1033	2	US-10-029-347-4	Sequence 4, Appl1	1251	69	3.9	951	2	US-09-949-016-6954	Sequence 6954, Ap
1179	69.5	3.9	1172	2	US-09-712-363-176	Sequence 176, App	1252	69	3.9	924	2	US-09-438-185A-704	Sequence 704, App
1180	69.5	3.9	1222	2	US-08-506-296B-21	Sequence 21, Appl	1253	69	3.9	949	2	US-10-104-047-2435	Sequence 2435, Ap
1181	69.5	3.9	1222	2	US-09-194-612A-1	Sequence 1, Appl1	1254	69	3.9	949	2	US-09-196-387-10	Sequence 10, Appl
1182	69.5	3.9	1722	2	US-09-949-002-535	Sequence 341, App	1255	69	3.9	1068	2	US-09-215-694-7	Sequence 7, Appl1
1183	69.5	3.9	1740	2	US-09-949-002-535	Sequence 335, App	1256	69	3.9	1068	2	US-10-109-310-7	Sequence 10, Appl
1184	69.5	3.9	108	1	US-08-378-939-30	Sequence 3, Appl	1257	69	3.9	1327	2	US-09-196-387-2	Sequence 2, Appl1
1185	69	3.9	127	2	US-09-136-315-4	Sequence 4, Appl1	1258	69	3.9	1327	2	US-09-196-387-2	Sequence 2, Appl1
1186	69	3.9	127	2	US-09-767-888-4	Sequence 4, Appl1	1259	69	3.9	1327	2	US-09-841-835-2	Sequence 2, Appl1
1187	69	3.9	156	2	US-08-821-894-42	Sequence 42, Appl1	1260	69	3.9	1327	2	US-09-971-115A-8	Sequence 8, Appl1
1188	69	3.9	256	2	US-09-107-532A-6856	Sequence 6856, Ap	1261	69	3.9	2032	2	US-09-071-035-458	Sequence 458, App
1189	69	3.9	269	1	US-08-727-311-3	Sequence 3, Appl1	1262	69	3.9	2032	2	US-09-071-035-462	Sequence 462, App
1190	69	3.9	329	2	US-09-651-200-18	Sequence 18, Appl	1263	69	3.9	2032	2	US-09-071-035-466	Sequence 466, App
1191	69	3.9	329	2	US-09-303-040-6	Sequence 6, Appl1	1264	69	3.9	2032	2	US-10-206-576-458	Sequence 458, App
1192	69	3.9	329	2	US-09-710-279-414	Sequence 414, App	1265	69	3.9	2032	2	US-10-206-576-462	Sequence 462, App
1193	69	3.9	331	2	US-09-134-001C-5258	Sequence 5258, Ap	1266	69	3.9	2032	2	US-10-206-576-466	Sequence 466, App
1194	69	3.9	332	2	US-09-646-561-26	Sequence 26, Appl	1267	69	3.9	2054	2	US-09-134-000C-6612	Sequence 6612, Ap
1195	69	3.9	335	2	US-09-902-540-11829	Sequence 11829, A	1268	69	3.9	3892	2	US-09-328-352-5503	Sequence 5503, Ap



1269	69	3.9	4536	2	US-09-180-422B-27	Sequence 27, Appl	1342	68.5	3.9	714	2	US-09-107-532A-4039	Sequence 4039, Ap
1270	69	3.9	4535	2	US-09-079-030-1	Sequence 1, Appl	1343	68.5	3.9	822	2	US-09-252-991A-29534	Sequence 2953, A
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GENERAL INFORMATION:						
; APPLICANT: Ashkenazi, Avi J.						
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; APPLICANT: Wood, William I.						
; APPLICANT: Zhang, Zemin						
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Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 MAGSPCLTLLIYILKOLTSAAAGPYKELVGSYGAVTTPPLSKKQVDSIWTFTTTL 60
QY      61 VTIOPGGTITVTONNRRRVPDPDGSYSLKSLKKNDSGIYVGSYSSIQDPTQRY 120
DB      61 VTIOPGGTITVTONNRRRVPDPDGSYSLKSLKKNDSGIYVGSYSSIQDPTQRY 120
QY      121 VLVVYHLSKPYVMGLQSNKNGCTVNTLTCMEHSEEDVITYWKALGOANESHNGSIL 180
DB      121 VLVVYHLSKPYVMGLQSNKNGCTVNTLTCMEHSEEDVITYWKALGOANESHNGSIL 180
QY      121 VLVVYHLSKPYVMGLQSNKNGCTVNTLTCMEHSEEDVITYWKALGOANESHNGSIL 180
DB      121 VLVVYHLSKPYVMGLQSNKNGCTVNTLTCMEHSEEDVITYWKALGOANESHNGSIL 180
QY      181 PISWRGSDMTFICVARNPVSRNFSPIIARKLCEGAADDPDSSMWLLCLLVPLLSL 240
DB      181 PISWRGSDMTFICVARNPVSRNFSPIIARKLCEGAADDPDSSMWLLCLLVPLLSL 240
QY      241 FVLGLFLWFLKRRQREYIEBKRRVDICRETPNICHSSENTYDTIPIHTNTILKEDA 300
DB      241 FVLGLFLWFLKRRQREYIEBKRRVDICRETPNICHSSENTYDTIPIHTNTILKEDA 300
QY      301 NTYVSTVEIKKMNPHSLITMPDTPRLPAYENVI 335
DB      301 NTYVSTVEIKKMNPHSLITMPDTPRLPAYENVI 335

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US-09-990-444-253
; Sequence 253, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/091978  
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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 4e-183;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAGSPTCLTIYIIMQLTGSAAAGPVKELVGSVGATVFPKSKKKQVDSIVMTFTTPL 60  
QY VTIOPEGGTTIVTONRNERVDFPDGYSKLKSKLKNDSGIYYGYIYSSSIQOPSTOBY 120  
DB 61 VTIOPEGGTTIVTONRNERVDFPDGYSKLKSKLKNDSGIYYGYIYSSSIQOPSTOBY 120  
QY 121 VLAHYEHLKSKPVTVGLQSNKNGTCVTNI/TCMEHGEEDVIYTWKALQOANESHNGSIL 180  
DB 121 VLAHYEHLKSKPVTVGLQSNKNGTCVTNI/TCMEHGEEDVIYTWKALQOANESHNGSIL 180  
QY 181 PISMRWGESDMFTFCVARNPVSRNFSPTLARKLCEGAADDPDSMTLCLLVPLLLSL 240  
DB 181 PISMRWGESDMFTFCVARNPVSRNFSPTLARKLCEGAADDPDSMTLCLLVPLLLSL 240  
QY 241 FYLGLFLWFLKREEREEYIEKKRVDICRETPNICPSGENTXYTTPHRTTIKEDPA 300  
DB 241 FYLGLFLWFLKREEREEYIEKKRVDICRETPNICPSGENTXYTTPHRTTIKEDPA 300  
QY 301 NTVYSTVEIPKKMENPHSLTMPDTPRLFAYENV 335  
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RESULT 3  
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; Sequence 253, Application US/09997333  
; Patent No. 6953836  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bostein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerliessen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Guirney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paom, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin



TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC27  
CURRENT APPLICATION NUMBER: US/09/997,333  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-07-09

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Query Match      100.0%; Score 1772; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 4e-183;
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DB 61 VTIOEGGTTIVTQNNRRRVDPPDGGYSLKSLKKNDSGIYVYSSIQOPSTORY 120
QY 121 VLAHVEHLSKPYVTGLQSNKNGTCVTNLTCCMEHGEERVIYTWKALGQAANESHNGSL 180
DB 121 VLAHVEHLSKPYVTGLQSNKNGTCVTNLTCCMEHGEERVIYTWKALGQAANESHNGSL 180
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DB 181 PISMRGESDMTFICVARNPVSRNFSSPILARKLCEGADDDSSWVLCLLVPLLSL 240
QY 241 FVLGLFLWFLKKEOEYIEKKRVDICRETPNICHSSENTYDTIPTNRTILKEDPA 300
DB 241 FVLGLFLWFLKKEOEYIEKKRVDICRETPNICHSSENTYDTIPTNRTILKEDPA 300
QY 301 NTVYSTVEIPKKNENPHSLITMPDTPRLPAYENVI 335
DB 301 NTVYSTVEIPKKNENPHSLITMPDTPRLPAYENVI 335

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RESULT 4
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; Sequence 253, Application US/09992598

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#### GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
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; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734

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PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-26
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 1772; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 4e-183;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MAGSPCTCLTLYILMOLTGSAAAGPVKEIVSGVGAATPPLSKRYKOVDSIVMTFNTPL 60
DB      1  MAGSPCTCLTLYILMOLTGSAAAGPVKEIVSGVGAATPPLSKRYKOVDSIVMTFNTPL 60
QY      61  VTIOPEGATIIIVTONRRRERYDPDGGYSLKLSKLKXNDGSIYVGIYSSILOQPSIOEY 120
DB      61  VTIOPEGATIIIVTONRRRERYDPDGGYSLKLSKLKXNDGSIYVGIYSSILOQPSIOEY 120
QY      121  VLAHYEHLSPKRYVTMGLOSNKNGTCVTNLTCMEHGEEDVIYTKALGOANESHNGSIL 180
DB      121  VLAHYEHLSPKRYVTMGLOSNKNGTCVTNLTCMEHGEEDVIYTKALGOANESHNGSIL 180
QY      121  VLAHYEHLSPKRYVTMGLOSNKNGTCVTNLTCMEHGEEDVIYTKALGOANESHNGSIL 180
DB      121  VLAHYEHLSPKRYVTMGLOSNKNGTCVTNLTCMEHGEEDVIYTKALGOANESHNGSIL 180
QY      181  PISWRMGESDMTFCVARNPVSRRFSSPIIARKLCEGAADDPDSMWLLCILLVPLILSL 240
DB      181  PISWRMGESDMTFCVARNPVSRRFSSPIIARKLCEGAADDPDSMWLLCILLVPLILSL 240
QY      241  FVLGLFWMFLKRGEOEYIEBKRRVDICRETPNICPSGENTEXTDTPHTRTIILKEDPA 300
DB      241  FVLGLFWMFLKRGEOEYIEBKRRVDICRETPNICPSGENTEXTDTPHTRTIILKEDPA 300
QY      301  NTVYSTVIEIPKQMPHSLTMDPTPRLFAVENYI 335
DB      301  NTVYSTVIEIPKQMPHSLTMDPTPRLFAVENYI 335

RESULT 5
US-09-513-999C-4472
Sequence 4472, Application US/0951399C
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Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Ducloux, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4472
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -22...-1
; OTHER INFORMATION: score 5.9
; OTHER INFORMATION: seq LYLIMQLTGSAA/SG
US-09-513-999C-4472
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Query Match      28.1%; Score 498; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.9e-46;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MAGSPCTCTIYIIMQLTGSAAAGVYKLVSGVAGATFPLSKRYQVDSTVMTFPL 60
Qy 61 VTIOPEGGITVTONRNRERYDFPDGYSLSKLSK 97
Db 61 VTIOPEGGITVTONRNRERYDFPDGYSLSKLSK 97
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RESULT 6
US-09-949-016-6428
; Sequence 6428, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6428
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6428
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Query Match      20.5%; Score 362.5; DB 2; Length 328;
Best Local Similarity 31.5%; Pred. No. 2.1e-30;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;
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Qy 14 LMOI-----TGSAGSPVVELV---GSVGAATFPLK-SKVRQVDSIVTFTFPLVTLQ 64
Db 6 LMIILICLOTWPEAKGDSRIETVNGIIGESVTFFPNIDEPQVKIATISTSVAYVTP 65
Qy 65 PEGGT---IIVTONRNRERYDFPDGYSLSKLSKKNDSIYVVGISYSSLSQOFTQERY 121
Db 65 PEGGT---IIVTONRNRERYDFPDGYSLSKLSKKNDSIYVVGISYSSLSQOFTQERY 121
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Db 126 LQYRRRLGKPKITQSLASVSTCNVTITCSVEKEKNVYNNMPLDE-----EGNVLQ 179
Qy 182 ISMRGSDMTFCVARNPVSRNPSPLARKLCEGAADPD-----SNVLLCLLVP 235
Db 180 IFQPEQELTYTTAONPVSN-SDSISARQLCADIAMGRTHTHTGLSLVAMPFLVL 238
Qy 236 LLSLFLVGLFLWFLKEROEYIEKRVYDICTETPNICPHSGENTETPTNRTIL 295
Db 239 ILSVFLFRLF-----KRQDASAKKTIYTYIMASHTQD--AESRIYDEILQSKVLPS 290
Qy 296 KEDPANTVSTVEIIPKQENPHSLITMPDPRFLAYERNV 335
Db 291 KEPPNTVYSEVQFADKMGKASTQDSKP--PGTSYEVIV 328
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RESULT 7
US-09-149-476-483
; Sequence 483, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
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; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,502
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
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; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
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1	EARLIER	FILING DATE: 1997-08-22	60/056, 636
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3	EARLIER	FILING DATE: 1997-08-22	
4	EARLIER	FILING DATE: 1997-08-22	
5	EARLIER	APPLICATION NUMBER: 60/056, 874	
6	EARLIER	FILING DATE: 1997-08-22	
7	EARLIER	APPLICATION NUMBER: 60/056, 910	
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10	EARLIER	FILING DATE: 1997-08-22	
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15	EARLIER	APPLICATION NUMBER: 60/056, 892	
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18	EARLIER	FILING DATE: 1997-08-22	
19	EARLIER	APPLICATION NUMBER: 60/047, 595	
20	EARLIER	FILING DATE: 1997-05-23	
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37	EARLIER	APPLICATION NUMBER: 60/047, 593	
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39	EARLIER	APPLICATION NUMBER: 60/047, 614	
40	EARLIER	FILING DATE: 1997-05-23	
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42	EARLIER	FILING DATE: 1997-04-11	
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44	EARLIER	FILING DATE: 1997-04-11	
45	EARLIER	APPLICATION NUMBER: 60/047, 501	
46	EARLIER	FILING DATE: 1997-05-23	
47	EARLIER	APPLICATION NUMBER: 60/043, 670	
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66	EARLIER	FILING DATE: 1997-08-22	
67	EARLIER	APPLICATION NUMBER: 60/048, 964	
68	EARLIER	FILING DATE: 1997-06-06	
69	EARLIER	APPLICATION NUMBER: 60/057, 652	
70	EARLIER	FILING DATE: 1997-09-05	
71	EARLIER	APPLICATION NUMBER: 60/056, 884	
72	EARLIER	FILING DATE: 1997-08-22	
73	EARLIER	APPLICATION NUMBER: 60/057, 669	
74	EARLIER	FILING DATE: 1997-09-05	
75	EARLIER	APPLICATION NUMBER: 60/049, 610	
76	EARLIER	FILING DATE: 1997-06-13	



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; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match          20.5%; Score 362.5; DB 2; Length 329;
Best Local Similarity 31.5%; Pred. No. 2.1e-30;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

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QY 65 PEGGT---IYTONRNRERVDPPGGYSIKLSKLKKNDSGIYVGIYSSSLQOPESTQRY 121
DB 66 GDSFAPVYVTVTHRYRYERIHAGPNYMLVLSDLMEBAGDYKADINTQADPYITTKRYN 125
QY 122 LHVYHLSKPKYTMGLQSNKNGCTVTNLTCCMEHGBDYTYWKALGOANESHNGSLTP 181
DB 126 LQYRRLGPKITQSLMASVNSTCVNLTLCVSKEKEKNVTYNNSPLEB-----EGNVLQ 179
QY 182 ISRWGSDMTFTICVARNPVSRNFSPIIARKLCGGAADDDPS-----SMVLCILLVP 235
DB 180 IFQPEDELTYYTCAQNPVSN--SDSISARQLADIAMGFRTHHTGLSLVAMFLLVL 238
QY 236 LLLSLFVLGLFWLFLKRRQREYEIEKKRVDICRETPNICPSGENTEDYTPHTNRTIL 295
DB 239 ILSVFLRLP-----KRDQDASKTIYTYIMASRNTQF--AESRIYDEILQSKVLPS 290
QY 296 KEDPANTYSTEVEIPKKNENPHSLTMPDTRLPAYENVI 335
DB 291 KEEPVNTYSEVQFADKWKGRKASTQDSKP--PQTSSYEIVI 328

RESULT 8
US-09-949-016-7327
; Sequence 7327, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7327
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7327

Query Match          20.5%; Score 362.5; DB 2; Length 332;
Best Local Similarity 31.5%; Pred. No. 2.1e-30;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;
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QY 182 ISRWGSDMTFTICVARNPVSRNFSPIIARKLCGGAADDDPS-----SMVLCILLVP 235
DB 184 IFQPEDELTYYTCAQNPVSN--SDSISARQLADIAMGFRTHHTGLSLVAMFLLVL 242
QY 236 LLLSLFVLGLFWLFLKRRQREYEIEKKRVDICRETPNICPSGENTEDYTPHTNRTIL 295
DB 243 ILSVFLRLP-----KRDQDASKTIYTYIMASRNTQF--AESRIYDEILQSKVLPS 294
QY 296 KEDPANTYSTEVEIPKKNENPHSLTMPDTRLPAYENVI 335
DB 295 KEEPVNTYSEVQFADKWKGRKASTQDSKP--PQTSSYEIVI 332

RESULT 9
US-08-348-792-10
; Sequence 10, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,792
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CHUNG, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-348-792-10

Query Match          10.5%; Score 186; DB 1; Length 343;
Best Local Similarity 24.3%; Pred. No. 3e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;
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Db 173 DH-VYVSSDAGTHLSRANRSH---LHHTLSNQHDSIYNCTASNPVSSISSTFN-- 226  
Qy 209 ILARKICGAADDPSSMWLLCLLVPLLSLFLVGLFWMFLKREOREYIE---EKKRV 265  
Db 227 -LSSQACKQSSSESPMWQYTLVPLGVIIIFILVFTALIMKRGKSNHCQPPVEKSL 285  
Qy 266 DICRETENICPSGENTGYDTIPTHNRITLKEDPANTVY--STVEIPKGMENP-----HS 318  
Db 286 TIYAQVQKSGPO--EKKLHD-----ALTDODPCTTIYVATBPAPESVQEPNPTTYVA 336  
Qy 319 LITMPDT 325  
Db 337 SVTLPEB 343  
RESULT 10  
US-08-462-738-10  
; Sequence 10, Application US/08462738  
; Patent No. 5977303  
; GENERAL INFORMATION:  
; APPLICANT: Averea, Gregorio  
; APPLICANT: Chang, Chia-Chun J.  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: de Vries, Jan B.  
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL  
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,738  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/348,792  
; FILING DATE: 02-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0436GB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 343 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-462-738-10  
Query Match 10.5%; Score 186; DB 1; Length 343;  
Best Local Similarity 24.3%; Pred. No. 3e-11;  
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;

Qy 100 SGIIYVGIYS-SLQOPSTQEVLAHYEHLKSP--KYTMGIQSNKNGCVTNLTCCMEHG 156  
Db 116 EGMVIVSVEENVSVQCFCKQ---LKLHYQVSPPEIKVNTKQENENGTCISLLACTVKKG 172  
Qy 157 EEDVITYTK-----ALGOANESHNSILPIPSMRGESDMTFICVARRPV---SNFSSP 208  
Db 173 DH-VYVSSDAGTHLSRANRSH---LHHTLSNQHDSIYNCTASNPVSSISSTFN-- 226  
Qy 209 ILARKICGAADDPSSMWLLCLLVPLLSLFLVGLFWMFLKREOREYIE---EKKRV 265  
Db 227 -LSSQACKQSSSESPMWQYTLVPLGVIIIFILVFTALIMKRGKSNHCQPPVEKSL 285  
Qy 266 DICRETENICPSGENTGYDTIPTHNRITLKEDPANTVY--STVEIPKGMENP-----HS 318  
Db 286 TIYAQVQKSGPO--EKKLHD-----ALTDODPCTTIYVATBPAPESVQEPNPTTYVA 336  
Qy 319 LITMPDT 325  
Db 337 SVTLPEB 343  
RESULT 11  
US-09-199-955-10  
; Sequence 10, Application US/09199955  
; Patent No. 6372899  
; GENERAL INFORMATION:  
; APPLICANT: Averea, Gregorio  
; APPLICANT: Chang, Chia-Chun J.  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: de Vries, Jan B.  
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL  
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/199,955  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/461,473  
; FILING DATE: 05-JUN-1995  
; APPLICATION NUMBER: US 08/348,792  
; FILING DATE: 02-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0436GC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 343 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-199-955-10  
Query Match 10.5%; Score 186; DB 2; Length 343;  
Best Local Similarity 24.3%; Pred. No. 3e-11;  
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;



Qy	8	TLIIYIMQJTSASG----	PVKELVGSVGAIVTEPL-----	SKYQVDSIYWTEN	56
		: : : :	: : : :	: : : :	
Db	12	LIFLFLAEFLSIVGTGGVWDCPV-	LLOKLGQDTMLPLTNEHINXSVKSVIIV-TMA	68	
		: : : :	: : : :	: : : :	
Qy	57	TTPLVLTIOPEGGIIIVTONRNERVDF-----	PD--GGY-----	SLKLSKLKQND	99
		: : : :	: : : :	: : : :	
Db	69	TSP-----	GSKSNKKIVSFPDLSKSGSYPHLEBGFYHQSNLSLKITGNRRS	115	
		: : : :	: : : :	: : : :	
Qy	100	SGIYYVGIYSS-SLQOPSTQEVYLAHYEHLSK--	KYTMGLQSNKNGTCYTNLTCCMEHG	156	
		: : : :	: : : :	: : : :	
Db	116	BGMVYVSEVENVSVOQFCRQ--	LKLYEQVSPBEIKVTKTOENENGTCSLILACVYKKG	172	
		: : : :	: : : :	: : : :	
Qy	157	BEDEVLYTKM-----	ALGOANSHNSIILPISRMWBSDMTFICVARNPY----	SRNFPSP	208
		: : : :	: : : :	: : : :	
Db	173	DH-VIYSWDEAGHTILSPRANSH--	LHITLSNOHODSIYCTASNPVVISIRTFN--	226	
		: : : :	: : : :	: : : :	
Qy	209	ILARKLCESANADDPSSMWILCLILVPLLSLFLVLGLFLFLFREROEBYTE--	EKKRV	265	
		: : : :	: : : :	: : : :	
Db	227	-LSSQACRQESSSESPPMWOYTLTVPLGVAIIFLVLPAIIMMRQGSNHCQCPVEKSL	285		
		: : : :	: : : :	: : : :	
Qy	266	DICRETPNICPSGENTERYDTLPHNRTLIKEDPANNTV--	STVEIIPKXKMP-----	HS	318
		: : : :	: : : :	: : : :	
Db	286	TIYAAOVQKSGPQ--EKKLAD-----	ALTDQDPCCTIYVAATEPAESVOEBNPTTVYA	336	
		: : : :	: : : :	: : : :	
Qy	319	LLTMPDT	325		
		: : : :	: : : :	: : : :	
Db	337	SVTLPRS	343		

RESULT 12  
US-08-880-875-10  
; Sequence 10, Application US/08880875

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1 GENERAL INFORMATION:
2 APPLICANT: Aversa, Gregorio
3 APPLICANT: Chang, Chia-Chun J.
4 APPLICANT: Cocke, Benjamin G.
5 APPLICANT: de Vries, Jan E.
6 TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
7 TITLE OF INVENTION: SURFACE ANTIGENS, PROTEINS AND ANTIBODIES
8 NUMBER OF SEQUENCES: 12
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: DMAX Research Institute
11 STREET: 901 California Avenue
12 CITY: Palo Alto
13 STATE: California
14 COUNTRY: USA
15 ZIP: 94304-1104
16
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: Patent In Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/880,875
24 FILING DATE:
25 CLASSIFICATION: 435
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 08/481,777
28 FILING DATE: 07-JUN-1995
29 APPLICATION NUMBER: US 08/348,792
30 FILING DATE: 02-DEC-1994
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Ching, Edwin P.
33 REGISTRATION NUMBER: 34,090
34 REFERENCE/DOCKET NUMBER: DX0436K
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 415-852-9196
37 TELEFAX: 415-496-1200
38 INFORMATION FOR SEQ. ID NO.: 10:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 343 amino acids

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;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-880-875-10

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Query Match	10.5%;	Score 186;	DB 2;	Length 343;
Best Local Similarity	24.3%;	Pred. No. 3e-11;		
Matches	89;	Conservative	64;	Mismatches 130;
			Indels	84;
			Gaps	21;

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QY      8 LTLIYIIMQLOISSLASG-----PKELVSVSGAATVPFL-----KSKVQOYDSIVATFN 56
Db      12 LILFSLAELELSTGTGGVWDCPV--ILQKLGODTWMPLTNEHQINKSVKSVRIIV-TAA 68
QY      57 TPLPLTIQPEGGTLIVTONRNERVDF-----PD--GGY-----SLKLSKLKUD 99
Db      69 TSP-----GSKSNKKIIVSFDLSKSGSYDHLDEGHHFQSGKNLSLKILGNRRS 115
QY      100 SGIYVYGIVYS-SLQOPSTOEYVLHVYEHLSRP--KVTMGLQSNKNGTCVTMLTCMHEG 156
Db      116 ESMYLVSVENVSVOQFCQK--LKLVEQVSPBEIKVINKTQENENGTCSLILACTVWKKG 172
QY      157 ESDVLYYTK-----ALGOANESHNGSLIPISMRNGESDMTFLCVARNV---SRNFPSSP 208
Db      173 DH-VTVSSDSEAGETHLSRPNRSH--LHAILTSLNODSIYNTCTASNPVSSIRFTN-- 226
QY      209 ILARKLCGGAADDPSSMWLTLCLILVPLLSFLVGLFLPFLKREKROEBYIE---EKRY 265
Db      227 -LSSQACQOESSSESSPMMQYTLVPLGVIIPIVLVFTALIMKRQCKSHNCQPPVEKSL 285
QY      266 DICRETPNICPHSGENTEYDTIPIHTNRITLKEDPANTV--STVEIPKCMENP-----HS 318
Db      286 TTYAQQVQSGPQ--EKKLHD-----ALTDODPCTTIVAAATEPAPESVOENPPTVYA 336
QY      319 LLTMPDT 325
Db      337 SVTLPE 343

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RESULT 13  
US-08-348-792-2  
; Sequence 2, Application US/08348792

GENERAL INFORMATION:  
 APPLICANT: Averna, Gregorio  
 APPLICANT: Chang, Chia-Chun J.  
 APPLICANT: Cocks, Benjamin G.  
 APPLICANT: de Vries, Jan E.  
 TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL  
 TITLE OF INVENTION: SURFACE ANTIGENS, PROTEINS AND ANTIBODIES  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DNAX Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/348,792  
 FILING DATE: 02-DEC-1994  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34, 090  
 REFERENCE/DOCKET NUMBER: DX0436  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-9196  
 TELEFAX: 415-496-1200



;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 335 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-348-792-2

Query Match 10.3%; Score 182.5; DB 1; Length 335;  
Best Local Similarity 22.5%; Pred. No. 6.9e-11;  
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

QY 8 LTLIYILM-QLTGSASGP-----VKELVSGVGAATFPL-----KSKYKQVDSIYWT 54  
DB 7 LSLTFVLFLSLAFGASVGTGGRMNCPIKLRLQLSKVLPLTYERINKSMNKSIIHVWTM 66  
QY 55 FNT-----TFLVITQP-EGGTIIYTONRNRVDPDGGYSLKLSKLNDSGIYYGI 107  
DB 67 AKSLNSVENKIVSLDPSBAG---PPRYLGRYKYFIENLTLGIRSRKDEBGMVLTML 122  
QY 108 YSS-SLOPSTQEVYLAHYEHLSPKVTWGLQSNKNGTCVTNLTCMEHGEEDVIYTW-- 164  
DB 123 EKNSVQRFCLQ---LRLEYQVSTPEIKVLTAKTQENGCTLLIGCTVEKGKH-VAYSMSB 178  
QY 165 KALGQANESHNGSILPISWRGSDMTFCVARNPVSRRFS--SPIIARLCEGAADP 222  
DB 179 KAGTHPLNPANSHLSLTLPQHADNIYICTVSNPISNNSQTFSF-----WPCGRDTP 232  
QY 223 DSSM-----VLCLLLVPLLSLFLGLFLMFLKREKREBYIE--EKKRVNIC 268  
DB 233 SETKPMAYVAGLGGVIMLIMVILQ-----LRRGKKNHQTVEKKSILTY 281  
QY 269 RETPNICPSGENTVDTPHTNRTILKEDPANTVY--STVEIPKKNPMSL-----LT 321  
DB 282 AQVQKPGP---LQKKLDSFP-----AQDPTTIYVAATPVPESVQETNSITVYASVT 331  
QY 322 MPDT 325  
DB 332 LPES 335

RESULT 14  
US-08-462-738-2  
; Sequence 2, Application US/08462738  
; Patent No. 5977303  
; GENERAL INFORMATION:  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Chang, Chia-Chun J.  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: de Vries, Jan E.  
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL  
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,738  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/348,792  
; FILING DATE: 02-DEC-1994  
; ATTORNEY/AGENT INFORMATION:

;; NAME: Ching, Edwin P.  
;; REGISTRATION NUMBER: 34,090  
;; REFERENCE/DOCKET NUMBER: DX0436GB  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-852-9196  
;; TELEFAX: 415-496-1200  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 335 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-462-738-2

Query Match 10.3%; Score 182.5; DB 1; Length 335;  
Best Local Similarity 22.5%; Pred. No. 6.9e-11;  
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

QY 8 LTLIYILM-QLTGSASGP-----VKELVSGVGAATFPL-----KSKYKQVDSIYWT 54  
DB 7 LSLTFVLFLSLAFGASVGTGGRMNCPIKLRLQLSKVLPLTYERINKSMNKSIIHVWTM 66  
QY 55 FNT-----TFLVITQP-EGGTIIYTONRNRVDPDGGYSLKLSKLNDSGIYYGI 107  
DB 67 AKSLNSVENKIVSLDPSBAG---PPRYLGRYKYFIENLTLGIRSRKDEBGMVLTML 122  
QY 108 YSS-SLOPSTQEVYLAHYEHLSPKVTWGLQSNKNGTCVTNLTCMEHGEEDVIYTW-- 164  
DB 123 EKNSVQRFCLQ---LRLEYQVSTPEIKVLTAKTQENGCTLLIGCTVEKGKH-VAYSMSB 178  
QY 165 KALGQANESHNGSILPISWRGSDMTFCVARNPVSRRFS--SPIIARLCEGAADP 222  
DB 179 KAGTHPLNPANSHLSLTLPQHADNIYICTVSNPISNNSQTFSF-----WPCGRDTP 232  
QY 223 DSSM-----VLCLLLVPLLSLFLGLFLMFLKREKREBYIE--EKKRVNIC 268  
DB 233 SETKPMAYVAGLGGVIMLIMVILQ-----LRRGKKNHQTVEKKSILTY 281  
QY 269 RETPNICPSGENTVDTPHTNRTILKEDPANTVY--STVEIPKKNPMSL-----LT 321  
DB 282 AQVQKPGP---LQKKLDSFP-----AQDPTTIYVAATPVPESVQETNSITVYASVT 331  
QY 322 MPDT 325  
DB 332 LPES 335

RESULT 15  
US-09-199-955-2  
; Sequence 2, Application US/09199955  
; Patent No. 6372899  
; GENERAL INFORMATION:  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Chang, Chia-Chun J.  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: de Vries, Jan E.  
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL  
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/199,955







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OM protein - protein search, using sw model

Run on: December 16, 2005, 11:08:20 ; Search time 13 Seconds  
(without alignments)  
173.601 Million cell updates/sec

Perfect score: 1772  
Sequence: 1 MAGSPTCTLIYILMQLTGS.....PMSLTMPDTRLFAYENV 335

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 51470 seqs, 6736768 residues

Total number of hits satisfying chosen parameters: 51470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

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2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	335	US-11-102-240-46	Sequence 46, Appl
2	1315.5	17.8	346	US-11-174-150-33	Sequence 33, Appl
3	251	14.2	220	US-11-174-150-32	Sequence 32, Appl
4	124.5	7.0	344	US-11-080-991-4	Sequence 4, Appl
5	124.5	7.0	344	US-11-186-284-20	Sequence 20, Appl
6	124.5	7.0	344	US-11-077-386-16	Sequence 16, Appl
7	119.5	6.7	365	US-11-102-978-9	Sequence 9, Appl
8	119.5	6.7	365	US-11-080-991-78	Sequence 7, Appl
9	117	6.6	324	US-11-077-386-15	Sequence 15, Appl
11	98.5	5.6	404	US-11-069-642-115	Sequence 115, Appl
12	93	5.2	419	US-10-821-234-1664	Sequence 1664, Appl
14	92.5	5.2	299	US-11-000-463-275	Sequence 275, Appl
15	92.5	5.2	299	US-11-000-463-747	Sequence 747, Appl
16	92.5	5.2	299	US-11-000-463-748	Sequence 748, Appl
17	92.5	5.2	299	US-11-173-037-7	Sequence 7, Appl
19	92	5.2	298	US-11-080-991-54	Sequence 54, Appl
20	92	5.2	2828	US-11-186-284-49	Sequence 49, Appl
21	89.5	5.1	845	US-11-147-047-46	Sequence 46, Appl
22	87	4.9	583	US-11-080-991-64	Sequence 64, Appl
23	86	4.9	259	US-11-000-463-276	Sequence 276, Appl
24	85.5	4.8	2491	US-10-995-561-769	Sequence 769, Appl
25	84	4.7	668	US-11-111-239-13	Sequence 13, Appl
28	83.5	4.7	515	US-11-093-274-38	Sequence 38, Appl
29	82	4.6	567	US-11-016-503-10	Sequence 10, Appl
30	81.5	4.6	7968	US-11-186-731-5	Sequence 5, Appl
31	81	4.6	254	US-11-054-515-1843	Sequence 1843, Appl

32	81	4.6	829	7	US-11-090-739-122	Sequence 122, Appl
33	81	4.6	829	7	US-11-186-284-18	Sequence 18, Appl
34	80.5	4.5	313	6	US-10-723-207-3	Sequence 3, Appl
35	79.5	4.5	859	7	US-11-188-743-16	Sequence 16, Appl
36	79	4.5	490	7	US-11-063-343-31	Sequence 31, Appl
37	78.5	4.4	212	7	US-11-025-834A-16	Sequence 16, Appl
38	78.5	4.4	628	7	US-11-080-991-108	Sequence 108, Appl
39	78.5	4.4	727	6	US-10-995-561-864	Sequence 864, Appl
40	78.5	4.4	782	6	US-10-995-561-861	Sequence 861, Appl
41	78.5	4.4	847	6	US-10-995-561-863	Sequence 863, Appl
42	78.5	4.4	847	6	US-10-821-234-1635	Sequence 1635, Appl
43	77	4.3	1897	6	US-10-821-234-1635	Sequence 1635, Appl
44	77	4.3	1907	7	US-11-000-463-250	Sequence 250, Appl
45	76.5	4.3	1451	6	US-10-995-561-829	Sequence 829, Appl
46	76	4.3	462	7	US-11-016-503-8	Sequence 8, Appl
47	76	4.3	567	7	US-11-016-503-2	Sequence 2, Appl
48	76	4.3	1694	7	US-11-135-855-36	Sequence 36, Appl
49	76	4.3	1709	7	US-11-135-855-35	Sequence 35, Appl
50	75	4.2	527	7	US-11-113-424-81	Sequence 81, Appl
51	74.5	4.2	555	6	US-10-821-234-1015	Sequence 1015, Appl
52	74.5	4.2	4655	6	US-10-995-561-586	Sequence 586, Appl
53	74	4.2	1488	6	US-10-821-234-1333	Sequence 1333, Appl
54	74	4.2	343	7	US-11-080-091-4	Sequence 4, Appl
55	74	4.2	1649	6	US-10-995-561-974	Sequence 974, Appl
56	74	4.2	1709	6	US-10-995-561-973	Sequence 973, Appl
57	73.5	4.1	304	7	US-11-025-834A-21	Sequence 21, Appl
58	73.5	4.1	334	7	US-11-113-424-80	Sequence 10, Appl
59	73.5	4.1	257	7	US-11-067-121-18	Sequence 18, Appl
61	73	4.1	257	7	US-11-000-463-377	Sequence 377, Appl
62	73	4.1	406	7	US-11-000-463-849	Sequence 849, Appl
63	73	4.1	406	7	US-11-194-246-343	Sequence 343, Appl
64	73	4.1	864	7	US-10-821-234-1385	Sequence 1385, Appl
66	72.5	4.1	426	6	US-11-016-503-6	Sequence 6, Appl
67	72	4.1	452	7	US-10-793-626-1930	Sequence 1930, Appl
68	72	4.1	528	6	US-11-016-503-4	Sequence 4, Appl
69	72	4.1	557	7	US-11-108-117-1102	Sequence 1102, Appl
70	72	4.1	840	7	US-10-821-234-1155	Sequence 1155, Appl
71	72	4.1	4419	6	US-11-080-091-9	Sequence 9, Appl
72	71.5	4.0	298	7	US-11-143-980-56	Sequence 56, Appl
73	71.5	4.0	314	7	US-10-995-561-670	Sequence 670, Appl
74	71.5	4.0	391	6	US-10-392-234A-67	Sequence 67, Appl
75	71.5	4.0	1032	6	US-11-186-284-26	Sequence 26, Appl
76	71.5	4.0	3063	7	US-11-080-091-12	Sequence 12, Appl
77	71	4.0	362	7	US-10-995-561-860	Sequence 860, Appl
78	71	4.0	488	6	US-10-821-234-1622	Sequence 1622, Appl
79	71	4.0	1338	7	US-11-109-156-23	Sequence 23, Appl
80	71	4.0	1338	7	US-10-499-715-2	Sequence 715, Appl
81	71	4.0	2897	6	US-10-995-561-672	Sequence 672, Appl
82	71	4.0	3588	6	US-10-995-561-671	Sequence 671, Appl
83	71	4.0	4346	6	US-10-995-561-670	Sequence 670, Appl
84	71	4.0	4347	6	US-10-878-556A-48	Sequence 48, Appl
85	70.5	4.0	246	7	US-10-793-626-1352	Sequence 1352, Appl
86	70.5	4.0	333	6	US-11-144-987-22	Sequence 22, Appl
87	70.5	4.0	472	6	US-11-062	Sequence 7, Appl
88	70.5	4.0	644	6	US-10-995-561-905	Sequence 905, Appl
89	70.5	4.0	915	7	US-10-995-561-904	Sequence 904, Appl
90	70.5	4.0	1095	7	US-10-995-561-906	Sequence 906, Appl
91	70.5	4.0	1133	7	US-11-093-274-41	Sequence 41, Appl
92	70.5	4.0	1306	6	US-11-192-219-7	Sequence 4, Appl
93	70.5	4.0	1356	6	US-10-467-657-962	Sequence 962, Appl
94	70.5	4.0	1356	6	US-11-025-834A-14	Sequence 14, Appl
95	70	4.0	783	7	US-11-137-465-43	Sequence 43, Appl
96	70	4.0	1070	7	US-10-793-626-414	Sequence 414, Appl
97	70	4.0	180	6	US-11-147-725-2	Sequence 2, Appl
98	69.5	3.9	298	7	US-10-467-657-1418	Sequence 1418, Appl
99	69.5	3.9	1062	6	US-11-075-646-8	Sequence 8, Appl
100	69.5	3.9	329	6	US-11-137-465-62	Sequence 62, Appl
101	69	3.9	447	7		
102	69	3.9	447	7		
103	69	3.9	447	7		
104	69	3.9	751	6		
105	69	3.9	1161	7		
106	69	3.9	1250	7		



107	68.5	3.9	972	6	US-10-821-234-1587	Sequence 1587, Ap	183	63.5	3.6	923	7	US-11-192-219-4	Sequence 4, Appli
108	68	3.8	155	7	US-11-194-246-319	Sequence 319, App	184	63.5	3.6	932	7	US-11-188-743-17	Sequence 17, Appl
109	68	3.8	340	6	US-10-467-962B-79	Sequence 79, Appl	185	63.5	3.6	932	7	US-11-188-743-18	Sequence 18, Appl
110	68	3.8	837	6	US-10-995-5561-698	Sequence 698, App	186	63.5	3.6	952	7	US-11-174-166-18	Sequence 18, Appl
111	68	3.8	963	7	US-11-174-166-20	Sequence 20, Appl	187	63.5	3.6	964	7	US-11-089-551A-30	Sequence 30, Appl
112	68	3.8	1174	6	US-10-995-5561-697	Sequence 697, App	188	63.5	3.6	1165	7	US-11-192-219-2	Sequence 2, Appli
113	67.5	3.8	4374	6	US-11-128-572-2	Sequence 2, Appli	189	63.5	3.6	2314	7	US-11-013-759-11	Sequence 11, Appl
114	67	3.8	367	6	US-10-793-626-102	Sequence 1202, Ap	190	63	3.6	108	7	US-11-054-669-84	Sequence 94, Appl
115	67	3.8	590	7	US-11-131-212-73	Sequence 73, Appl	191	63	3.6	251	7	US-11-054-515-85	Sequence 85, Appl
116	67	3.8	617	6	US-10-995-5561-890	Sequence 890, App	192	63	3.6	251	7	US-11-054-515-1840	Sequence 1840, Ap
117	67	3.8	740	7	US-11-137-465-61	Sequence 61, Appl	193	63	3.6	251	6	US-10-401-386B-38	Sequence 38, Appl
118	67	3.8	820	7	US-11-147-047-31	Sequence 31, Appl	194	63	3.6	252	6	US-10-401-386B-38	Sequence 32, Appl
119	67	3.8	1115	7	US-11-113-751-46	Sequence 46, Appl	195	63	3.6	340	6	US-10-999-866-32	Sequence 32, Appl
120	67	3.8	1170	6	US-10-831-997-2	Sequence 2, Appli	196	63	3.6	340	7	US-11-061-821-32	Sequence 32, Appl
121	67	3.8	1170	6	US-10-995-5561-594	Sequence 594, App	197	63	3.6	497	6	US-10-999-866-34	Sequence 34, Appl
122	67	3.8	1170	6	US-10-995-5561-595	Sequence 595, App	198	63	3.6	497	7	US-11-061-821-34	Sequence 34, Appl
123	67	3.8	1170	6	US-10-995-5561-596	Sequence 596, App	199	63	3.6	794	6	US-10-485-517-355	Sequence 355, App
124	67	3.8	1170	7	US-11-046-456-28	Sequence 28, App	200	63	3.6	977	7	US-11-093-274-39	Sequence 39, Appl
125	67	3.8	1170	7	US-11-046-644-28	Sequence 28, App	201	63	3.6	1126	6	US-10-485-517-248	Sequence 248, App
126	66.5	3.8	193	6	US-10-967-527A-28	Sequence 28, Appl	202	62.5	3.5	130	6	US-10-667-295-159	Sequence 159, App
127	66.5	3.8	199	6	US-10-967-527A-4	Sequence 4, Appli	203	62.5	3.5	176	6	US-10-793-626-1262	Sequence 3262, Ap
128	66.5	3.8	398	6	US-10-996-628-4	Sequence 4, Appli	204	62.5	3.5	346	6	US-10-793-626-2034	Sequence 2034, Ap
129	66.5	3.8	2353	7	US-11-097-728-6	Sequence 6, Appli	205	62.5	3.5	374	7	US-11-084-220-3	Sequence 3, Appli
132	66	3.7	738	6	US-10-995-561-682	Sequence 692, App	206	62.5	3.5	519	7	US-11-080-991-106	Sequence 106, App
133	66	3.7	738	6	US-10-995-561-693	Sequence 693, App	207	62.5	3.5	610	6	US-10-793-626-482	Sequence 482, App
134	66	3.7	766	6	US-10-821-234-1691	Sequence 1691, Ap	208	62.5	3.5	648	6	US-10-793-626-568	Sequence 568, App
135	66	3.7	769	6	US-10-485-517-401	Sequence 401, App	209	62.5	3.5	898	7	US-11-166-720-3	Sequence 3, Appli
136	66	3.7	1101	6	US-10-878-556A-107	Sequence 107, App	210	62.5	3.5	909	7	US-11-076-187-4	Sequence 4, Appli
137	66	3.7	1263	6	US-10-485-517-127	Sequence 127, App	211	62.5	3.5	914	7	US-11-108-1172-1066	Sequence 1066, Ap
138	65.5	3.7	262	6	US-10-793-626-516	Sequence 516, App	212	62.5	3.5	958	7	US-11-148-108-41	Sequence 41, Appl
139	65.5	3.7	298	7	US-11-138-949-9	Sequence 9, Appli	213	62.5	3.5	974	7	US-11-108-1172-1087	Sequence 1087, Ap
140	65.5	3.7	509	6	US-10-793-626-2880	Sequence 2880, Ap	214	62.5	3.5	974	7	US-11-115-086-7	Sequence 7, Appli
141	65.5	3.7	1614	7	US-11-108-528-82	Sequence 82, Appl	215	62	3.5	248	7	US-11-054-515-1254	Sequence 1254, Ap
142	65.5	3.7	1981	6	US-10-374-954-23	Sequence 23, Appl	216	62	3.5	250	7	US-11-054-669-110	Sequence 110, App
143	65.5	3.7	1998	6	US-10-374-954-21	Sequence 21, Appl	217	62	3.5	258	6	US-10-995-5561-555	Sequence 555, App
144	65.5	3.7	2009	6	US-10-401-386B-34	Sequence 34, Appl	218	62	3.5	258	7	US-11-054-515-1239	Sequence 1239, Ap
145	65	3.7	255	6	US-11-082-389-220	Sequence 220, App	219	62	3.5	258	7	US-11-054-515-1245	Sequence 1245, Ap
146	65	3.7	388	7	US-10-467-657-2272	Sequence 2272, Ap	220	62	3.5	332	6	US-10-467-657-128	Sequence 3310, App
147	65	3.7	487	6	US-11-176-863-2	Sequence 2, Appli	221	62	3.5	340	7	US-11-092-353-1	Sequence 69, Appl
149	65	3.7	607	7	US-10-624-932-2	Sequence 105, App	222	62	3.5	371	7	US-11-129-143-69	Sequence 2714, Ap
150	65	3.7	898	6	US-11-069-642-105	Sequence 1834, Ap	223	62	3.5	412	6	US-10-467-657-2114	Sequence 326, App
151	65	3.7	1058	7	US-11-054-515-1834	Sequence 615, App	224	62	3.5	457	7	US-11-194-246-326	Sequence 877, App
152	64.5	3.6	246	7	US-11-054-515-615	Sequence 1376, Ap	225	62	3.5	463	7	US-10-650-326B-12	Sequence 12, Appl
153	64.5	3.6	252	7	US-11-054-515-1376	Sequence 1036, Ap	226	62	3.5	472	6	US-11-092-353-3	Sequence 3, Appli
154	64.5	3.6	260	7	US-11-196-475-13	Sequence 13, Appl	227	62	3.5	511	7	US-11-012-762-48	Sequence 48, Appl
155	64.5	3.6	273	7	US-11-000-463-346	Sequence 346, App	228	62	3.5	748	6	US-10-821-234-1479	Sequence 1479, Ap
156	64.5	3.6	551	6	US-10-510-386-8	Sequence 8, Appli	229	62	3.5	970	6	US-10-770-726-86	Sequence 86, Appl
157	64.5	3.6	643	6	US-11-080-991-32	Sequence 32, Appl	230	62	3.5	1346	7	US-11-060-005-2	Sequence 2954, Ap
158	64.5	3.6	647	7	US-11-029-003-6	Sequence 6, Appli	231	62	3.5	89	6	US-10-467-657-2954	Sequence 7, Appli
159	64.5	3.6	671	7	US-11-144-987-24	Sequence 24, Appl	232	61.5	3.5	204	7	US-11-128-440-7	Sequence 394, App
160	64.5	3.6	917	7	US-10-485-517-131	Sequence 26, Appl	233	61.5	3.5	359	7	US-11-080-091-1	Sequence 1, Appli
161	64.5	3.6	948	6	US-11-054-515-1533	Sequence 1531, App	234	61.5	3.5	359	7	US-11-116-939-15	Sequence 15, Appl
162	64.5	3.6	948	6	US-11-074-176-100	Sequence 1500, App	235	61.5	3.5	378	7	US-11-080-091-3	Sequence 3, Appli
163	64.5	3.6	243	7	US-11-138-949-6	Sequence 328, App	236	61.5	3.5	448	6	US-10-967-527A-16	Sequence 16, Appl
164	64	3.6	279	7	US-11-000-463-400	Sequence 400, App	237	61.5	3.5	708	6	US-10-658-986-2	Sequence 2, Appli
165	64	3.6	418	7	US-10-821-234-1473	Sequence 1473, Ap	238	61.5	3.5	748	6	US-10-658-986-2	Sequence 888, App
166	64	3.6	567	6	US-10-878-556A-63	Sequence 1068, Ap	239	61.5	3.5	777	6	US-10-658-986-4	Sequence 4, Appl
167	64	3.6	1058	6	US-11-108-172-1068	Sequence 20, Appl	240	61.5	3.5	918	6	US-10-995-5561-696	Sequence 696, App
168	64	3.6	1058	6	US-11-125-837-20	Sequence 137, App	241	61.5	3.5	978	6	US-10-510-524-1	Sequence 1, Appli
169	64	3.6	5179	7	US-10-667-295-137	Sequence 2306, App	242	61.5	3.5	1458	6	US-11-096-274-2	Sequence 2, Appli
170	64	3.6	187	6	US-10-467-657-2306	Sequence 2218, Ap	243	61.5	3.5	1474	6	US-10-995-561-873	Sequence 873, App
171	63.5	3.6	251	6	US-10-793-626-3160	Sequence 3160, App	244	61.5	3.5	1615	7	US-11-080-991-96	Sequence 96, Appl
172	63.5	3.6	423	6	US-11-139-499-8	Sequence 8, Appli	245	61.5	3.5	1798	7	US-10-995-5561-913	Sequence 913, App
173	63.5	3.6	478	7	US-10-793-626-1024	Sequence 1024, Ap	246	61.5	3.5	1818	6	US-10-995-5561-913	Sequence 29, Appl
174	63.5	3.6	535	6	US-10-518-599-22	Sequence 1106, Ap	247	61.5	3.5	1960	7	US-11-077-386-29	Sequence 27, Appl
175	63.5	3.6	732	6	US-10-467-657-1106	Sequence 3, Appli	248	61.5	3.5	2061	7	US-10-995-561-633	Sequence 633, App
176	63.5	3.6	809	6			249	61.5	3.5	2296	6		
177	63.5	3.6	896	7			250	61.5	3.5				
178	63.5	3.6					251	61.5	3.5				
179	63.5	3.6					252	61.5	3.5				
180	63.5	3.6					253	61.5	3.5				
181	63.5	3.6					254	61.5	3.5				
182	63.5	3.6					255	61.5	3.5				



257	61.5	3.5	2355	6	US-10-995-561-623	Sequence 627, App	330	60	3.4	612	6	US-10-821-234-1101	Sequence 1101, Ap
258	61.5	3.5	2355	6	US-10-995-561-627	Sequence 627, App	331	60	3.4	824	6	US-10-821-234-1108	Sequence 1008, Ap
259	61.5	3.5	2384	6	US-10-821-234-1545	Sequence 1545, Ap	332	60	3.4	1259	6	US-10-995-561-625	Sequence 625, App
260	61.5	3.5	2386	6	US-10-995-561-626	Sequence 626, App	333	60	3.4	1286	6	US-10-995-561-628	Sequence 628, App
261	61	3.4	131	6	US-10-469-561-24	Sequence 24, App	334	60	3.4	1315	6	US-10-995-561-630	Sequence 630, App
262	61	3.4	215	6	US-10-374-954-9	Sequence 9, Appl1	335	60	3.4	1341	6	US-10-995-561-621	Sequence 621, App
263	61	3.4	267	7	US-11-186-284-215	Sequence 215, Appl1	336	60	3.4	1348	6	US-10-995-561-624	Sequence 624, App
264	61	3.4	288	6	US-10-821-234-1062	Sequence 1062, App	337	59.5	3.4	112	7	US-11-054-515-1069	Sequence 1, Appl1
265	61	3.4	300	7	US-11-055-822-536	Sequence 536, App	338	59.5	3.4	244	7	US-11-054-515-1069	Sequence 2069, Ap
266	61	3.4	300	7	US-11-055-822-630	Sequence 630, App	339	59.5	3.4	245	7	US-11-054-515-1950	Sequence 1950, Ap
267	61	3.4	304	6	US-10-793-626-1652	Sequence 1652, Ap	340	59.5	3.4	246	7	US-11-128-440-18	Sequence 18, Appl
268	61	3.4	370	7	US-11-129-143-68	Sequence 68, Appl	341	59.5	3.4	248	7	US-11-054-515-921	Sequence 921, App
269	61	3.4	380	7	US-11-090-439-54	Sequence 54, Appl	342	59.5	3.4	249	7	US-11-128-440-19	Sequence 19, App
270	61	3.4	469	6	US-10-510-386-14	Sequence 14, Appl	343	59.5	3.4	248	7	US-11-054-515-126	Sequence 326, App
271	61	3.4	476	7	US-11-139-499-4	Sequence 4, Appl1	344	59.5	3.4	250	7	US-11-128-440-20	Sequence 20, Appl
272	61	3.4	510	6	US-10-793-626-2860	Sequence 2860, Ap	345	59.5	3.4	257	7	US-11-054-515-1327	Sequence 1327, Ap
273	61	3.4	649	7	US-11-102-240-132	Sequence 132, App	346	59.5	3.4	259	7	US-11-056-825-7	Sequence 7, Appl1
274	61	3.4	711	7	US-11-087-100-18	Sequence 18, Appl	347	59.5	3.4	263	6	US-10-467-657-6102	Sequence 6102, Ap
275	61	3.4	711	7	US-11-087-084-18	Sequence 18, Appl	348	59.5	3.4	273	6	US-10-353-783-55	Sequence 55, Appl
276	61	3.4	711	7	US-11-087-085-18	Sequence 18, Appl	349	59.5	3.4	293	6	US-10-793-626-2542	Sequence 2542, Ap
277	61	3.4	1142	7	US-11-044-051-73	Sequence 73, Appl	350	59.5	3.4	311	7	US-11-000-463-829	Sequence 829, App
278	61	3.4	1238	7	US-11-078-735-21	Sequence 21, Appl	351	59.5	3.4	353	7	US-10-999-439-9	Sequence 9, Appl1
279	61	3.4	2910	7	US-11-087-100-2	Sequence 2, Appl1	352	59.5	3.4	354	6	US-10-999-866-31	Sequence 31, Appl
280	61	3.4	2910	7	US-11-087-084-2	Sequence 2, Appl1	353	59.5	3.4	354	7	US-11-064-821-31	Sequence 31, Appl
281	61	3.4	2910	7	US-11-087-085-2	Sequence 2, Appl1	354	59.5	3.4	369	6	US-10-510-386-190	Sequence 190, App
282	60.5	3.4	62	6	US-10-467-657-5768	Sequence 5768, Ap	355	59.5	3.4	455	6	US-10-847-867-29	Sequence 29, Appl
283	60.5	3.4	108	6	US-10-925-366A-292	Sequence 292, App	356	59.5	3.4	594	6	US-10-997-247-2	Sequence 2, Appl1
284	60.5	3.4	139	6	US-10-467-657-2748	Sequence 2748, Ap	357	59.5	3.4	595	6	US-10-995-561-995	Sequence 995, App
285	60.5	3.4	206	7	US-11-128-440-5	Sequence 5, Appl1	358	59.5	3.4	662	7	US-11-090-439-9	Sequence 9, Appl1
286	60.5	3.4	231	7	US-11-128-440-16	Sequence 16, Appl	359	59.5	3.4	707	7	US-11-069-662-113	Sequence 113, App
287	60.5	3.4	231	7	US-11-128-440-17	Sequence 17, Appl	360	59.5	3.4	737	6	US-10-878-556A-99	Sequence 99, Appl
288	60.5	3.4	276	7	US-11-091-100-16	Sequence 16, Appl	361	59.5	3.4	794	7	US-11-102-476-34	Sequence 34, Appl
289	60.5	3.4	292	6	US-10-821-234-966	Sequence 966, App	362	59.5	3.4	1049	7	US-11-137-465-42	Sequence 42, Appl
290	60.5	3.4	335	7	US-11-182-946-7	Sequence 7, Appl	363	59.5	3.4	1061	7	US-11-000-463-347	Sequence 347, App
291	60.5	3.4	360	6	US-10-467-657-5722	Sequence 5722, Ap	364	59.5	3.4	1091	7	US-11-000-463-348	Sequence 348, App
292	60.5	3.4	429	7	US-11-093-274-37	Sequence 37, Appl	365	59.5	3.4	1141	6	US-10-995-561-1009	Sequence 1009, Ap
293	60.5	3.4	444	7	US-11-172-320-6	Sequence 6, Appl1	366	59.5	3.4	1141	6	US-10-995-561-1010	Sequence 1010, Ap
294	60.5	3.4	444	7	US-11-173-969-6	Sequence 6, Appl1	367	59.5	3.4	1149	7	US-11-110-082-30	Sequence 30, Appl
295	60.5	3.4	466	6	US-10-467-657-2360	Sequence 2360, Ap	368	59.5	3.4	1405	6	US-10-995-561-515-629	Sequence 529, App
296	60.5	3.4	669	7	US-11-076-187-3	Sequence 3, Appl	369	59.5	3.4	245	7	US-11-054-515-665	Sequence 665, App
297	60.5	3.4	747	7	US-11-182-592-2	Sequence 2, Appl1	370	59.5	3.4	1214	7	US-11-102-476-4	Sequence 4, Appl1
298	60.5	3.4	821	7	US-11-087-127-90	Sequence 90, Appl	371	59	3.3	120	7	US-11-080-991-64	Sequence 94, Appl
299	60.5	3.4	832	7	US-11-108-172-1081	Sequence 1081, Ap	372	59	3.3	193	7	US-11-125-837-36	Sequence 36, Appl
300	60.5	3.4	853	6	US-10-420-192-6	Sequence 6, Appl1	373	59	3.3	242	7	US-11-085-775-4	Sequence 4, Appl1
301	60.5	3.4	858	6	US-10-613-744-6	Sequence 6, Appl1	374	59	3.3	245	7	US-11-054-515-1830	Sequence 1830, Ap
302	60.5	3.4	1029	6	US-10-821-234-908	Sequence 908, App	375	59	3.3	245	7	US-11-054-515-1651	Sequence 1516, Ap
303	60.5	3.4	1187	6	US-10-821-234-955	Sequence 955, App	376	59	3.3	251	7	US-11-054-515-665	Sequence 665, App
304	60.5	3.4	1730	7	US-11-192-967-4	Sequence 4, Appl1	377	59	3.3	251	7	US-11-054-515-304	Sequence 304, App
305	60.5	3.4	1730	7	US-11-193-715-4	Sequence 4, Appl1	378	59	3.3	256	7	US-11-054-515-1027	Sequence 1027, Ap
306	60	3.4	104	7	US-11-000-463-939	Sequence 939, App	379	59	3.3	258	7	US-11-054-515-865	Sequence 865, App
307	60	3.4	106	7	US-10-463-467	Sequence 467, App	380	59	3.3	258	7	US-11-054-515-1029	Sequence 1029, Ap
308	60	3.4	136	6	US-10-821-234-913	Sequence 913, App	381	59	3.3	259	7	US-11-054-515-1277	Sequence 1277, Ap
309	60	3.4	226	6	US-10-467-657-2428	Sequence 2428, Ap	382	59	3.3	259	7	US-11-054-515-1481	Sequence 1481, Ap
310	60	3.4	228	6	US-10-793-626-3190	Sequence 3190, Ap	383	59	3.3	277	6	US-10-924-074-24	Sequence 24, Appl
311	60	3.4	236	6	US-10-927-641-72	Sequence 72, Appl	384	59	3.3	277	6	US-11-182-946-10	Sequence 10, Appl
312	60	3.4	248	7	US-11-054-515-1037	Sequence 1037, Ap	385	59	3.3	279	6	US-10-467-657-7232	Sequence 3232, Ap
313	60	3.4	249	7	US-11-054-515-739	Sequence 739, App	386	59	3.3	281	7	US-11-055-822-260	Sequence 260, App
314	60	3.4	251	7	US-11-054-515-1229	Sequence 1229, Ap	387	59	3.3	425	6	US-10-995-561-616	Sequence 616, App
315	60	3.4	253	7	US-11-054-515-909	Sequence 909, App	388	59	3.3	455	7	US-11-182-946-3	Sequence 3, Appl1
316	60	3.4	253	7	US-11-054-515-1167	Sequence 1167, Ap	389	59	3.3	476	7	US-11-008-727-22	Sequence 22, Appl
317	60	3.4	253	7	US-11-054-515-1235	Sequence 1235, Ap	390	59	3.3	493	6	US-10-995-561-511	Sequence 611, App
318	60	3.4	253	7	US-11-054-515-1375	Sequence 1375, Ap	391	59	3.3	532	6	US-10-857-780-18	Sequence 18, Appl
319	60	3.4	254	7	US-11-054-515-844	Sequence 844, App	392	59	3.3	532	6	US-10-995-561-619	Sequence 897, App
320	60	3.4	257	7	US-11-054-515-1710	Sequence 1710, Ap	393	59	3.3	532	7	US-11-104-812-2	Sequence 2, Appl1
321	60	3.4	271	6	US-10-793-626-1156	Sequence 1156, Ap	394	59	3.3	532	7	US-11-105-279-2	Sequence 2, Appl1
322	60	3.4	285	6	US-10-821-234-1304	Sequence 1304, Ap	395	59	3.3	592	7	US-11-135-855-24	Sequence 24, Appl
323	60	3.4	286	6	US-10-793-626-2192	Sequence 2192, Ap	396	59	3.3	832	6	US-10-512-109-29	Sequence 29, Appl
324	60	3.4	336	6	US-11-113-424-83	Sequence 83, Appl	397	59	3.3	1158	7	US-11-075-646-6	Sequence 6, Appl1
325	60	3.4	380	7	US-11-090-439-52	Sequence 52, Appl	398	59	3.3	1179	7	US-11-097-125-1	Sequence 12, Appl1
326	60	3.4	421	6	US-10-793-626-1144	Sequence 144, App	399	59	3.3	1196	6	US-10-995-561-921	Sequence 921, App
327	60	3.4	463	7	US-11-102-240-86	Sequence 86, Appl	401	59	3.3	1436	6	US-10-995-561-531	Sequence 531, App
328	60	3.4	502	6	US-10-793-626-3136	Sequence 3136, Ap	402	59	3.3	1532	6	US-10-821-234-914	Sequence 914, App
329	60	3.4	610	6	US-10-606-302-1	Sequence 1, Appl1	403	59	3.3	1857	7	US-11-057-058-60	Sequence 60, Appl



404	59	3.3	1857	7	US-11-057-058-61	Sequence 61, Appl	479	57.5	3.2	244	6	US-10-793-626-2780	Sequence 2780, Ap
405	58.5	3.3	135	7	US-11-012-353-81	Sequence 81, Appl	480	57.5	3.2	249	7	US-11-054-515-340	Sequence 340, Ap
406	58.5	3.3	135	7	US-11-012-353-85	Sequence 85, Appl	481	57.5	3.2	249	7	US-11-054-515-957	Sequence 957, Ap
407	58.5	3.3	166	6	US-10-793-626-1978	Sequence 1978, Ap	482	57.5	3.2	253	7	US-11-054-515-1964	Sequence 1964, Ap
408	58.5	3.3	175	6	US-10-967-527A-7	Sequence 7, Appl	483	57.5	3.2	256	7	US-11-054-515-1026	Sequence 1026, Ap
409	58.5	3.3	179	6	US-10-793-626-1092	Sequence 1092, Ap	484	57.5	3.2	256	7	US-11-054-515-1600	Sequence 1600, Ap
410	58.5	3.3	245	7	US-11-054-515-1532	Sequence 1532, Ap	485	57.5	3.2	308	6	US-10-467-657-1192	Sequence 1192, Ap
411	58.5	3.3	255	7	US-11-054-515-1642	Sequence 1642, Ap	486	57.5	3.2	344	7	US-11-108-172-1085	Sequence 1085, Ap
412	58.5	3.3	276	6	US-11-029-003-18	Sequence 18, Appl	487	57.5	3.2	379	7	US-11-129-143-66	Sequence 66, Appl
413	58.5	3.3	289	6	US-10-987-663-2	Sequence 2, Appl	488	57.5	3.2	380	6	US-10-485-517-89	Sequence 289, Ap
414	58.5	3.3	290	7	US-11-113-424-78	Sequence 78, Appl	489	57.5	3.2	384	7	US-11-000-463-805	Sequence 804, Ap
415	58.5	3.3	305	7	US-11-080-091-2	Sequence 2, Appl	490	57.5	3.2	384	7	US-11-000-463-806	Sequence 806, Ap
416	58.5	3.3	311	7	US-11-000-463-817	Sequence 817, Ap	491	57.5	3.2	384	7	US-11-000-463-807	Sequence 807, Ap
417	58.5	3.3	326	6	US-10-485-517-306	Sequence 306, Appl	492	57.5	3.2	384	7	US-11-000-463-875	Sequence 375, Ap
418	58.5	3.3	349	6	US-10-515-419-2	Sequence 2, Appl	493	57.5	3.2	423	7	US-11-120-338-25	Sequence 25, Appl
419	58.5	3.3	352	6	US-10-515-419-3	Sequence 3, Appl	494	57.5	3.2	451	7	US-11-120-338-17	Sequence 17, Appl
420	58.5	3.3	352	6	US-10-995-561-712	Sequence 712, Ap	495	57.5	3.2	452	7	US-11-139-499-12	Sequence 12, Appl
421	58.5	3.3	359	6	US-10-995-561-716	Sequence 716, Ap	496	57.5	3.2	476	6	US-10-984-376-1	Sequence 1, Appl
422	58.5	3.3	359	6	US-10-995-561-713	Sequence 713, Ap	497	57.5	3.2	488	6	US-10-984-376-4	Sequence 4, Appl
423	58.5	3.3	388	6	US-10-995-561-713	Sequence 713, Ap	498	57.5	3.2	488	6	US-10-984-376-184	Sequence 3184, Ap
424	58.5	3.3	391	7	US-11-058-727-119	Sequence 119, Ap	499	57.5	3.2	567	6	US-11-053-100-45	Sequence 45, Ap
425	58.5	3.3	391	7	US-11-058-727-121	Sequence 121, Ap	501	57.5	3.2	736	7	US-11-053-100-61	Sequence 1523, Ap
426	58.5	3.3	391	7	US-11-058-727-123	Sequence 123, Ap	503	57.5	3.2	897	6	US-10-821-234-1523	Sequence 19, Appl
427	58.5	3.3	391	7	US-11-108-389-119	Sequence 119, Ap	504	57.5	3.2	934	7	US-11-108-864-19	Sequence 1097, Ap
428	58.5	3.3	391	7	US-11-108-389-121	Sequence 121, Ap	505	57.5	3.2	1094	6	US-10-821-234-1097	Sequence 3, Appl
429	58.5	3.3	391	7	US-11-108-389-123	Sequence 123, Ap	506	57.5	3.2	1122	7	US-11-191-374-3	Sequence 3, Appl
430	58.5	3.3	394	6	US-10-995-561-714	Sequence 714, Ap	507	57.5	3.2	1122	7	US-11-191-375-3	Sequence 3, Appl
431	58.5	3.3	455	6	US-10-847-867-1	Sequence 1, Appl	508	57.5	3.2	1170	6	US-11-053-100-71	Sequence 71, Appl
432	58.5	3.3	479	7	US-11-194-246-310	Sequence 310, Ap	509	57.5	3.2	1186	7	US-11-096-051-4	Sequence 4, Appl
433	58.5	3.3	480	6	US-10-847-867-3	Sequence 3, Appl	510	57.5	3.2	2376	7	US-11-096-051-2	Sequence 51, Appl
434	58.5	3.3	500	7	US-11-102-240-84	Sequence 84, Appl	511	57.5	3.2	2715	7	US-11-113-424-51	Sequence 51, Appl
435	58.5	3.3	636	6	US-10-485-517-170	Sequence 170, Ap	512	57.5	3.2	2715	7	US-11-113-424-51	Sequence 51, Appl
437	58.5	3.3	685	7	US-11-078-735-19	Sequence 19, Appl	513	57.5	3.2	2715	7	US-11-096-051-10	Sequence 10, Appl
438	58.5	3.3	729	7	US-11-099-691-3	Sequence 3, Appl	514	57.5	3.2	2721	7	US-11-096-051-8	Sequence 8, Appl
439	58.5	3.3	995	7	US-11-113-424-62	Sequence 62, Appl	515	57.5	3.2	2725	7	US-11-096-051-8	Sequence 24, Appl
440	58.5	3.3	1148	7	US-11-110-082-29	Sequence 29, Appl	516	57.5	3.2	4868	7	US-11-044-111-24	Sequence 189, Ap
441	58.5	3.3	5405	7	US-11-108-172-1116	Sequence 116, Ap	517	57.5	3.2	77	7	US-11-113-424-189	Sequence 189, Ap
442	58	3.3	177	6	US-10-999-866-61	Sequence 61, Appl	518	57	3.2	116	6	US-10-793-626-1680	Sequence 1680, Ap
443	58	3.3	199	6	US-10-967-527A-25	Sequence 25, Appl	519	57	3.2	241	7	US-11-054-515-1888	Sequence 1888, Ap
444	58	3.3	205	6	US-10-995-561-1028	Sequence 1028, Ap	520	57	3.2	244	7	US-11-054-515-1491	Sequence 1491, Ap
445	58	3.3	233	6	US-10-995-561-1029	Sequence 1029, Ap	521	57	3.2	244	7	US-11-054-515-1582	Sequence 1582, Ap
446	58	3.3	233	6	US-10-858-730-234	Sequence 234, Ap	522	57	3.2	250	7	US-11-054-515-1540	Sequence 1540, Ap
447	58	3.3	233	6	US-11-055-822-54	Sequence 54, Appl	523	57	3.2	251	7	US-11-054-515-165	Sequence 165, Ap
448	58	3.3	251	7	US-11-054-515-196	Sequence 196, Ap	524	57	3.2	254	7	US-11-054-515-1469	Sequence 1469, Ap
449	58	3.3	253	7	US-11-054-515-1125	Sequence 1125, Ap	525	57	3.2	256	7	US-11-054-515-1258	Sequence 1258, Ap
450	58	3.3	257	7	US-11-054-515-1240	Sequence 1240, Ap	526	57	3.2	257	7	US-11-054-515-1028	Sequence 1028, Ap
451	58	3.3	257	7	US-11-054-515-1252	Sequence 1252, Ap	527	57	3.2	257	7	US-11-054-515-1283	Sequence 1283, Ap
452	58	3.3	258	7	US-11-054-515-1243	Sequence 1243, Ap	528	57	3.2	258	7	US-11-054-515-1265	Sequence 1265, Ap
453	58	3.3	258	7	US-11-054-515-1255	Sequence 1255, Ap	529	57	3.2	258	7	US-11-054-515-1274	Sequence 1274, Ap
454	58	3.3	258	7	US-11-054-515-1276	Sequence 1276, Ap	530	57	3.2	258	7	US-11-054-515-1365	Sequence 1365, Ap
455	58	3.3	259	7	US-11-054-515-1034	Sequence 1034, Ap	531	57	3.2	258	7	US-11-054-515-1365	Sequence 1365, Ap
456	58	3.3	259	7	US-11-054-515-1043	Sequence 1043, Ap	532	57	3.2	259	7	US-11-054-515-1032	Sequence 1032, Ap
457	58	3.3	259	7	US-11-054-515-147	Sequence 147, Ap	533	57	3.2	259	7	US-11-054-515-1041	Sequence 1041, Ap
458	58	3.3	259	7	US-11-054-515-1247	Sequence 1247, Ap	534	57	3.2	286	7	US-11-179-977-9	Sequence 9, Appl
459	58	3.3	259	7	US-11-054-515-1263	Sequence 1263, Ap	535	57	3.2	324	6	US-10-793-626-640	Sequence 640, Ap
460	58	3.3	259	7	US-11-054-515-1270	Sequence 1270, Ap	536	57	3.2	367	6	US-10-793-626-2876	Sequence 2876, Ap
461	58	3.3	260	7	US-11-054-515-1250	Sequence 1250, Ap	537	57	3.2	447	7	US-11-196-475-162	Sequence 162, Ap
462	58	3.3	260	7	US-11-054-515-1382	Sequence 1382, Ap	538	57	3.2	451	6	US-10-923-327-9	Sequence 9, Appl
463	58	3.3	261	7	US-11-054-515-1503	Sequence 1503, Ap	539	57	3.2	451	6	US-10-923-327-9	Sequence 9, Appl
464	58	3.3	263	7	US-11-116-939-10	Sequence 10, Appl	540	57	3.2	451	6	US-10-923-327-11	Sequence 11, Appl
465	58	3.3	293	7	US-11-116-939-12	Sequence 12, Appl	541	57	3.2	456	7	US-11-074-176-238	Sequence 238, Ap
466	58	3.3	312	6	US-10-858-730-92	Sequence 92, Appl	542	57	3.2	497	6	US-10-821-234-1358	Sequence 1358, Ap
467	58	3.3	324	6	US-11-116-939-19	Sequence 19, Appl	543	57	3.2	545	6	US-10-467-657-1408	Sequence 1408, Ap
468	58	3.3	451	6	US-10-793-626-210	Sequence 210, Ap	544	57	3.2	545	6	US-10-467-657-1408	Sequence 624, Ap
469	58	3.3	824	7	US-11-116-939-11	Sequence 11, Appl	545	57	3.2	569	6	US-11-174-150-28	Sequence 28, Appl
470	58	3.3	860	7	US-11-022-562-217	Sequence 217, Ap	546	57	3.2	589	7	US-11-074-176-306	Sequence 306, Ap
471	58	3.3	1060	7	US-11-090-739-120	Sequence 120, Ap	547	57	3.2	713	7	US-11-074-176-18	Sequence 18, Appl
472	58	3.3	1271	6	US-10-770-726-46	Sequence 46, Appl	548	57	3.2	723	7	US-11-174-150-29	Sequence 29, Appl
473	58	3.3	1271	6	US-10-770-726-45	Sequence 45, Appl	549	57	3.2	801	7	US-11-077-550-128	Sequence 128, Ap
474	58	3.3	135	6	US-11-012-353-77	Sequence 77, Appl	550	57	3.2	876	7	US-11-077-550-126	Sequence 126, Ap
475	57.5	3.2	135	6	US-10-467-657-4246	Sequence 4246, Ap	551	57	3.2	877	7	US-11-077-550-130	Sequence 130, Ap
476	57.5	3.2	145	6	US-10-793-626-826	Sequence 826, Ap	552	57	3.2	877	7	US-11-077-550-124	Sequence 124, Ap
477	57.5	3.2	182	6	US-11-170-653-60	Sequence 60, Appl	553	57	3.2	902	7	US-11-077-550-132	Sequence 132, Ap
478	57.5	3.2	217	7			554	57	3.2				
							555	57	3.2				



556	57	3.2	912	7	US-11-077-550-116	Sequence 116, App	633	56	3.2	291	6	US-10-821-234-1025	Sequence 1025, Ap
557	57	3.2	914	7	US-11-077-550-120	Sequence 120, App	634	56	3.2	331	6	US-10-821-234-1650	Sequence 1650, Ap
558	57	3.2	914	7	US-11-077-550-122	Sequence 122, App	635	56	3.2	351	6	US-11-095-624-5	Sequence 5, App11
559	57	3.2	950	7	US-11-077-550-118	Sequence 118, App	636	56	3.2	357	6	US-10-793-626-1360	Sequence 1360, Ap
560	57	3.2	1073	6	US-10-467-657-5230	Sequence 5230, Ap	637	56	3.2	447	6	US-10-884-730-379	Sequence 379, App
561	57	3.2	1225	7	US-11-102-476-2	Sequence 2, App11	638	56	3.2	459	6	US-10-793-626-2462	Sequence 2462, Ap
562	57	3.2	1254	6	US-10-528-031-47	Sequence 47, App1	639	56	3.2	473	6	US-10-793-626-60	Sequence 60, App1
563	57	3.2	2314	6	US-11-097-728-2	Sequence 2, App11	640	56	3.2	495	6	US-10-613-744-5	Sequence 5, App11
564	57	3.2	3056	7	US-11-109-156-20	Sequence 20, App1	641	56	3.2	548	7	US-11-022-289-3	Sequence 3, App11
565	57	3.2	100	7	US-11-054-669-75	Sequence 75, App1	642	56	3.2	652	6	US-10-821-234-1016	Sequence 1016, Ap
566	56.5	3.2	100	7	US-11-084-554-107	Sequence 107, App	643	56	3.2	654	7	US-11-046-668-4	Sequence 4, App1
567	56.5	3.2	100	7	US-11-084-554-118	Sequence 118, App	644	56	3.2	683	7	US-11-046-668-2	Sequence 2, App11
568	56.5	3.2	112	7	US-11-012-353-58	Sequence 58, App1	645	56	3.2	685	7	US-11-089-551A-2	Sequence 2, App11
569	56.5	3.2	158	6	US-10-467-657-2650	Sequence 2650, App	646	56	3.2	734	7	US-11-093-274-40	Sequence 40, App1
570	56.5	3.2	158	6	US-10-467-657-3592	Sequence 3592, Ap	647	56	3.2	805	6	US-11-045-517-198	Sequence 198, App
571	56.5	3.2	158	6	US-10-467-657-6438	Sequence 6438, Ap	648	56	3.2	814	6	US-10-878-556A-161	Sequence 161, App
572	56.5	3.2	160	6	US-10-467-657-5090	Sequence 5090, Ap	649	56	3.2	857	6	US-10-613-744-11	Sequence 11, App1
573	56.5	3.2	168	6	US-11-108-172-198	Sequence 198, App	650	56	3.2	859	7	US-11-000-463-423	Sequence 423, App
574	56.5	3.2	216	6	US-10-467-657-482	Sequence 482, App	651	56	3.2	859	7	US-11-000-463-895	Sequence 895, App
575	56.5	3.2	236	7	US-11-144-248-51	Sequence 51, App1	652	56	3.2	859	7	US-11-113-751-36	Sequence 36, App1
576	56.5	3.2	242	7	US-11-054-515-1884	Sequence 1884, Ap	653	56	3.2	1151	7	US-11-194-246-439	Sequence 439, App
577	56.5	3.2	242	7	US-11-054-515-2084	Sequence 2084, Ap	654	56	3.2	1159	7	US-11-078-735-20	Sequence 20, App1
578	56.5	3.2	248	7	US-11-054-515-1988	Sequence 1988, Ap	655	56	3.2	1218	7	US-10-995-561-691	Sequence 691, App
579	56.5	3.2	250	7	US-11-054-515-1804	Sequence 1804, Ap	656	56	3.2	2813	6	US-10-995-561-688	Sequence 688, App
580	56.5	3.2	250	7	US-11-056-825-2	Sequence 2, App11	657	56	3.2	2919	6	US-10-821-234-1133	Sequence 1133, Ap
581	56.5	3.2	273	6	US-10-353-783-54	Sequence 54, App1	658	55.5	3.1	100	7	US-11-054-669-91	Sequence 91, App1
582	56.5	3.2	279	6	US-10-793-626-870	Sequence 870, App1	659	55.5	3.1	100	7	US-11-054-669-112	Sequence 112, App
583	56.5	3.2	305	7	US-11-080-091-13	Sequence 13, App1	660	55.5	3.1	100	7	US-11-012-353-60	Sequence 60, App1
584	56.5	3.2	334	7	US-11-140-417-8	Sequence 8, App11	661	55.5	3.1	112	7	US-11-022-289-11	Sequence 11, App1
585	56.5	3.2	334	7	US-10-995-561-704	Sequence 704, App	662	55.5	3.1	125	6	US-11-789-273-6	Sequence 6, App11
587	56.5	3.2	335	6	US-11-141-947-2	Sequence 2, App11	663	55.5	3.1	126	6	US-11-128-440-13	Sequence 13, App1
588	56.5	3.2	344	7	US-11-083-800-10	Sequence 10, App1	664	55.5	3.1	244	7	US-11-054-515-1568	Sequence 1568, Ap
589	56.5	3.2	344	7	US-11-083-800-10	Sequence 10, App1	665	55.5	3.1	248	7	US-11-054-515-2094	Sequence 2094, Ap
590	56.5	3.2	348	6	US-10-467-657-6602	Sequence 6602, Ap	666	55.5	3.1	250	7	US-11-054-515-1439	Sequence 1439, Ap
591	56.5	3.2	348	6	US-10-467-657-7662	Sequence 7662, Ap	667	55.5	3.1	250	7	US-11-054-515-1581	Sequence 1581, Ap
594	56.5	3.2	451	7	US-11-120-338-22	Sequence 22, App	668	55.5	3.1	252	7	US-11-054-515-1646	Sequence 1646, Ap
595	56.5	3.2	452	7	US-11-120-338-14	Sequence 14, App1	669	55.5	3.1	273	6	US-10-353-783-42	Sequence 42, App1
596	56.5	3.2	458	7	US-11-016-503-16	Sequence 16, App1	670	55.5	3.1	275	6	US-10-995-561-735	Sequence 735, App
597	56.5	3.2	458	7	US-11-089-803-6	Sequence 6, App11	671	55.5	3.1	287	6	US-10-995-561-730	Sequence 730, App
598	56.5	3.2	458	7	US-10-467-657-2612	Sequence 2612, Ap	672	55.5	3.1	295	6	US-10-987-663-30	Sequence 30, App1
599	56.5	3.2	471	6	US-10-858-730-125	Sequence 125, App	673	55.5	3.1	305	7	US-11-000-463-391	Sequence 391, App
600	56.5	3.2	485	6	US-11-508-263-22	Sequence 22, App1	674	55.5	3.1	305	7	US-11-000-463-863	Sequence 863, App
601	56.5	3.2	496	7	US-11-110-082-31	Sequence 31, App1	675	55.5	3.1	325	6	US-10-793-626-698	Sequence 698, App
602	56.5	3.2	509	7	US-11-008-727-16	Sequence 16, App1	676	55.5	3.1	325	6	US-10-793-626-1330	Sequence 1330, Ap
603	56.5	3.2	524	6	US-10-467-657-8122	Sequence 8122, Ap	677	55.5	3.1	330	7	US-11-022-289-11	Sequence 11, App1
604	56.5	3.2	581	7	US-11-045-802-30	Sequence 30, App1	678	55.5	3.1	330	7	US-11-075-351-1	Sequence 1, App1
605	56.5	3.2	687	7	US-11-117-169-6	Sequence 6, App11	679	55.5	3.1	330	7	US-11-165-141-15	Sequence 15, App1
606	56.5	3.2	727	7	US-11-117-169-8	Sequence 8, App11	680	55.5	3.1	330	7	US-11-024-251-35	Sequence 35, App1
607	56.5	3.2	745	6	US-10-995-561-659	Sequence 659, App	681	55.5	3.1	335	7	US-10-999-866-35	Sequence 35, App1
608	56.5	3.2	745	6	US-11-109-156-14	Sequence 14, App1	682	55.5	3.1	339	6	US-11-061-821-35	Sequence 35, App1
609	56.5	3.2	879	7	US-11-022-562-340	Sequence 340, App	683	55.5	3.1	339	7	US-10-875-716-9	Sequence 9, App11
610	56.5	3.2	932	7	US-11-071-581-1	Sequence 1, App11	684	55.5	3.1	365	6	US-11-117-169-12	Sequence 12, App1
611	56.5	3.2	1116	7	US-11-113-751-34	Sequence 34, App1	685	55.5	3.1	367	7	US-11-055-822-180	Sequence 180, App
612	56.5	3.2	1138	7	US-11-012-762-28	Sequence 28, App1	686	55.5	3.1	370	7	US-11-055-822-190	Sequence 190, App
613	56.5	3.2	1403	7	US-11-091-928-1	Sequence 1, App11	687	55.5	3.1	370	7	US-10-858-730-286	Sequence 286, App
614	56.5	3.2	1476	6	US-10-647-956A-4	Sequence 4, App11	688	55.5	3.1	377	6	US-11-055-822-178	Sequence 178, App
615	56.5	3.2	1476	6	US-11-144-248-20	Sequence 20, App1	689	55.5	3.1	377	7	US-11-055-822-188	Sequence 188, App
616	56	3.2	216	7	US-11-186-284-217	Sequence 217, App	690	55.5	3.1	377	7	US-11-055-822-188	Sequence 188, App
617	56	3.2	217	7	US-11-186-284-217	Sequence 217, App	691	55.5	3.1	377	7	US-11-055-822-188	Sequence 188, App
618	56	3.2	230	7	US-11-188-281-18	Sequence 18, App1	692	55.5	3.1	402	7	US-11-024-251-31	Sequence 31, App1
619	56	3.2	232	6	US-10-467-657-3352	Sequence 3352, Ap	693	55.5	3.1	421	6	US-10-763-712A-2	Sequence 2, App11
620	56	3.2	237	6	US-11-083-055-2	Sequence 2, App11	694	55.5	3.1	421	6	US-10-763-712A-2	Sequence 2, App11
621	56	3.2	244	7	US-11-054-515-1498	Sequence 1498, Ap	695	55.5	3.1	438	7	US-11-074-176-152	Sequence 152, App
622	56	3.2	248	7	US-11-054-515-1267	Sequence 1267, Ap	696	55.5	3.1	438	7	US-11-120-338-15	Sequence 15, App1
623	56	3.2	249	7	US-11-054-515-604	Sequence 604, App	697	55.5	3.1	454	7	US-11-136-475-160	Sequence 160, App
624	56	3.2	249	7	US-11-054-515-628	Sequence 628, App	698	55.5	3.1	474	7	US-11-000-463-384	Sequence 384, App
625	56	3.2	249	7	US-11-054-515-783	Sequence 783, App	699	55.5	3.1	477	7	US-11-000-463-395	Sequence 395, App
626	56	3.2	250	7	US-11-054-515-1022	Sequence 1022, Ap	700	55.5	3.1	531	6	US-10-485-517-776	Sequence 776, App
627	56	3.2	251	7	US-11-054-515-187	Sequence 187, App	701	55.5	3.1	551	7	US-11-022-289-7	Sequence 7, App11
628	56	3.2	265	6	US-10-793-626-2422	Sequence 2422, Ap	702	55.5	3.1	551	7	US-11-022-289-8	Sequence 8, App11
629	56	3.2	266	7	US-11-054-515-3229	Sequence 3229, Ap	703	55.5	3.1	557	7	US-11-022-289-2	Sequence 2, App11
630	56	3.2	271	7	US-11-089-551A-17	Sequence 17, App1	704	55.5	3.1	557	7	US-11-022-289-4	Sequence 4, App11
631	56	3.2	286	6	US-10-793-626-1020	Sequence 1020, Ap	705	55.5	3.1	557	7	US-11-022-289-5	Sequence 5, App11
632	56	3.2	286	7	US-11-194-246-320	Sequence 320, App	706	55.5	3.1	557	7	US-11-022-289-6	Sequence 6, App11



708	55.5	3.1	564	7	US-11-022-289-10	Sequence 10, Appl	782	55	3.1	400	6	US-10-793-626-1056	Sequence 1056, Ap
709	55.5	3.1	579	7	US-11-174-186-41	Sequence 41, Appl	783	55	3.1	407	6	US-10-793-626-886	Sequence 886, App
710	55.5	3.1	656	6	US-10-995-561-871	Sequence 871, App	784	55	3.1	430	7	US-11-016-503-17	Sequence 17, Appl
711	55.5	3.1	664	6	US-10-485-517-308	Sequence 308, App	785	55	3.1	430	7	US-11-194-246-138	Sequence 438, App
712	55.5	3.1	679	6	US-10-995-561-872	Sequence 872, App	786	55	3.1	445	6	US-10-793-626-1294	Sequence 1294, Ap
713	55.5	3.1	708	7	US-11-174-150-25	Sequence 25, Appl	787	55	3.1	458	7	US-11-016-503-12	Sequence 12, Appl
714	55.5	3.1	715	7	US-11-089-551A-47	Sequence 47, Appl	788	55	3.1	458	7	US-11-089-803-2	Sequence 2, Appl
716	55.5	3.1	736	7	US-11-174-150-26	Sequence 26, Appl	789	55	3.1	470	7	US-11-008-727-20	Sequence 20, Appl
717	55.5	3.1	963	6	US-10-995-561-923	Sequence 923, App	790	55	3.1	546	7	US-11-143-980-38	Sequence 38, Appl
718	55.5	3.1	1066	7	US-11-055-822-370	Sequence 370, Appl	791	55	3.1	550	7	US-11-184-380-14	Sequence 14, Appl
719	55.5	3.1	1066	7	US-11-055-822-1002	Sequence 1002, Ap	792	55	3.1	581	6	US-10-793-626-28	Sequence 28, Appl
720	55.5	3.1	1092	6	US-10-821-234-999	Sequence 999, App	793	55	3.1	581	6	US-10-793-626-1080	Sequence 1080, Ap
721	55.5	3.1	1113	6	US-11-055-822-368	Sequence 368, App	794	55	3.1	592	6	US-10-995-561-994	Sequence 994, App
722	55.5	3.1	1113	7	US-11-055-822-1000	Sequence 1000, Ap	795	55	3.1	615	6	US-10-995-561-940	Sequence 940, App
723	55.5	3.1	1141	6	US-10-601-368-24	Sequence 24, Appl	796	55	3.1	659	6	US-10-995-561-573	Sequence 573, App
724	55.5	3.1	1158	6	US-10-858-730-70	Sequence 70, Appl	797	55	3.1	662	6	US-10-995-561-943	Sequence 943, App
725	55.5	3.1	1166	6	US-10-601-368-22	Sequence 22, Appl	798	55	3.1	701	6	US-10-995-561-575	Sequence 575, App
726	55.5	3.1	1188	6	US-10-601-368-21	Sequence 21, Appl	799	55	3.1	702	6	US-10-995-561-942	Sequence 942, App
727	55.5	3.1	1410	6	US-10-878-356A-136	Sequence 136, App	801	55	3.1	716	6	US-11-147-047-52	Sequence 52, App
728	55.5	3.1	1538	6	US-10-995-561-772	Sequence 772, App	802	55	3.1	751	6	US-10-995-561-578	Sequence 578, App
729	55.5	3.1	1586	6	US-10-821-234-901	Sequence 901, App	803	55	3.1	752	6	US-10-793-626-1036	Sequence 1036, Ap
730	55.5	3.1	1889	7	US-11-102-476-46	Sequence 46, Appl	804	55	3.1	754	6	US-10-995-561-941	Sequence 941, App
731	55.5	3.1	1970	6	US-10-821-234-1641	Sequence 1641, Ap	805	55	3.1	808	6	US-10-995-561-574	Sequence 574, App
732	55.5	3.1	3002	6	US-10-821-234-916	Sequence 916, App	806	55	3.1	808	7	US-11-105-268-53	Sequence 53, Appl
733	55.5	3.1	5335	6	US-10-995-561-777	Sequence 777, App	807	55	3.1	808	7	US-11-110-082-38	Sequence 38, Appl
734	55.5	3.1	5406	6	US-10-995-561-774	Sequence 774, App	808	55	3.1	838	6	US-10-645-441-9	Sequence 9, Appl
735	55.5	3.1	5415	6	US-10-995-561-779	Sequence 779, App	809	55	3.1	844	6	US-10-763-712A-48	Sequence 48, Appl
736	55.5	3.1	5464	6	US-10-995-561-775	Sequence 775, App	810	55	3.1	881	7	US-11-191-374-12	Sequence 12, Appl
737	55.5	3.1	5935	6	US-10-995-561-776	Sequence 776, App	811	55	3.1	897	7	US-11-137-465-35	Sequence 35, Appl
738	55	3.1	97	7	US-11-144-248-44	Sequence 44, Appl	812	55	3.1	993	7	US-11-137-465-36	Sequence 36, Appl
739	55	3.1	97	7	US-11-054-669-51	Sequence 51, Appl	813	55	3.1	1005	7	US-11-113-424-63	Sequence 63, Appl
740	55	3.1	117	7	US-11-012-353-162	Sequence 53, Appl	814	55	3.1	1137	6	US-10-499-715-4	Sequence 4, Appl
741	55	3.1	125	7	US-11-096-074-57	Sequence 57, Appl	815	55	3.1	1162	6	US-10-451-375-3	Sequence 3, Appl
742	55	3.1	168	6	US-10-793-626-2068	Sequence 2068, Ap	816	55	3.1	1663	6	US-10-982-545-6	Sequence 6, Appl
743	55	3.1	236	7	US-11-008-727-4	Sequence 4, Appl	817	55	3.1	2323	6	US-10-793-626-760	Sequence 760, App
744	55	3.1	240	6	US-10-793-626-1972	Sequence 1972, App	818	55	3.1	248	7	US-11-054-515-2000	Sequence 2000, Ap
745	55	3.1	241	7	US-11-054-515-1887	Sequence 1887, App	819	55	3.1	249	7	US-11-054-515-327	Sequence 327, App
746	55	3.1	244	7	US-11-054-515-1845	Sequence 1845, App	820	55	3.1	249	7	US-11-054-515-445	Sequence 445, App
747	55	3.1	245	7	US-11-054-515-1521	Sequence 1521, App	821	55	3.1	249	7	US-11-054-515-495	Sequence 495, App
748	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	822	55	3.1	249	7	US-11-054-515-1833	Sequence 1833, Ap
749	55	3.1	247	6	US-10-884-730-356	Sequence 356, App	823	55	3.1	251	7	US-11-054-515-1505	Sequence 1505, App
750	55	3.1	247	6	US-10-793-626-1972	Sequence 1972, App	824	55	3.1	252	7	US-11-054-515-1475	Sequence 1475, App
751	55	3.1	247	6	US-11-054-515-1887	Sequence 1887, App	825	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
752	55	3.1	247	7	US-11-054-515-1901	Sequence 1901, App	826	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
753	55	3.1	247	7	US-11-054-515-1844	Sequence 1844, App	827	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
754	55	3.1	247	7	US-11-054-515-1515	Sequence 1515, App	828	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
755	55	3.1	247	7	US-11-054-515-1863	Sequence 1863, App	829	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
756	55	3.1	247	7	US-11-054-515-1124	Sequence 1124, App	830	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
757	55	3.1	247	7	US-11-054-515-1669	Sequence 1669, App	831	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
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759	55	3.1	247	7	US-11-054-515-1521	Sequence 1521, App	833	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
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761	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	835	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
762	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	836	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
763	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	837	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
764	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	838	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
765	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	839	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
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767	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	841	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
768	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	842	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
769	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	843	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
770	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	844	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
771	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	845	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
772	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	846	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
773	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	847	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
774	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	848	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
775	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	849	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
776	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	850	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
777	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	851	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
778	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	852	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
779	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	853	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
780	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	854	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
781	55	3.1	247	7	US-11-054-515-1528	Sequence 1528, App	855	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App



858	54.5	3.1	455	6	US-10-847-867-30	Sequence 30, Appl	932	54	3.0	535	6	US-10-995-561-510	Sequence 610, App
859	54.5	3.1	455	6	US-10-847-867-31	Sequence 31, Appl	933	54	3.0	538	6	US-10-793-626-3134	Sequence 3134, Ap
860	54.5	3.1	455	6	US-10-847-867-33	Sequence 33, Appl	934	54	3.0	617	7	US-11-172-145-8	Sequence 8, Appl
861	54.5	3.1	455	6	US-10-847-867-34	Sequence 34, Appl	935	54	3.0	687	6	US-10-467-657-1300	Sequence 1300, Ap
862	54.5	3.1	455	7	US-11-016-503-14	Sequence 14, Appl	936	54	3.0	733	6	US-10-821-234-1147	Sequence 1147, Ap
863	54.5	3.1	455	7	US-11-089-803-4	Sequence 4, Appl	937	54	3.0	791	6	US-10-467-657-5014	Sequence 5014, Ap
864	54.5	3.1	497	6	US-10-984-376-3	Sequence 3, Appl	938	54	3.0	827	6	US-10-821-224-1685	Sequence 1685, Ap
865	54.5	3.1	547	6	US-10-770-726-87	Sequence 87, Appl	939	54	3.0	829	6	US-10-512-109-27	Sequence 27, Appl
866	54.5	3.1	585	7	US-11-074-176-190	Sequence 190, App	940	54	3.0	896	7	US-11-080-991-98	Sequence 27, Appl
867	54.5	3.1	597	6	US-10-884-730-381	Sequence 381, App	941	54	3.0	953	7	US-11-057-058-56	Sequence 56, Appl
868	54.5	3.1	700	6	US-10-995-561-922	Sequence 922, App	942	54	3.0	1041	6	US-10-995-561-780	Sequence 780, App
869	54.5	3.1	700	6	US-10-995-561-924	Sequence 924, App	943	54	3.0	1041	6	US-10-995-561-782	Sequence 782, App
870	54.5	3.1	700	6	US-11-196-475-74	Sequence 74, Appl	944	54	3.0	1122	6	US-10-821-234-1657	Sequence 1657, Ap
871	54.5	3.1	746	6	US-10-793-626-652	Sequence 652, App	946	54	3.0	1531	7	US-11-087-227-24	Sequence 24, Appl
872	54.5	3.1	781	7	US-11-194-246-344	Sequence 344, App	947	54	3.0	1531	7	US-11-186-284-211	Sequence 211, App
873	54.5	3.1	793	6	US-10-995-561-925	Sequence 925, App	948	54	3.0	1596	7	US-11-060-005-4	Sequence 4, Appl
874	54.5	3.1	816	7	US-11-090-439-48	Sequence 48, Appl	949	54	3.0	4128	6	US-10-770-726-77	Sequence 77, Appl
875	54.5	3.1	862	7	US-11-128-420-11	Sequence 11, Appl	950	54	3.0	7968	7	US-11-143-980-49	Sequence 49, Appl
876	54.5	3.1	865	6	US-10-467-962B-33	Sequence 33, Appl	951	53.5	3.0	99	7	US-11-084-554-206	Sequence 206, App
877	54.5	3.1	984	7	US-11-113-424-60	Sequence 60, Appl	952	53.5	3.0	108	6	US-10-925-366A-149	Sequence 149, App
879	54.5	3.1	1042	7	US-11-067-811-1	Sequence 1, Appl	953	53.5	3.0	120	7	US-11-102-201-1	Sequence 1, Appl
880	54.5	3.1	1096	6	US-10-995-561-710	Sequence 710, App	954	53.5	3.0	217	7	US-11-128-440-11	Sequence 11, Appl
881	54.5	3.1	1311	6	US-10-509-422-5	Sequence 4, Appl	955	53.5	3.0	218	7	US-11-188-281-6	Sequence 6, Appl
882	54.5	3.1	2256	7	US-11-144-368-4	Sequence 4, Appl	956	53.5	3.0	218	7	US-11-188-281-17	Sequence 17, Appl
883	54	3.0	91	7	US-11-075-351-58	Sequence 58, Appl	957	53.5	3.0	221	6	US-10-793-626-2216	Sequence 2216, Ap
884	54	3.0	97	7	US-11-054-669-52	Sequence 52, Appl	958	53.5	3.0	234	6	US-10-821-234-1515	Sequence 3, Appl
885	54	3.0	109	7	US-11-053-076-20	Sequence 20, Appl	959	53.5	3.0	247	7	US-11-054-515-2072	Sequence 2072, Ap
886	54	3.0	119	6	US-10-467-657-5240	Sequence 5240, Ap	960	53.5	3.0	248	7	US-11-054-515-1456	Sequence 1456, Ap
887	54	3.0	128	7	US-11-096-074-24	Sequence 24, Appl	961	53.5	3.0	248	7	US-11-054-515-1890	Sequence 1890, Ap
888	54	3.0	129	6	US-10-967-527A-11	Sequence 11, Appl	962	53.5	3.0	248	7	US-11-054-515-1921	Sequence 321, App
889	54	3.0	136	6	US-10-839-799-29	Sequence 29, Appl	963	53.5	3.0	249	7	US-11-054-515-246	Sequence 346, App
890	54	3.0	159	7	US-11-132-285-7	Sequence 7, Appl	964	53.5	3.0	249	7	US-11-054-515-454	Sequence 454, App
891	54	3.0	199	6	US-10-793-626-1342	Sequence 1342, Ap	965	53.5	3.0	249	7	US-11-054-515-410	Sequence 410, App
892	54	3.0	226	7	US-11-132-285-5	Sequence 5, Appl	966	53.5	3.0	249	7	US-11-054-515-420	Sequence 420, App
893	54	3.0	232	6	US-10-510-386-116	Sequence 116, App	967	53.5	3.0	249	7	US-11-054-515-462	Sequence 466, App
894	54	3.0	236	7	US-11-139-499-10	Sequence 10, Appl	968	53.5	3.0	249	7	US-11-054-515-496	Sequence 499, App
895	54	3.0	241	6	US-10-467-657-1400	Sequence 1400, Ap	969	53.5	3.0	249	7	US-11-054-515-542	Sequence 542, App
896	54	3.0	244	7	US-11-054-515-1513	Sequence 1513, Ap	970	53.5	3.0	249	7	US-11-054-515-703	Sequence 703, App
897	54	3.0	244	7	US-11-054-515-1524	Sequence 1524, Ap	971	53.5	3.0	249	7	US-11-054-515-753	Sequence 753, App
898	54	3.0	248	7	US-11-054-515-1705	Sequence 1705, Ap	972	53.5	3.0	251	7	US-11-054-515-1023	Sequence 1023, Ap
899	54	3.0	249	7	US-11-054-515-462	Sequence 462, App	973	53.5	3.0	251	7	US-11-054-515-1162	Sequence 1162, Ap
900	54	3.0	249	7	US-11-054-515-519	Sequence 519, App	974	53.5	3.0	252	6	US-10-512-184-28	Sequence 28, Appl
901	54	3.0	249	7	US-11-054-515-570	Sequence 570, App	975	53.5	3.0	254	7	US-11-054-515-977	Sequence 977, App
902	54	3.0	249	7	US-11-054-515-700	Sequence 700, App	976	53.5	3.0	255	7	US-11-054-515-1153	Sequence 1153, Ap
903	54	3.0	249	7	US-11-054-515-708	Sequence 708, App	977	53.5	3.0	258	7	US-11-054-515-2090	Sequence 2090, Ap
904	54	3.0	249	7	US-11-113-424-30	Sequence 30, Appl	978	53.5	3.0	266	7	US-11-082-544-10	Sequence 10, Appl
905	54	3.0	251	6	US-10-793-626-3050	Sequence 3050, Ap	979	53.5	3.0	281	6	US-10-821-234-1288	Sequence 1288, Ap
906	54	3.0	251	7	US-11-054-515-123	Sequence 123, App	980	53.5	3.0	283	7	US-11-008-331-6	Sequence 6, Appl
907	54	3.0	251	7	US-11-054-515-252	Sequence 252, App	981	53.5	3.0	290	7	US-11-113-424-77	Sequence 77, Appl
908	54	3.0	252	7	US-11-054-515-1164	Sequence 1164, Ap	982	53.5	3.0	310	7	US-11-000-463-357	Sequence 357, App
909	54	3.0	253	7	US-11-054-515-1987	Sequence 1987, Ap	983	53.5	3.0	322	6	US-10-793-626-1912	Sequence 1912, Ap
910	54	3.0	256	7	US-11-054-515-1253	Sequence 1253, Ap	984	53.5	3.0	322	6	US-11-109-156-33	Sequence 33, Appl
911	54	3.0	256	7	US-11-054-515-1693	Sequence 1693, Ap	985	53.5	3.0	332	6	US-10-793-626-2562	Sequence 2562, Ap
912	54	3.0	265	6	US-10-467-657-5000	Sequence 5000, Ap	986	53.5	3.0	338	6	US-10-878-556A-19	Sequence 19, Appl
913	54	3.0	269	6	US-10-467-657-7302	Sequence 7302, Ap	987	53.5	3.0	391	7	US-11-105-172-4	Sequence 4, Appl
914	54	3.0	296	6	US-10-510-386-58	Sequence 58, Appl	988	53.5	3.0	398	6	US-10-821-234-1583	Sequence 1583, Ap
915	54	3.0	303	6	US-10-467-962B-16	Sequence 16, Appl	989	53.5	3.0	402	7	US-11-174-150-47	Sequence 47, Appl
916	54	3.0	303	6	US-10-467-962B-45	Sequence 45, Appl	990	53.5	3.0	413	7	US-11-060-029-4	Sequence 4, Appl
917	54	3.0	353	7	US-11-067-884-6	Sequence 6, Appl	991	53.5	3.0	436	7	US-11-080-991-102	Sequence 102, App
918	54	3.0	354	6	US-10-821-234-1618	Sequence 1618, Ap	992	53.5	3.0	441	6	US-10-510-386-162	Sequence 162, App
919	54	3.0	376	6	US-10-485-517-218	Sequence 218, App	993	53.5	3.0	455	6	US-10-847-867-32	Sequence 32, Appl
920	54	3.0	384	6	US-10-999-866-33	Sequence 33, Appl	994	53.5	3.0	467	6	US-10-510-386-56	Sequence 56, Appl
921	54	3.0	384	7	US-11-061-882-33	Sequence 33, Appl	995	53.5	3.0	490	7	US-11-066-642-23	Sequence 23, Appl
922	54	3.0	397	7	US-11-192-219-47	Sequence 47, Appl	996	53.5	3.0	564	6	US-10-485-517-98	Sequence 298, App
923	54	3.0	431	7	US-11-092-140-6	Sequence 6, Appl	997	53.5	3.0	579	6	US-10-528-673-2	Sequence 2, Appl
924	54	3.0	443	6	US-10-467-657-5762	Sequence 5762, Ap	998	53.5	3.0	693	6	US-11-196-475-72	Sequence 72, Appl
925	54	3.0	479	7	US-11-024-251-33	Sequence 33, Appl	999	53.5	3.0	915	7	US-11-144-987-16	Sequence 16, Appl
926	54	3.0	491	6	US-10-793-626-2808	Sequence 2808, Ap	1000	53.5	3.0	917	7	US-11-144-987-18	Sequence 18, Appl
927	54	3.0	493	7	US-11-067-121-10	Sequence 10, Appl	1001	53.5	3.0	985	7	US-11-113-424-61	Sequence 61, Appl
928	54	3.0	520	6	US-10-508-252-26	Sequence 26, Appl	1002	53.5	3.0	1070	7	US-11-000-463-721	Sequence 721, App
929	54	3.0	520	6	US-10-878-556A-38	Sequence 38, Appl	1003	53.5	3.0	1137	7	US-11-012-762-70	Sequence 70, Appl
930	54	3.0	522	6	US-10-793-626-456	Sequence 456, App	1004	53.5	3.0	1167	6	US-10-601-368-18	Sequence 18, Appl
931	54	3.0	522	6	US-10-793-626-2042	Sequence 2042, Ap	1005	53.5	3.0				



1006	53.5	3.0	1194	7	US-11-000-463-249	Sequence 249, App	1079	53	3.0	433	7	US-11-074-176-162	Sequence 162, App
1007	53.5	3.0	1206	6	US-10-467-657-72	Sequence 72, Appl	1080	53	3.0	450	7	US-11-025-712-12	Sequence 12, Appl
1008	53.5	3.0	1206	6	US-10-467-657-3892	Sequence 3892, Ap	1081	53	3.0	461	7	US-11-082-389-176	Sequence 176, App
1009	53.5	3.0	1210	7	US-11-108-172-692	Sequence 692, App	1082	53	3.0	474	6	US-10-467-657-5978	Sequence 5978, Ap
1010	53.5	3.0	1234	7	US-10-995-561-870	Sequence 870, App	1083	53	3.0	476	6	US-10-467-657-7518	Sequence 7518, Ap
1011	53.5	3.0	1365	6	US-10-995-561-867	Sequence 867, App	1084	53	3.0	475	6	US-10-510-386-98	Sequence 98, Appl
1012	53.5	3.0	1366	6	US-10-995-561-868	Sequence 868, App	1085	53	3.0	491	7	US-11-098-662-14	Sequence 14, Appl
1013	53.5	3.0	1366	6	US-10-995-561-868	Sequence 868, App	1086	53	3.0	491	7	US-11-165-141-2	Sequence 2, Appl1
1014	53.5	3.0	1411	6	US-10-995-561-869	Sequence 869, App	1087	53	3.0	540	6	US-10-770-726-80	Sequence 80, Appl1
1015	53.5	3.0	1437	7	US-11-074-176-96	Sequence 96, App	1088	53	3.0	567	6	US-10-420-192-8	Sequence 8, Appl1
1016	53.5	3.0	1548	7	US-11-108-172-1095	Sequence 1095, Ap	1089	53	3.0	591	6	US-10-510-386-22	Sequence 22, Appl
1017	53.5	3.0	1992	7	US-11-013-759-13	Sequence 3, Appl1	1090	53	3.0	609	6	US-10-821-234-1611	Sequence 1611, Ap
1018	53.5	3.0	1992	7	US-11-013-759-13	Sequence 13, Appl1	1092	53	3.0	653	7	US-11-135-855-25	Sequence 25, Appl
1019	53.5	3.0	2047	7	US-11-013-759-4	Sequence 4, Appl1	1094	53	3.0	688	7	US-11-113-424-48	Sequence 48, Appl
1020	53.5	3.0	2047	7	US-11-013-759-7	Sequence 7, Appl1	1095	53	3.0	688	7	US-11-113-424-48	Sequence 49, Appl
1021	53.5	3.0	2107	6	US-10-995-561-827	Sequence 827, App	1096	53	3.0	688	7	US-11-113-424-48	Sequence 140, App
1022	53.5	3.0	2480	6	US-10-995-561-825	Sequence 825, App	1097	53	3.0	694	7	US-11-074-176-150	Sequence 150, App
1023	53.5	3.0	2647	6	US-10-821-234-1303	Sequence 1303, Ap	1098	53	3.0	697	7	US-11-074-176-150	Sequence 66, Appl
1024	53.5	3.0	3116	6	US-10-995-561-826	Sequence 826, App	1099	53	3.0	700	7	US-11-196-475-66	Sequence 26, Appl
1025	53.5	3.0	3433	6	US-10-714-781A-67	Sequence 67, Appl	1100	53	3.0	751	7	US-11-012-762-26	Sequence 103, App
1026	53	3.0	97	7	US-11-144-248-36	Sequence 36, Appl	1101	53	3.0	786	6	US-10-467-962B-103	Sequence 83, Appl
1027	53	3.0	97	7	US-11-054-669-42	Sequence 42, Appl	1102	53	3.0	841	6	US-10-770-726-88	Sequence 134, App
1028	53	3.0	97	7	US-11-084-554-54	Sequence 54, Appl	1103	53	3.0	1189	7	US-11-074-176-134	Sequence 89, App
1029	53	3.0	99	7	US-11-084-554-208	Sequence 208, App	1104	53	3.0	1375	6	US-10-995-561-809	Sequence 809, App
1030	53	3.0	107	6	US-10-793-626-1586	Sequence 1586, Ap	1105	53	3.0	2432	6	US-10-932-334-61	Sequence 61, Appl
1031	53	3.0	108	6	US-10-473-037-50	Sequence 50, Appl	1106	52.5	3.0	113	6	US-10-932-334-61	Sequence 83, Appl
1032	53	3.0	108	6	US-10-999-866-6	Sequence 6, Appl1	1107	52.5	3.0	117	6	US-11-012-353-53	Sequence 5, Appl1
1033	53	3.0	108	7	US-11-061-821-6	Sequence 6, Appl1	1108	52.5	3.0	132	6	US-10-789-273-5	Sequence 11, Appl
1034	53	3.0	118	6	US-10-932-334-75	Sequence 75, Appl	1109	52.5	3.0	143	6	US-10-789-273-11	Sequence 8684, Ap
1035	53	3.0	120	6	US-11-173-071-2	Sequence 2, Appl1	1110	52.5	3.0	168	7	US-11-020-772-35	Sequence 35, Appl
1036	53	3.0	128	6	US-10-473-037-2	Sequence 2, Appl1	1111	52.5	3.0	213	7	US-11-174-186-42	Sequence 42, Appl
1037	53	3.0	184	6	US-10-742-634-9	Sequence 9, Appl1	1112	52.5	3.0	225	6	US-11-209-208-1	Sequence 1, Appl1
1038	53	3.0	184	6	US-10-967-527A-8	Sequence 8, Appl1	1113	52.5	3.0	225	6	US-11-209-208-4	Sequence 20, Appl1
1039	53	3.0	199	6	US-10-467-657-2368	Sequence 2368, Ap	1114	52.5	3.0	225	6	US-10-209-208-10	Sequence 40, Appl1
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1041	53	3.0	248	7	US-11-054-515-895	Sequence 895, App	1116	52.5	3.0	226	7	US-11-170-653-63	Sequence 28, Appl
1042	53	3.0	248	7	US-11-054-515-970	Sequence 970, App	1117	52.5	3.0	233	7	US-11-170-653-28	Sequence 418, App
1043	53	3.0	249	7	US-11-054-515-310	Sequence 310, App	1118	52.5	3.0	236	7	US-11-022-289-12	Sequence 12, Appl
1044	53	3.0	249	7	US-11-054-515-485	Sequence 485, App	1119	52.5	3.0	238	6	US-10-995-561-725	Sequence 725, App
1045	53	3.0	249	7	US-11-054-515-588	Sequence 588, App	1120	52.5	3.0	249	7	US-11-054-515-637	Sequence 637, App
1046	53	3.0	249	7	US-11-054-515-612	Sequence 612, App	1121	52.5	3.0	249	7	US-11-054-515-638	Sequence 433, App
1047	53	3.0	249	7	US-11-054-515-640	Sequence 640, App	1122	52.5	3.0	248	7	US-11-054-515-1991	Sequence 506, App
1048	53	3.0	249	7	US-11-054-515-740	Sequence 740, App	1123	52.5	3.0	249	7	US-11-054-515-406	Sequence 540, App
1049	53	3.0	250	7	US-11-054-515-1142	Sequence 1142, Ap	1124	52.5	3.0	249	7	US-11-054-515-412	Sequence 412, App
1050	53	3.0	251	7	US-11-054-515-1851	Sequence 1851, Ap	1125	52.5	3.0	249	7	US-11-054-515-418	Sequence 418, App
1051	53	3.0	251	7	US-11-054-515-118	Sequence 118, App	1126	52.5	3.0	249	7	US-11-054-515-433	Sequence 433, App
1052	53	3.0	251	7	US-11-054-515-209	Sequence 209, App	1127	52.5	3.0	249	7	US-11-054-515-438	Sequence 438, App
1053	53	3.0	251	7	US-11-054-515-270	Sequence 270, App	1128	52.5	3.0	249	7	US-11-054-515-506	Sequence 506, App
1054	53	3.0	251	7	US-11-054-515-288	Sequence 288, App	1129	52.5	3.0	249	7	US-11-054-515-540	Sequence 540, App
1055	53	3.0	251	7	US-11-054-515-1542	Sequence 1542, Ap	1130	52.5	3.0	249	7	US-11-054-515-599	Sequence 599, App
1056	53	3.0	252	6	US-10-485-517-156	Sequence 156, App	1131	52.5	3.0	249	7	US-11-054-515-637	Sequence 637, App
1057	53	3.0	252	6	US-10-467-657-276	Sequence 276, App	1132	52.5	3.0	249	7	US-11-054-515-747	Sequence 747, App
1058	53	3.0	252	6	US-10-467-657-4008	Sequence 4008, Ap	1133	52.5	3.0	249	7	US-11-054-515-829	Sequence 829, App
1059	53	3.0	252	7	US-11-054-515-1201	Sequence 1201, Ap	1134	52.5	3.0	249	7	US-11-054-515-833	Sequence 833, App
1060	53	3.0	252	7	US-11-054-515-1994	Sequence 1994, Ap	1135	52.5	3.0	253	6	US-11-054-515-1530	Sequence 1530, Ap
1061	53	3.0	253	7	US-11-054-515-1000	Sequence 1000, Ap	1136	52.5	3.0	256	7	US-11-054-515-1015	Sequence 1015, Ap
1062	53	3.0	253	7	US-11-054-515-1042	Sequence 1042, Ap	1137	52.5	3.0	257	7	US-11-054-515-1596	Sequence 1596, Ap
1063	53	3.0	259	7	US-11-054-515-1260	Sequence 1260, Ap	1138	52.5	3.0	265	6	US-10-995-561-724	Sequence 724, App
1064	53	3.0	259	7	US-11-054-515-864	Sequence 864, App	1139	52.5	3.0	265	6	US-10-995-561-733	Sequence 733, App
1065	53	3.0	259	7	US-11-054-515-1025	Sequence 1025, App	1140	52.5	3.0	273	6	US-11-113-424-75	Sequence 75, Appl
1066	53	3.0	260	7	US-11-054-515-1262	Sequence 1262, Ap	1141	52.5	3.0	286	7	US-10-878-556A-120	Sequence 120, App
1067	53	3.0	260	7	US-11-054-515-1244	Sequence 1244, Ap	1142	52.5	3.0	286	7	US-11-089-551A-17	Sequence 17, Appl
1068	53	3.0	283	7	US-11-087-072-2	Sequence 2, Appl1	1143	52.5	3.0	310	7	US-11-025-834A-15	Sequence 15, Appl
1069	53	3.0	288	6	US-10-467-657-1870	Sequence 1870, Ap	1144	52.5	3.0	312	7	US-11-055-822-16	Sequence 16, Appl
1070	53	3.0	307	7	US-11-053-185-20	Sequence 20, Appl	1145	52.5	3.0	325	7	US-11-074-176-368	Sequence 368, App
1071	53	3.0	330	6	US-11-085-812-2	Sequence 2, Appl1	1146	52.5	3.0	358	7	US-11-095-624-6	Sequence 6, Appl1
1072	53	3.0	332	6	US-10-467-657-3868	Sequence 3868, Ap	1147	52.5	3.0	362	6	US-10-821-234-1148	Sequence 1148, Ap
1073	53	3.0	347	7	US-10-467-657-7154	Sequence 7154, App	1148	52.5	3.0	374	7	US-11-000-463-453	Sequence 453, App
1074	53	3.0	360	7	US-11-186-284-226	Sequence 226, App	1149	52.5	3.0				
1075	53	3.0	360	7	US-11-082-389-90	Sequence 90, Appl	1150	52.5	3.0				
1076	53	3.0	428	6	US-10-793-626-484	Sequence 92, Appl	1151	52.5	3.0				
1077	53	3.0	428	7	US-11-074-176-344	Sequence 484, App	1152	52.5	3.0				
1078	53	3.0	432	7	US-11-056-354-4	Sequence 344, App	1153	52.5	3.0				
						Sequence 4, Appl1	1154	52.5	3.0				
							1155	52.5	3.0				



1156	52.5	3.0	381	6	US-10-510-386-168	Sequence 168, App	1230	52	2.9	250	7	US-11-054-515-1017	Sequence 1017, Ap
1157	52.5	3.0	382	6	US-10-392-234A-55	Sequence 65, Appl	1231	52	2.9	250	7	US-11-054-515-1563	Sequence 1563, Ap
1158	52.5	3.0	413	6	US-10-821-234-989	Sequence 989, App	1232	52	2.9	250	7	US-11-054-515-1564	Sequence 1564, Ap
1159	52.5	3.0	416	7	US-11-061-863-18	Sequence 18, Appl	1233	52	2.9	250	7	US-11-054-515-1574	Sequence 1574, Ap
1160	52.5	3.0	422	7	US-11-055-822-626	Sequence 626, App	1234	52	2.9	252	7	US-11-054-515-1874	Sequence 1874, Ap
1161	52.5	3.0	429	6	US-10-793-628-3174	Sequence 3174, App	1235	52	2.9	252	7	US-11-054-515-1954	Sequence 1954, Ap
1162	52.5	3.0	442	6	US-10-821-234-1594	Sequence 1594, Ap	1236	52	2.9	253	7	US-11-054-515-1349	Sequence 1349, Ap
1163	52.5	3.0	443	7	US-11-054-385-4	Sequence 4, Appl1	1237	52	2.9	253	7	US-11-054-515-1848	Sequence 1848, Ap
1164	52.5	3.0	447	6	US-10-967-527A-14	Sequence 14, Appl	1238	52	2.9	254	7	US-11-054-515-173	Sequence 873, App
1165	52.5	3.0	466	7	US-11-102-240-104	Sequence 104, App	1239	52	2.9	254	7	US-11-054-515-888	Sequence 888, App
1166	52.5	3.0	494	6	US-10-467-657-4376	Sequence 4376, Ap	1240	52	2.9	254	7	US-11-054-515-1087	Sequence 1087, App
1167	52.5	3.0	499	6	US-10-508-263-94	Sequence 94, Appl	1241	52	2.9	254	7	US-11-054-515-1186	Sequence 1186, Ap
1168	52.5	3.0	503	7	US-11-113-424-72	Sequence 72, Appl	1242	52	2.9	254	7	US-11-067-373-784	Sequence 784, App
1169	52.5	3.0	524	6	US-10-507-106-4	Sequence 4, Appl1	1243	52	2.9	258	7	US-11-054-515-1716	Sequence 1716, Ap
1170	52.5	3.0	541	7	US-11-000-463-238	Sequence 238, App	1244	52	2.9	258	7	US-11-054-515-1083	Sequence 2083, Ap
1172	52.5	3.0	570	7	US-11-113-424-69	Sequence 69, Appl	1245	52	2.9	267	6	US-10-623-155-352	Sequence 352, App
1173	52.5	3.0	570	7	US-11-113-424-71	Sequence 71, Appl	1246	52	2.9	278	6	US-10-957-569-55	Sequence 45, Appl
1174	52.5	3.0	620	7	US-11-113-424-70	Sequence 70, Appl	1247	52	2.9	284	6	US-10-467-657-536	Sequence 536, App
1175	52.5	3.0	638	6	US-10-995-561-1025	Sequence 1025, Ap	1248	52	2.9	295	7	US-11-143-980-31	Sequence 31, Appl
1176	52.5	3.0	693	7	US-11-167-856-2	Sequence 2, Appl1	1249	52	2.9	301	6	US-10-793-626-206	Sequence 206, App
1177	52.5	3.0	720	7	US-11-113-424-28	Sequence 28, Appl	1250	52	2.9	319	6	US-10-493-210A-1	Sequence 1, Appl1
1178	52.5	3.0	743	6	US-10-467-657-4082	Sequence 4082, Ap	1251	52	2.9	319	6	US-10-793-626-192	Sequence 792, App
1179	52.5	3.0	747	7	US-11-113-424-26	Sequence 26, Appl	1252	52	2.9	319	6	US-10-793-626-208	Sequence 208, Ap
1180	52.5	3.0	826	7	US-11-055-822-214	Sequence 214, App	1253	52	2.9	333	6	US-10-846-172A-6	Sequence 6, Appl1
1181	52.5	3.0	826	7	US-11-055-822-712	Sequence 712, App	1254	52	2.9	348	6	US-10-821-234-1614	Sequence 1614, Ap
1182	52.5	3.0	833	7	US-11-055-822-212	Sequence 212, App	1255	52	2.9	348	6	US-10-857-780-24	Sequence 24, Appl
1183	52.5	3.0	833	7	US-11-055-822-710	Sequence 710, App	1256	52	2.9	359	6	US-10-467-657-1676	Sequence 1676, Ap
1184	52.5	3.0	912	7	US-11-042-988-12	Sequence 12, Appl	1258	52	2.9	377	7	US-11-152-892-8	Sequence 8, Appl1
1185	52.5	3.0	922	7	US-11-115-086-9	Sequence 9, Appl1	1259	52	2.9	390	7	US-11-184-380-2	Sequence 2, Appl1
1186	52.5	3.0	1121	7	US-11-113-751-13	Sequence 13, Appl	1260	52	2.9	397	6	US-10-467-657-1944	Sequence 3944, Ap
1187	52.5	3.0	1127	6	US-10-858-730-13	Sequence 13, Appl	1261	52	2.9	399	7	US-11-147-047-35	Sequence 35, Appl
1188	52.5	3.0	1144	6	US-10-467-962B-89	Sequence 89, Appl	1262	52	2.9	403	7	US-11-109-156-39	Sequence 39, Appl
1189	52.5	3.0	1159	6	US-11-113-751-27	Sequence 27, Appl	1263	52	2.9	408	7	US-11-055-822-910	Sequence 910, App
1190	52.5	3.0	1160	6	US-10-995-561-1019	Sequence 1019, Ap	1264	52	2.9	416	6	US-10-821-234-1375	Sequence 1375, Ap
1191	52.5	3.0	1221	6	US-10-858-730-222	Sequence 222, App	1265	52	2.9	421	7	US-11-055-822-366	Sequence 366, App
1192	52.5	3.0	1302	6	US-10-995-561-1024	Sequence 1024, Ap	1266	52	2.9	432	7	US-11-056-354-2	Sequence 2, Appl1
1193	52.5	3.0	1306	6	US-10-995-561-1027	Sequence 1027, Ap	1267	52	2.9	436	6	US-10-467-962B-77	Sequence 77, Appl
1194	52.5	3.0	1438	6	US-10-511-559-73	Sequence 73, Appl	1268	52	2.9	443	7	US-11-196-475-166	Sequence 166, App
1195	52.5	3.0	1467	6	US-10-507-956-1	Sequence 1, Appl1	1269	52	2.9	447	6	US-10-467-657-4836	Sequence 4836, Ap
1196	52.5	3.0	1613	7	US-11-108-528-84	Sequence 84, Appl	1270	52	2.9	465	7	US-11-037-829A-14	Sequence 904, App
1197	52.5	3.0	1614	6	US-10-821-234-903	Sequence 903, App	1271	52	2.9	467	6	US-10-821-234-904	Sequence 68, Appl
1198	52.5	3.0	2096	6	US-10-995-561-606	Sequence 606, App	1272	52	2.9	468	7	US-11-055-822-68	Sequence 2956, Ap
1199	52.5	3.0	2351	6	US-10-995-561-608	Sequence 608, App	1273	52	2.9	479	6	US-10-793-626-3956	Sequence 3956, Ap
1200	52.5	3.0	2630	7	US-11-186-731-2	Sequence 2, Appl1	1274	52	2.9	489	6	US-10-467-657-6158	Sequence 6158, Ap
1201	52.5	3.0	4384	6	US-10-821-234-1120	Sequence 1120, Ap	1275	52	2.9	561	7	US-11-029-465-12	Sequence 12, Appl
1202	52	2.9	97	7	US-11-054-669-53	Sequence 53, Appl	1276	52	2.9	562	6	US-10-507-928-10	Sequence 10, Appl
1203	52	2.9	107	7	US-11-105-268-18	Sequence 18, Appl	1277	52	2.9	562	6	US-10-507-928-12	Sequence 12, Appl
1204	52	2.9	115	6	US-10-467-657-480	Sequence 490, App	1278	52	2.9	562	7	US-11-029-465-10	Sequence 30, Appl
1205	52	2.9	120	6	US-10-932-334-71	Sequence 71, Appl	1279	52	2.9	567	7	US-11-167-856-30	Sequence 30, Appl
1206	52	2.9	120	6	US-10-932-334-72	Sequence 72, Appl	1280	52	2.9	574	6	US-10-518-341-1	Sequence 1, Appl1
1207	52	2.9	154	6	US-10-721-763-25	Sequence 25, Appl	1281	52	2.9	574	7	US-11-022-562-214	Sequence 214, App
1208	52	2.9	169	6	US-10-467-657-784	Sequence 784, App	1282	52	2.9	584	7	US-11-045-802-91	Sequence 91, Appl
1209	52	2.9	200	7	US-11-055-822-1022	Sequence 1022, Ap	1283	52	2.9	588	6	US-10-821-234-1137	Sequence 1137, Ap
1210	52	2.9	204	7	US-11-128-440-3	Sequence 3, Appl1	1284	52	2.9	588	7	US-11-196-475-122	Sequence 122, App
1211	52	2.9	220	6	US-10-965-972-3	Sequence 3, Appl1	1285	52	2.9	610	7	US-11-184-380-3	Sequence 3, Appl1
1212	52	2.9	231	6	US-10-467-657-4662	Sequence 4662, Ap	1286	52	2.9	621	6	US-10-632-150-28	Sequence 28, Appl
1213	52	2.9	232	7	US-11-000-463-343	Sequence 343, App	1287	52	2.9	621	7	US-11-073-457-18	Sequence 28, Appl
1214	52	2.9	246	7	US-11-054-515-1241	Sequence 1241, Ap	1288	52	2.9	621	7	US-11-073-457-28	Sequence 28, Appl
1215	52	2.9	247	7	US-11-113-424-76	Sequence 76, Appl	1289	52	2.9	655	7	US-11-045-802-39	Sequence 29, Appl
1216	52	2.9	248	7	US-11-054-515-1816	Sequence 1816, Ap	1290	52	2.9	687	6	US-10-485-517-274	Sequence 274, App
1217	52	2.9	248	7	US-11-054-515-1955	Sequence 1955, Ap	1291	52	2.9	693	7	US-11-196-475-68	Sequence 68, Appl
1218	52	2.9	248	7	US-11-054-515-2091	Sequence 2091, Ap	1292	52	2.9	698	6	US-10-995-561-339	Sequence 939, App
1219	52	2.9	249	7	US-11-054-515-402	Sequence 402, App	1293	52	2.9	721	7	US-11-060-920-5	Sequence 5, Appl1
1220	52	2.9	249	7	US-11-054-515-536	Sequence 536, App	1294	52	2.9	725	6	US-10-995-561-938	Sequence 938, App
1221	52	2.9	249	7	US-11-054-515-689	Sequence 689, App	1295	52	2.9	732	6	US-10-467-657-8888	Sequence 888, Ap
1222	52	2.9	249	7	US-11-054-515-707	Sequence 707, App	1296	52	2.9	757	7	US-11-110-082-35	Sequence 35, Appl
1223	52	2.9	249	7	US-11-054-515-729	Sequence 722, App	1297	52	2.9	761	7	US-11-110-082-224	Sequence 24, Appl
1224	52	2.9	249	7	US-11-054-515-789	Sequence 789, App	1298	52	2.9	792	7	US-11-088-686-39	Sequence 39, Appl
1225	52	2.9	249	7	US-11-054-515-1570	Sequence 1570, Ap	1299	52	2.9	824	6	US-10-957-569-31	Sequence 31, Appl
1226	52	2.9	249	7	US-11-054-515-1618	Sequence 1618, Ap	1300	52	2.9	858	6	US-10-645-441-35	Sequence 35, Appl
1227	52	2.9	249	7	US-11-054-515-1838	Sequence 1838, Ap	1301	52	2.9	866	7	US-11-147-047-32	Sequence 32, Appl
1228	52	2.9	250	7	US-11-054-515-942	Sequence 942, App	1302	52	2.9	902	7	US-11-144-987-12	Sequence 12, Appl
1229	52	2.9	250	7	US-11-054-515-964	Sequence 964, App	1303	52	2.9	902	7	US-11-144-987-14	Sequence 14, Appl



1304	52	2.9	980	7	US-11-064-246-10	Sequence 10, Appl	1378	51.5	2.9	376	7	US-11-055-822-422	Sequence 422, Appl
1305	52	2.9	1018	7	US-11-067-121-17	Sequence 17, Appl	1379	51.5	2.9	380	6	US-10-624-932-22	Sequence 22, Appl
1307	52	2.9	1410	6	US-10-858-730-208	Sequence 108, App	1379	51.5	2.9	389	7	US-11-129-143-82	Sequence 82, Appl
1308	52	2.9	1151	6	US-10-793-626-2448	Sequence 2448, Ap	1381	51.5	2.9	395	7	US-11-053-185-8	Sequence 8, Appl1
1309	52	2.9	1167	6	US-10-601-368-4	Sequence 4, Appl1	1382	51.5	2.9	404	6	US-10-793-626-1204	Sequence 1204, Ap
1310	52	2.9	1167	6	US-10-942-072-13	Sequence 13, Appl	1383	51.5	2.9	419	6	US-10-821-234-1556	Sequence 1556, Ap
1311	52	2.9	1167	6	US-11-097-125-2	Sequence 2, Appl1	1385	51.5	2.9	445	7	US-11-074-176-182	Sequence 182, App
1312	52	2.9	1168	6	US-10-942-072-11	Sequence 11, Appl	1387	51.5	2.9	468	7	US-11-102-240-150	Sequence 150, App
1313	52	2.9	1188	6	US-10-601-368-3	Sequence 3, Appl1	1388	51.5	2.9	474	7	US-11-037-829A-13	Sequence 13, Appl
1314	52	2.9	1188	6	US-11-000-463-338	Sequence 338, App	1389	51.5	2.9	483	7	US-11-113-424-34	Sequence 24, Appl
1315	52	2.9	1188	7	US-11-000-463-810	Sequence 810, Appl	1390	51.5	2.9	492	6	US-10-467-657-1804	Sequence 1804, Ap
1316	52	2.9	1360	7	US-11-188-743-22	Sequence 22, Appl	1391	51.5	2.9	497	6	US-10-763-712A-24	Sequence 24, Appl
1317	52	2.9	1387	7	US-11-077-386-26	Sequence 26, Appl	1392	51.5	2.9	497	6	US-10-763-712A-91	Sequence 91, Appl
1318	52	2.9	1406	6	US-10-995-561-530	Sequence 530, App	1393	51.5	2.9	518	7	US-11-055-822-420	Sequence 420, App
1319	52	2.9	1481	7	US-11-077-386-30	Sequence 30, Appl	1394	51.5	2.9	524	7	US-11-113-424-64	Sequence 64, App
1320	52	2.9	1637	6	US-10-821-234-1204	Sequence 1204, Ap	1395	51.5	2.9	547	6	US-10-995-561-785	Sequence 785, App
1321	52	2.9	1827	7	US-11-057-056-62	Sequence 62, Appl	1396	51.5	2.9	547	6	US-10-995-561-787	Sequence 787, App
1322	52	2.9	2657	6	US-10-821-234-1262	Sequence 1262, Ap	1397	51.5	2.9	553	7	US-11-090-439-18	Sequence 18, Appl
1323	52	2.9	3803	6	US-10-995-561-773	Sequence 773, App	1398	51.5	2.9	583	6	US-10-793-626-1358	Sequence 1358, Ap
1324	52	2.9	3960	6	US-10-995-561-771	Sequence 771, App	1399	51.5	2.9	591	7	US-11-082-389-386	Sequence 386, App
1325	51.5	2.9	98	7	US-11-144-248-34	Sequence 34, Appl	1400	51.5	2.9	614	7	US-11-126-841A-2	Sequence 2, Appl1
1326	51.5	2.9	98	7	US-11-054-669-34	Sequence 34, Appl	1401	51.5	2.9	614	7	US-11-126-841A-13	Sequence 13, Appl
1327	51.5	2.9	99	7	US-11-054-669-37	Sequence 37, Appl	1402	51.5	2.9	646	6	US-10-995-561-695	Sequence 695, App
1328	51.5	2.9	100	6	US-10-789-227-7	Sequence 7, Appl1	1403	51.5	2.9	651	6	US-10-821-234-1666	Sequence 1666, Ap
1329	51.5	2.9	100	6	US-11-012-353-59	Sequence 59, Appl	1404	51.5	2.9	759	6	US-10-467-657-4186	Sequence 4186, Ap
1330	51.5	2.9	100	7	US-11-054-669-78	Sequence 78, Appl	1405	51.5	2.9	870	7	US-11-082-389-384	Sequence 384, App
1331	51.5	2.9	100	7	US-11-054-669-79	Sequence 79, Appl	1406	51.5	2.9	871	6	US-10-933-025-3	Sequence 3, Appl1
1332	51.5	2.9	100	7	US-11-054-669-80	Sequence 80, Appl	1407	51.5	2.9	979	6	US-10-636-320-6	Sequence 6, Appl1
1333	51.5	2.9	100	7	US-11-084-554-109	Sequence 109, App	1408	51.5	2.9	1178	6	US-10-995-561-651	Sequence 85, App
1334	51.5	2.9	100	7	US-11-084-554-110	Sequence 110, App	1409	51.5	2.9	1381	6	US-10-467-657-178	Sequence 178, App
1335	51.5	2.9	101	7	US-11-084-554-115	Sequence 115, App	1410	51.5	2.9	1400	6	US-10-821-234-1045	Sequence 3726, Ap
1336	51.5	2.9	101	7	US-11-084-554-117	Sequence 117, App	1411	51.5	2.9	1463	6	US-10-971-982-3	Sequence 1045, Ap
1337	51.5	2.9	108	6	US-10-925-366A-158	Sequence 158, App	1412	51.5	2.9	1613	7	US-11-108-528-86	Sequence 86, Appl
1338	51.5	2.9	128	7	US-11-155-775-54	Sequence 54, Appl	1413	51.5	2.9	2053	7	US-11-013-759-9	Sequence 9, Appl1
1339	51.5	2.9	132	6	US-10-793-626-404	Sequence 404, App	1414	51.5	2.9	2504	7	US-10-647-956A-8	Sequence 8, Appl1
1340	51.5	2.9	142	6	US-10-763-712A-117	Sequence 117, App	1415	51.5	2.9	2725	6	US-11-113-424-52	Sequence 52, Appl
1341	51.5	2.9	212	6	US-10-793-626-1196	Sequence 1496, Ap	1416	51.5	2.9	98	7	US-11-012-353-74	Sequence 74, Appl
1342	51.5	2.9	223	7	US-11-112-882-88	Sequence 88, Appl	1417	51.5	2.9	98	7	US-11-054-669-94	Sequence 44, Appl
1343	51.5	2.9	231	7	US-11-170-653-25	Sequence 25, Appl	1418	51.5	2.9	99	7	US-11-054-669-91	Sequence 41, Appl
1344	51.5	2.9	234	7	US-11-128-440-21	Sequence 21, Appl	1419	51.5	2.9	99	7	US-11-054-669-93	Sequence 43, Appl
1345	51.5	2.9	247	7	US-11-054-515-1892	Sequence 1892, Ap	1420	51.5	2.9	99	7	US-11-054-669-94	Sequence 44, Appl
1346	51.5	2.9	248	7	US-11-054-515-1960	Sequence 1960, App	1421	51.5	2.9	99	7	US-11-084-554-52	Sequence 52, Appl
1347	51.5	2.9	249	7	US-11-054-515-408	Sequence 408, App	1422	51.5	2.9	99	7	US-11-084-554-55	Sequence 55, Appl
1348	51.5	2.9	249	7	US-11-054-515-474	Sequence 474, App	1423	51.5	2.9	106	7	US-11-144-248-26	Sequence 26, Appl
1349	51.5	2.9	249	7	US-11-054-515-617	Sequence 617, App	1424	51.5	2.9	106	7	US-11-024-251-29	Sequence 29, Appl
1350	51.5	2.9	249	7	US-11-054-515-746	Sequence 746, App	1425	51.5	2.9	107	6	US-11-165-141-17	Sequence 17, Appl
1351	51.5	2.9	249	7	US-11-054-515-831	Sequence 831, App	1426	51.5	2.9	107	6	US-10-839-799-131	Sequence 131, App
1352	51.5	2.9	250	7	US-11-054-515-963	Sequence 963, App	1427	51.5	2.9	107	6	US-10-999-866-40	Sequence 40, Appl
1353	51.5	2.9	250	7	US-11-054-515-1990	Sequence 1990, App	1428	51.5	2.9	107	7	US-11-025-712-5	Sequence 5, Appl1
1354	51.5	2.9	250	7	US-11-054-515-2073	Sequence 2073, Ap	1429	51.5	2.9	107	7	US-11-075-351-61	Sequence 61, Appl
1355	51.5	2.9	250	7	US-11-054-515-2095	Sequence 2095, Ap	1430	51.5	2.9	107	7	US-11-061-821-60	Sequence 40, Appl
1356	51.5	2.9	251	7	US-11-054-515-910	Sequence 910, App	1431	51.5	2.9	109	7	US-11-102-240-114	Sequence 114, App
1357	51.5	2.9	251	7	US-11-054-515-1459	Sequence 1459, App	1432	51.5	2.9	110	7	US-11-024-251-27	Sequence 27, Appl
1358	51.5	2.9	253	7	US-11-054-515-1664	Sequence 1364, App	1433	51.5	2.9	110	7	US-11-193-512-33	Sequence 33, Appl
1359	51.5	2.9	254	7	US-11-054-515-1266	Sequence 1266, App	1434	51.5	2.9	112	6	US-10-502-145-19	Sequence 19, Appl
1360	51.5	2.9	254	7	US-11-054-515-1302	Sequence 1302, App	1435	51.5	2.9	116	6	US-11-054-669-112	Sequence 112, App
1361	51.5	2.9	255	7	US-11-054-515-1849	Sequence 1849, App	1436	51.5	2.9	126	6	US-10-839-799-97	Sequence 87, Appl
1362	51.5	2.9	256	7	US-11-054-515-1607	Sequence 1607, App	1437	51.5	2.9	128	7	US-11-096-074-22	Sequence 22, Appl
1363	51.5	2.9	259	7	US-11-075-185-24	Sequence 24, Appl	1438	51.5	2.9	130	7	US-11-090-311-4	Sequence 4, Appl1
1364	51.5	2.9	268	6	US-10-995-561-718	Sequence 718, App	1439	51.5	2.9	132	6	US-10-468-361-22	Sequence 22, Appl
1365	51.5	2.9	271	7	US-11-091-100-17	Sequence 17, Appl	1440	51.5	2.9	138	6	US-11-090-311-8	Sequence 8, Appl1
1366	51.5	2.9	286	6	US-10-485-517-155	Sequence 155, App	1441	51.5	2.9	146	6	US-10-721-763-17	Sequence 17, Appl
1367	51.5	2.9	295	7	US-11-091-100-2	Sequence 2, Appl1	1442	51.5	2.9	159	6	US-10-689-742-130	Sequence 130, App
1368	51.5	2.9	298	6	US-10-467-657-2850	Sequence 2850, App	1443	51.5	2.9	167	6	US-10-689-742-130	Sequence 130, App
1369	51.5	2.9	298	6	US-10-467-657-6750	Sequence 6750, App	1444	51.5	2.9	177	7	US-10-793-626-1502	Sequence 1502, App
1370	51.5	2.9	298	7	US-11-085-812-4	Sequence 4, Appl1	1445	51.5	2.9	178	6	US-11-102-240-156	Sequence 156, App
1371	51.5	2.9	330	6	US-10-846-172A-7	Sequence 7, Appl1	1446	51.5	2.9	213	7	US-10-995-561-732	Sequence 732, App
1372	51.5	2.9	338	7	US-11-152-892-6	Sequence 6, Appl1	1447	51.5	2.9	213	7	US-11-172-320-4	Sequence 4, Appl1
1373	51.5	2.9	343	7	US-11-055-822-132	Sequence 132, App	1448	51.5	2.9	213	7	US-11-120-338-13	Sequence 13, Appl
1374	51.5	2.9	346	6	US-10-793-626-2514	Sequence 2514, App	1449	51.5	2.9	213	7	US-11-120-338-16	Sequence 16, Appl
1375	51.5	2.9	355	6	US-10-995-561-720	Sequence 720, App	1450	51.5	2.9	213	7	US-11-173-969-4	Sequence 4, Appl1
1376	51.5	2.9	367	6	US-10-821-234-1058	Sequence 1058, App	1451	51.5	2.9	213	7	US-11-173-969-8	Sequence 8, Appl1
1377	51.5	2.9	374	6	US-10-793-626-3096	Sequence 3096, App	1452	51.5	2.9	214	7	US-11-025-712-11	Sequence 11, Appl



1453	51	2.9	214	7	US-11-094-625-9	Sequence 9, Appli
1454	51	2.9	214	7	US-11-173-564-1	Sequence 1, Appli
1455	51	2.9	218	6	US-10-923-327-6	Sequence 6, Appli
1456	51	2.9	218	6	US-10-923-327-8	Sequence 8, Appli
1457	51	2.9	218	6	US-10-923-327-10	Sequence 10, Appli
1458	51	2.9	218	6	US-10-923-327-12	Sequence 12, Appli
1459	51	2.9	218	6	US-10-923-327-17	Sequence 17, Appli
1460	51	2.9	218	6	US-11-084-554-11	Sequence 11, Appli
1461	51	2.9	236	6	US-10-995-561-903	Sequence 903, App
1462	51	2.9	236	7	US-11-144-248-47	Sequence 47, Appl
1463	51	2.9	236	7	US-11-144-248-48	Sequence 48, Appl
1464	51	2.9	236	7	US-11-144-248-52	Sequence 52, Appl
1465	51	2.9	237	6	US-10-793-626-162	Sequence 162, App
1466	51	2.9	237	7	US-11-054-669-109	Sequence 109, App
1467	51	2.9	239	7	US-11-139-499-6	Sequence 6, Appli
1468	51	2.9	243	7	US-11-054-515-1943	Sequence 1943, Ap
1469	51	2.9	245	7	US-11-054-515-1895	Sequence 1896, Ap
1470	51	2.9	246	7	US-11-054-515-2075	Sequence 2075, Ap
1471	51	2.9	247	7	US-11-054-515-1651	Sequence 1651, Ap
1472	51	2.9	248	7	US-11-054-515-1440	Sequence 1440, Ap
1473	51	2.9	249	7	US-11-054-515-396	Sequence 396, App
1474	51	2.9	249	7	US-11-054-515-413	Sequence 413, App
1475	51	2.9	249	7	US-11-054-515-426	Sequence 426, App
1476	51	2.9	249	7	US-11-054-515-455	Sequence 455, App
1477	51	2.9	249	7	US-11-054-515-503	Sequence 503, App
1478	51	2.9	249	7	US-11-054-515-507	Sequence 507, App
1479	51	2.9	249	7	US-11-054-515-686	Sequence 686, App
1480	51	2.9	249	7	US-11-054-515-693	Sequence 693, App
1481	51	2.9	249	7	US-11-054-515-763	Sequence 763, App
1482	51	2.9	249	7	US-11-054-515-824	Sequence 824, App
1483	51	2.9	249	7	US-11-054-515-1572	Sequence 1572, Ap
1484	51	2.9	249	7	US-11-054-515-1573	Sequence 1573, Ap
1485	51	2.9	249	7	US-11-054-515-1956	Sequence 1956, Ap
1486	51	2.9	250	7	US-11-054-515-1228	Sequence 1228, Ap
1487	51	2.9	250	7	US-11-054-515-1548	Sequence 1548, Ap
1488	51	2.9	250	7	US-11-054-515-1565	Sequence 1565, Ap
1489	51	2.9	250	7	US-11-054-515-1566	Sequence 1566, Ap
1490	51	2.9	250	7	US-11-054-515-1715	Sequence 1715, Ap
1491	51	2.9	251	7	US-11-054-515-112	Sequence 112, App
1492	51	2.9	251	7	US-11-054-515-131	Sequence 131, App
1493	51	2.9	251	7	US-11-054-515-174	Sequence 174, App
1494	51	2.9	251	7	US-11-054-515-284	Sequence 284, App
1495	51	2.9	251	7	US-11-054-515-990	Sequence 990, App
1496	51	2.9	251	7	US-11-054-515-1148	Sequence 1148, Ap
1497	51	2.9	251	7	US-11-054-515-1397	Sequence 1397, Ap
1498	51	2.9	251	7	US-11-186-284-220	Sequence 220, App
1499	51	2.9	252	7	US-11-054-515-1048	Sequence 1048, App
1500	51	2.9	252	7	US-11-054-515-1208	Sequence 1208, Ap

Search completed: December 16, 2005, 11:21:27  
Job time : 20 secs



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GenCore version 5.1.6  
OM protein - protein search, using sw model ; Search time 191 Seconds  
Run on: December 16, 2005, 11:20:57 (without alignments)  
770.638 Million cell updates/sec

Title: US-10-063-549-46  
Perfect score: 335  
Sequence: 1 MAGSPROCTLITLIMQUTGS.....PHSLTMPDTPRLFAVENVI 335  
Scoring table: 011007  
Gapop 60.0 , Gapext 60.0  
Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Database : A\_Geneseq. 21:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV6701	standard;	protein;	335	AA.	
DE	Membrane-bound protein					PRO1138.
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 3;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 2						
ID	AAV70431	standard;	protein;	335	AA.	
DE	Human cell surface immunomodulator-1 (CSIMM-1).					
PN	WO200011150-A1.					
PD	02-MAR-2000.					
PA	(INCY-) INCYTE PHARM INC.					
Query Match		100.0%;	Score 335;	DB 3;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 3						
ID	AAV44609	standard;	protein;	335	AA.	
DE	Human myocardium protein-7.					
PN	WO9967387-A2.					
PD	29-DEC-1999.					
PA	(MILL-) MILLENNIUM PHARM INC.					
Query Match		100.0%;	Score 335;	DB 3;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 4						
ID	AAU29119	standard;	protein;	335	AA.	
DE	Human PRO polypeptide sequence #96.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 4;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 5						
ID	AAAB87548	standard;	protein;	335	AA.	
DE	Human PRO1138					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 4;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 6						
ID	AAAB7321	standard;	protein;	335	AA.	
DE	APBX-1.					
PN	WO200146260-A2.					
PD	28-JUN-2001.					

PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 100.0%; | Score 335; | DB 4; | Length 335; |  || Best Local Similarity | 100.0%; | Pred. No. 2.9e-314; |  |  |  |
RESULT 7						
ID	AAAB5224	standard;	protein;	335	AA.	
DE	Human PRO1138 (UNQ576) protein sequence SEQ ID NO:253.					
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 4;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 8						
ID	ABG95873	standard;	protein;	335	AA.	
DE	Human secreted/transmembrane protein PRO1138.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 5;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 9						
ID	ABU58495	standard;	protein;	335	AA.	
DE	Human PRO polypeptide #96.					
PN	US2003027272-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 10						
ID	ABU88043	standard;	protein;	335	AA.	
DE	Novel human secreted and transmembrane protein PRO1138.					
PN	US2003032127-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 11						
ID	ABU84358	standard;	protein;	335	AA.	
DE	Human secreted/transmembrane protein (PRO) #96.					
PN	US2003032112-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 12						
ID	ABR66232	standard;	protein;	335	AA.	
DE	Human secreted polypeptide PRO1138, SEQ ID NO:192.					
PN	US2003027278-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 13						
ID	ABR65622	standard;	protein;	335	AA.	
DE	Human secreted polypeptide PRO1138, SEQ ID NO:192.					
PN	US2003036159-A1.					
PD	20-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 14						
ID	ABU95952	standard;	protein;	335	AA.	
DE	Human secreted/transmembrane protein (PRO) #96.					
PN	US2003040070-A1.					
PD	27-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 15						
ID	ABU58039	standard;	protein;	335	AA.	
DE	Human PRO polypeptide #71.					
PN	US2003027163-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 16						
ID	ABU59117	standard;	protein;	335	AA.	
DE	Novel human secreted or transmembrane protein PRO1138.					
PN	US2002132252-A1.					
PD	19-SEP-2002.					



PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 17  
ID ABU82629 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 18  
ID ABU82801 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 19  
ID ABU8922 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 20  
ID ABR6171 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 21  
ID ABU60548 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, #100.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 22  
ID ABU96224 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 23  
ID ABU92655 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 24  
ID ABO08732 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 25  
ID ABO02784 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 26  
ID ABR74938 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 27  
ID ABR94700 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 28  
ID ABU13930 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 29  
ID ABU85673 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 30  
ID ABU9833 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 31  
ID ABU98048 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 32  
ID ABU91754 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 33  
ID ABU89447 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 34  
ID ABU86288 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 35  
ID ABU67501 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 36  
ID ABU80529 standard; protein; 335 AA.  
DE Human PRO protein #96.  
PN US2003036137-A1.  
PD 20-FEB-2003.



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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 37
ID ABU72515 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003005531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 38
ID ABU90898 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 39
ID ABO33957 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO138.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 40
ID ABR99447 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 41
ID ABR98837 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 42
ID ABO16360 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 43
ID ABR92260 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 44
ID ABO16901 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 45
ID ABR76322 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 46
ID ABU71974 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO138.
PD 20-FEB-2003.
PN US2003018183-A1.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 47
ID ABU85058 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 48
ID ABO00197 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 49
ID ABO11529 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 50
ID ABO02174 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 51
ID ABU88748 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 52
ID ABU83443 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 53
ID ABO06244 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 54
ID ABR59280 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 55
ID ABO09342 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 56
ID ABO19206 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036118-A1.
PD 20-FEB-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 57  
ID ABO11224 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 58  
ID ABR66842 standard; protein; 335 AA.  
DE Human secreted/polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 59  
ID ABO16055 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 60  
ID ABO13761 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 61  
ID ABU71528 standard; protein; 335 AA.  
DE Human secreted/polypeptide PRO1138.  
PN US2003033855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 62  
ID ABU65664 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, SEQ ID 192.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 63  
ID ABO07512 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 64  
ID ABO03699 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 65  
ID ABR67147 standard; protein; 335 AA.  
DE Human secreted/polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 66  
ID ABO15750 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.

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Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 67  
ID ABU56031 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, PRO1138.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 68  
ID ABU72309 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 69  
ID ABU65359 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 70  
ID ABU95304 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 71  
ID ABU71207 standard; protein; 335 AA.  
DE Human PRO1138 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 72  
ID ABO07817 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 73  
ID ABR70058 standard; protein; 335 AA.  
DE Human secreted/polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 74  
ID ABR69391 standard; protein; 335 AA.  
DE Human secreted/polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 75  
ID ABO01532 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 76  
ID ABU81334 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003017542-A1.  
PD 23-JAN-2003.



Best Local Similarity	100.0%;	Pred.	No. 2.9e-314;	
RESULT 87				
ID ABO94994 standard; protein; 335 AA.				
DE Novel human secreted and transmembrane protein PRO1138.				
FN US2003032123-A1.				
PD 13-FEB-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred.	No. 2.9e-314;	
RESULT 88				
ID ABO90542 standard; protein; 335 AA.				
DE Human secreted and transmembrane protein PRO1138.				
FN US2003032108-A1.				
PD 13-FEB-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred.	No. 2.9e-314;	
RESULT 89				
ID ABO84053 standard; protein; 335 AA.				
DE Human secreted/transmembrane protein (PRO) #96.				
FN US2003032111-A1.				
PD 13-FEB-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred.	No. 2.9e-314;	
RESULT 90				
ID ABO93704 standard; protein; 335 AA.				
DE Novel human secreted and transmembrane protein PRO1138.				
FN US2003032119-A1.				
PD 13-FEB-2003.				
PA (GENTECH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred.	No. 2.9e-314;	
RESULT 91				
ID ABO25961 standard; protein; 335 AA.				
DE Human PRO1138 polypeptide.				
FN US2002127576-A1.				
PD 12-SEP-2002.				
PA (GENTECH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335
Best Local Similarity	100.0%;	Pred.	No. 2.9e-314;	
RESULT 92				
ID ABR64949 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
FN US2003027263-A1.				
PD 06-FEB-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335
Best Local Similarity	100.0%;	Pred.	No. 2.9e-314;	
RESULT 93				
ID ABO27303 standard; protein; 335 AA.				
DE Human secreted/transmembrane polypeptide PRO138.				
FN US2003009012-A1.				
PD 09-JAN-2003.				
PA (GENTECH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred.	No. 2.9e-314;	
RESULT 94				
ID ABB68781 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
FN US2003027271-A1.				
PD 06-FEB-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335
Best Local Similarity	100.0%;	Pred.	No. 2.9e-314;	
RESULT 95				
ID ABO06597 standard; protein; 335 AA.				
DE Human secreted/transmembrane protein (PRO) #96.				
FN US2003036125-A1.				
PD 20-FEB-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335
Best Local Similarity	100.0%;	Pred.	No. 2.9e-314;	
RESULT 96				
ID ABR99142 standard; protecin; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
FN US2003040068-A1.				
PD 27-FEB-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335



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Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 97
ID ABU57026 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 98
ID ABU85978 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 99
ID ABU82265 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 100
ID ABU87276 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 101
ID ABU83748 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 102
ID ABO08122 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 103
ID ABU92498 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 104
ID ABU81833 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 105
ID ABU65997 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 106
ID ABU81168 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 107
ID ABR59626 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 108
ID ABU94014 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 109
ID ABU99867 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 110
ID ABR66537 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 111
ID ABR90955 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 112
ID ABO53283 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO138.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 113
ID ABU58970 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, #100.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 114
ID ABU94382 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 115
ID ABU79264 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 116
ID ABU86593 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
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RESULT 117
ID ABU86898 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 118
ID ABU94687 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 119
ID ABO04614 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 120
ID ABR70363 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 121
ID ABU92348 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 122
ID ABU98528 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 123
ID ABR65927 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 124
ID ABR64644 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 125
ID ABU59413 standard; protein; 335 AA.
DE Novel human secreted or transmembrane protein PRO1054.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 126
ID ABU79569 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 127
ID ABU92360 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 128
ID ABU95919 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 129
ID ABU91139 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 130
ID ABU90232 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 131
ID ABO09647 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 132
ID ABR58417 standard; protein; 335 AA.
DE Human NOV27a.
PN WO2003029423-A2.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 133
ID ABO10919 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 134
ID ABR70973 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 135
ID ABU98285 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002183493-A1.
PD 05-DEC-2002.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 136
ID ABU87581 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 137
ID ABU91449 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
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PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 138  
ID ABU89290 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US200303634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 139  
ID ABU84663 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 140  
ID ABR69753 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 141  
ID ABU80130 standard; protein; 335 AA.  
DE Human PRO protein #96.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 142  
ID ABU82497 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 143  
ID ABU92179 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 144  
ID ABU93399 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 145  
ID ABO09952 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 146  
ID ABO09037 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 147  
ID ABU96461 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003027993-A1.

PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 148  
ID ABU10685 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 149  
ID ABU10605 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein #96.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 150  
ID ABU81637 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 151  
ID ABU72131 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 152  
ID ABU95614 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 153  
ID ABU96823 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 154  
ID ABR70668 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 155  
ID ABO05019 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 156  
ID ABO08427 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;



RESULT 157  
ID AB088576 standard; protein; 335 AA.  
DE Human secreted and transmembrane polypeptide PRO1138.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 158  
ID ABO34090 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003017981-A1.  
PD 23-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 159  
ID ABO05634 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 160  
ID ABR74023 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 161  
ID ABR95615 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 162  
ID ABR80912 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 163  
ID ABR81217 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 164  
ID ABO00913 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 165  
ID ABR88515 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 166  
ID ABR77336 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054479-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 167  
ID ABO28820 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 168  
ID ABO31565 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 169  
ID ABO07982 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 170  
ID ABO40462 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 171  
ID ABO35887 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 172  
ID ABO44026 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 173  
ID ADA77944 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 174  
ID AEM24821 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 175  
ID ABO03089 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;



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Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 176
ID ABR90345 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 177
ID ABM1259 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 178
ID ABR95005 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 179
ID ABR95310 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 180
ID ADB17103 standard; protein; 335 AA.
DE Human transmembrane PRO polypeptide (SeqID 46).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 181
ID ABO21548 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 182
ID ABR97812 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 183
ID ABR87600 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 184
ID ABM77641 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 185
ID ABM27871 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 186
ID ABM06152 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 187
ID ABM03658 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 188
ID ABM35109 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 189
ID ABM26346 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 190
ID ABO48128 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 191
ID ABR92870 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 192
ID ABO24631 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 193
ID ADA37764 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 194
ID ABM11642 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064447-A1.
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PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 195  
ID AEM02743 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 196  
ID AEM16039 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 197  
ID ABO27600 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 198  
ID AEM29091 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 199  
ID AEM07067 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 200  
ID AEM21161 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 201  
ID AEM09507 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 202  
ID ABO41377 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 203  
ID ABO36192 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068703-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 204  
ID ABO43721 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 205  
ID AEM76421 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 206  
ID AEM76117 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 207  
ID AEM25736 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 208  
ID AEM26041 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 209  
ID ADA21450 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO1138.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 210  
ID ABO03394 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 211  
ID ABO02479 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 212  
ID ABO44261 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO 1138.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 213  
ID ABR90650 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036130-A1.



PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 214  
ID ABR73718 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 215  
ID ABO16970 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 216  
ID ABR94395 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 217  
ID ABR75902 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 218  
ID ABR71278 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 219  
ID ABR93175 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 220  
ID ABR93480 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 221  
ID ADA10237 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, PRO1138.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 222  
ID ABR87905 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 223

ID ABO27905 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 224  
ID ABO30040 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 225  
ID ABO33249 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 226  
ID ABO4937 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 227  
ID ABO0897 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 228  
ID ABO36497 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 229  
ID ABO35582 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 230  
ID ABO39547 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 231  
ID ABO10422 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 232  
ID ABO11947 standard; protein; 335 AA.



DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 233  
ID ABO52093 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 234  
ID ABO52398 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 235  
ID ADI19908 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 236  
ID ABO23716 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 237  
ID ADI17291 standard; protein; 335 AA.  
DE Human transmembrane PRO polypeptide (SeqId 46).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 238  
ID ADI17781 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 239  
ID ABR97202 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 240  
ID ABR86990 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 241  
ID ABM1032 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 242  
ID ABM28176 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 243  
ID ABO32175 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 244  
ID ABM15302 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 245  
ID ABM06457 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 246  
ID ABM04268 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 247  
ID ABM22381 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 248  
ID ABM07677 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 249  
ID ABO40767 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 250  
ID ABM35414 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.



Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 251  
ID ABM3177 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 252  
ID ABO52703 standard; protein; 335 AA.  
DE Human pro polypeptide #96.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 253  
ID ABO50263 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 254  
ID ABU99257 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 255  
ID ABO04309 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 256  
ID ABO05939 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 257  
ID ABM18479 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 258  
ID ADA27889 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 259  
ID ABR97507 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 260  
ID ABR80607 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049740-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 261  
ID ABM01218 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 262  
ID ABR8820 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 263  
ID ABM13472 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 264  
ID ABM20856 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 265  
ID ABO41987 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 266  
ID ABO42597 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 267  
ID ABM10117 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 268  
ID ABO38632 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 269  
ID ABM32872 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.



Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 270				
ID ABR22686 standard; protein, 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003087373-A1.				
PD 08-MAR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 271				
ID ABR74897 standard; protein, 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003096353-A1.				
PD 22-MAY-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 272				
ID ADA79736 standard; protein, 335 AA.				
DE Human secreted/transmembrane protein (PRO) #96.				
PN US2003073173-A1.				
PD 17-APR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 273				
ID ABR96287 standard; protein, 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003054458-A1.				
PD 20-MAR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 274				
ID ABR02438 standard; protein, 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003059886-A1.				
PD 27-MAR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 275				
ID ABR86380 standard; protein, 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003049758-A1.				
PD 13-MAR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 276				
ID ABR86685 standard; protein, 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003049772-A1.				
PD 13-MAR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 277				
ID ABR16649 standard; protein, 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003064448-A1.				
PD 03-APR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 278				
ID ABR29701 standard; protein, 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003064456-A1.				
PD 03-APR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 279				
ID ABO29125 standard; protein, 335 AA.				
DE Human secreted/transmembrane protein (PRO) #96.				

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Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 289  
ID AAM34397 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 290  
ID ABO20328 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 291  
ID ABO21243 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 292  
ID ABO22158 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 293  
ID ADA20080 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 294  
ID ABO34189 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO 1138.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 295  
ID ABR96592 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 296  
ID ADA94469 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003055832-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 297  
ID ABR85770 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 298  
ID ABR99752 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 299  
ID ABO0608 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 300  
ID ABO0303 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 301  
ID ABO29735 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 302  
ID AAM23601 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 303  
ID AAM23996 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 304  
ID ABO38327 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 305  
ID ABO45627 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 306  
ID AAM20551 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 307  
ID ADA81463 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003092121-A1.  
PD 15-MAY-2003.



PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 308  
ID ABO16665 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 309  
ID ABO18291 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 310  
ID ABO22718 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 311  
ID ABO23023 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 312  
ID ABR92565 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 313  
ID ABR81522 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 314  
ID ABR77946 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 315  
ID ABR89735 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 316  
ID ABR26651 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 317  
ID ABR13777 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 318  
ID ABO28515 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 319  
ID ABO30345 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 320  
ID ABR07372 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 321  
ID ABR03963 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 322  
ID ABO37107 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 323  
ID ABO41682 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 324  
ID ABO35277 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 325  
ID ABR25126 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 326  
ID ABO47518 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049742-A1.  
PD 13-MAR-2003.



PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 327  
ID ABO47823 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 328  
ID ABO48433 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 329  
ID ABO51483 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 330  
ID ABO51788 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 331  
ID ABO50568 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 332  
ID ABR79692 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 333  
ID ABM16954 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 334  
ID ABO17986 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 335  
ID ABO20938 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 336  
ID ABR96897 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 337  
ID ADA38694 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 338  
ID ABM12552 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 339  
ID ABM16344 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 340  
ID ABM24211 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 341  
ID ABM14692 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 342  
ID ABM04573 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 343  
ID ABM06762 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 344  
ID ABM09202 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 345  
ID ABO39242 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068775-A1.  
PD 10-APR-2003.



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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 346
ID ABR75507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 347
ID ABR25431 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 348
ID ABR19941 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 349
ID ABO46847 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 350
ID ABO47152 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 351
ID ADA83261 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 352
ID ABR71583 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 353
ID ABR72193 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 354
ID ABR98532 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 355
ID ABO06902 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 356
ID ABR84855 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 357
ID ABR73413 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 358
ID ABR76507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 359
ID ABR73108 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 360
ID ABR18174 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 361
ID ABO20633 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 362
ID ABO25376 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 363
ID ABO25681 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 364
ID ABR94090 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
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RESULT 365  
ID ADA92815 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 366  
ID ABR79997 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 367  
ID ABM1137 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 368  
ID ABO32944 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 369  
ID ABO30650 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 370  
ID ABO30955 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 371  
ID ABM27261 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 372  
ID ABM3006 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 373  
ID ABM05542 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 374  
ID ABM15607 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 375  
ID ABM08592 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 376  
ID ABO42292 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 377  
ID ABO38022 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 378  
ID ABO45932 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 379  
ID ABM66735 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 380  
ID ADB20304 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 381  
ID ABM19636 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 382  
ID ABO49348 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;  
Pred. No. 2.9e-314;  
RESULT 383  
ID ABO49653 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049775-A1.  
PD 13-MAR-2003.



PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 384  
ID AOA78556 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 385  
ID ABR88210 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 386  
ID ADA00377 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO 138.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 387  
ID AAM26956 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 388  
ID AAM03353 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 389  
ID ABO39852 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 390  
ID ABO49958 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 391  
ID ABO50873 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 392  
ID ABO05329 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;

Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 393  
ID ABR74633 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 394  
ID ABR77112 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 395  
ID ABM17869 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 396  
ID ABR95920 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 397  
ID ABO21853 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 398  
ID ABO20023 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 399  
ID ABO24326 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 400  
ID ABR86075 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 401  
ID ABM10727 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 402  
ID ABR76726 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054465-A1.  
PD 20-MAR-2003.



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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 403
ID ABR89430 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 404
ID ABM12557 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 405
ID ABM05847 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 406
ID ABO34972 standard; protein; 335 AA.
DE Human pro polypeptide #96.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 407
ID ABM03048 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 408
ID ABM19026 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 409
ID ABM19331 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 410
ID ABO46542 standard; protein; 335 AA.
DE Human pro polypeptide #96.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 411
ID ABO49043 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 412
ID ABR69086 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 413
ID ABR89125 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 414
ID ABR72498 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 415
ID ABR74328 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 416
ID ABO18596 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 417
ID ABR80302 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 418
ID ABM01523 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 419
ID ABM02133 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 420
ID ABR87295 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 421
ID ABM12862 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073186-A1.
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PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 422
ID AM30616 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 423
ID AM24516 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 424
ID ABO29430 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 425
ID ABO31260 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 426
ID ABM14387 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 427
ID AM09612 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 428
ID ABO38937 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 429
ID AM34702 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 430
ID ABO51178 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 431
ID ABO4004 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 432
ID ABO10474 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 433
ID ABO53176 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 434
ID ABR77717 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 435
ID ABR78927 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 436
ID ABO24021 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 437
ID ABR93785 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 438
ID AM01828 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 439
ID AM78251 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 440
ID ABR90040 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073177-A1.
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PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 441  
ID ADA22376 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO1138.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 442  
ID AM27566 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 443  
ID AM13167 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 444  
ID ABO31870 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 445  
ID AM14082 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 446  
ID AM08287 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 447  
ID ABO40157 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 448  
ID AM74592 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 449  
ID AM33787 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;

RESULT 450  
ID AM20246 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 451  
ID ABO48738 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 452  
ID ABO22546 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 453  
ID ABR72803 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 454  
ID ABO15445 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 455  
ID ABR85160 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 456  
ID ABO15140 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 457  
ID ABO17275 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 458  
ID AM17564 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 459  
ID ABO6542 standard; protein; 335 AA.  
DE Human secreted/transmembrane PRO polypeptide #71.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;



RESULT 460  
ID ADA39235 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003068782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 461  
ID ABR85465 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003048746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 462  
ID AMW7031 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 463  
ID ABO28210 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 464  
ID ABO28210 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 465  
ID AMW22991 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 466  
ID AMW21771 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 467  
ID AMW21466 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 468  
ID AMW14997 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 469  
ID ABO41072 standard; protein; 335 AA.

DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 470  
ID ABO36802 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 471  
ID ABO37412 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 472  
ID AMW5202 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 473  
ID AMW33482 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 474  
ID ABO46237 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 475  
ID ADA82627 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 476  
ID ADB85619 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 477  
ID ADB96261 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 478  
ID AMW31836 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068680-A1.



PD 10-APR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 479  
ID ABM31226 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 480  
ID ADB85935 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 481  
ID ABM32141 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 482  
ID ABM32446 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 483  
ID ADB68298 standard; protein; 335 AA.  
DE Human PRO1138 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 484  
ID ADB68105 standard; protein; 335 AA.  
DE Human PRO1138 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 485  
ID ABM31531 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 486  
ID ABM30921 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 487  
ID ADB90922 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 488  
ID ADC57733 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003027154-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 489  
ID ADC55097 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 490  
ID ADC11964 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003048681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 491  
ID ADC07002 standard; protein; 335 AA.  
DE Human PRO1138 protein.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 492  
ID ADC56386 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 493  
ID ADC17181 standard; protein; 335 AA.  
DE Mammalian PRO polypeptide (SeqID 46).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 494  
ID ADC07441 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 495  
ID ADC11431 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 496  
ID ADC14879 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 497  
ID ADC52374 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003138882-A1.  
PD 24-JUL-2003.



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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 498
ID AD014553 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 499
ID ADD06085 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 500
ID ADC81910 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 501
ID ADD07552 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 502
ID ADC82443 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 503
ID ADD05665 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 504
ID ADD06623 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 505
ID ADD06672 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 506
ID ADC89503 standard; protein; 335 AA.
DE Human natural killer cell surface receptor CSI.
PN US2003113332-A1.
PD 19-JUN-2003.
PA (UYNT-) UNIV NORTH TEXAS HEALTH SCI CENT.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 507
ID ADC83119 standard; protein; 335 AA.
DE Human PRO polypeptide #71.

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PN US2003059763-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 508
ID ADD67525 standard; protein; 335 AA.
DE Human Ly1728P protein SEQ ID NO:2.
PN NO2003062401-A2.
PD 31-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 509
ID ADD55226 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 510
ID ADD36050 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 511
ID ADD56184 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 512
ID ADD54622 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 513
ID ADE26776 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 514
ID ADE26243 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 515
ID ADP67180 standard; protein; 335 AA.
DE Human PRO1138 amino acid sequence SEQ ID NO:253.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 516
ID ADG01051 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 517

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ID ADG08604 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 518  
ID ADG02660 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 519  
ID ADG01367 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 520  
ID ADP95542 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 521  
ID ADP95225 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 522  
ID ADG1357 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 523  
ID ADH24078 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 524  
ID ADH34104 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 525  
ID ADH29937 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 526  
ID ADH32908 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.

PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 527  
ID ADH09017 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 528  
ID ADG85112 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 529  
ID ADH24588 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 530  
ID ADH37444 standard; protein; 335 AA.  
DE Human secreted and transmembrane protein PRO138 cDNA.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 531  
ID ADH02033 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 532  
ID ADH37614 standard; protein; 335 AA.  
DE Human secreted and transmembrane protein PRO138 cDNA.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 533  
ID ADG85652 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 534  
ID ADH24248 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 535  
ID ADH38542 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181643-A1.



[illegible]

PA	(GETH ) GENENTECH INC.	100.0%;	Score 335;	DB 7;	Length 335;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 545					
ID	ADH49684 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181639-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 335;	DB 7;	Length 335;
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 546					
ID	AD125394 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181696-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 335;	DB 7;	Length 335;
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 548					
ID	AD125564 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181699-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 335;	DB 7;	Length 335;
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 549					
ID	ADH97738 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181672-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 335;	DB 7;	Length 335;
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 550					
ID	AD135434 standard; protein; 335 AA.				
DE	Human PRO polypeptide #71.				
PN	US2003050457-A1.				
PD	13-MAR-2003.				
Query Match		100.0%;	Score 335;	DB 7;	Length 335;
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 551					
ID	AD103586 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181656-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 335;	DB 7;	Length 335;
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 552					
ID	AD111943 standard; protein; 335 AA.				
DE	Human PRO polypeptide #23.				
PN	US2003181686-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 335;	DB 7;	Length 335;
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 553					
ID	ADH90017 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181697-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 335;	DB 7;	Length 335;
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		



Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 554  
ID ADH9926 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 555  
ID ADH9418 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 556  
ID AD11093 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 557  
ID AD11603 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 558  
ID ADH9248 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 559  
ID ADH9658 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 560  
ID ADH9708 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 561  
ID AD10566 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 562  
ID AD10416 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO138.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 563

ID AD104811 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 564  
ID ADH78265 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 565  
ID AD119609 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 566  
ID ADH90357 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 567  
ID AD103076 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 568  
ID ADH77925 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 569  
ID ADH97908 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 570  
ID AD101293 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 571  
ID AD101988 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 572  
ID AD103246 standard; protein; 335 AA.



DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 573  
ID AD11433 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 574  
ID AD102335 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 575  
ID AD11773 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 576  
ID AD105410 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 577  
ID ADH79482 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 578  
ID AD119439 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 579  
ID AD105240 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 580  
ID ADH79652 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 581  
ID AD101478 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 582  
ID AD101648 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 583  
ID AD101818 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 584  
ID ADH79822 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 585  
ID AD104640 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 586  
ID AD102776 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 587  
ID ADH78095 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 588  
ID AD125734 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 589  
ID AD125904 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 590  
ID ADK65416 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003073821-A1.



PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 591  
ID ADH98758 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 592  
ID ADH79999 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 593  
ID ADL3798 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 594  
ID ADM30332 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 595  
ID ADL93730 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 596  
ID ADC52184 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 597  
ID ADE74329 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 598  
ID ADE74941 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 599  
ID ADF35379 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;

RESULT 600  
ID ADG11629 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 601  
ID ADF96154 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 602  
ID ADG04425 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 603  
ID ADG00585 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 604  
ID ADH06616 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 605  
ID ADH06446 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 606  
ID ADG68667 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 607  
ID ADH27757 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 608  
ID ADH25098 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 609  
ID ADH33730 standard; protein; 335 AA.



DE Human PRO polypeptide #23.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 610  
ID ADG82841 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 611  
ID ADH02373 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 612  
ID ADH07980 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 613  
ID ADG69377 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 614  
ID ADH3198 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 615  
ID ADH26122 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 616  
ID ADG83938 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 617  
ID ADH19499 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 618  
ID ADG85482 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 619  
ID ADH05276 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 620  
ID ADH31016 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 621  
ID ADH24418 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 622  
ID ADH33091 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 623  
ID ADG69547 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 624  
ID ADH07810 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 625  
ID ADG85822 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 626  
ID ADH39368 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 627  
ID ADH33560 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181637-A1.



PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 335; DB 8; Length 335;
Best Local Similarity	100.0%; Pred. No. 2.9e-314;
RESULT 628	
ID	ADH33900 standard; protein; 335 AA.
DE	Human PRO polypeptide #23.
PN	US2003181644-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 335; DB 8; Length 335;
Best Local Similarity	100.0%; Pred. No. 2.9e-314;
RESULT 629	
ID	ADH01110 standard; protein; 335 AA.
DE	Human PRO polypeptide #23.
PN	US2003180838-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 335; DB 8; Length 335;
Best Local Similarity	100.0%; Pred. No. 2.9e-314;
RESULT 630	
ID	AD069717 standard; protein; 335 AA.
DE	Novel human secreted and transmembrane protein PRO1138.
PN	US2003180843-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 335; DB 8; Length 335;
Best Local Similarity	100.0%; Pred. No. 2.9e-314;
RESULT 631	
ID	ADH20992 standard; protein; 335 AA.
DE	Human secreted/transmembrane protein PRO1138.
PN	US2003224358-A1.
PD	04-DEC-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 335; DB 8; Length 335;
Best Local Similarity	100.0%; Pred. No. 2.9e-314;
RESULT 632	
ID	ADH02203 standard; protein; 335 AA.
DE	Human PRO polypeptide #23.
PN	US2003180841-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 335; DB 8; Length 335;
Best Local Similarity	100.0%; Pred. No. 2.9e-314;
RESULT 633	
ID	AD069207 standard; protein; 335 AA.
DE	Novel human secreted and transmembrane protein PRO1138.
PN	US2003180847-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 335; DB 8; Length 335;
Best Local Similarity	100.0%; Pred. No. 2.9e-314;
RESULT 634	
ID	AD085992 standard; protein; 335 AA.
DE	Novel human secreted and transmembrane protein PRO1138.
PN	US2003180862-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 335; DB 8; Length 335;
Best Local Similarity	100.0%; Pred. No. 2.9e-314;
RESULT 635	
ID	ADH24928 standard; protein; 335 AA.
DE	Novel human secreted and transmembrane protein PRO1138.
PN	US2003180909-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 335; DB 8; Length 335;
Best Local Similarity	100.0%; Pred. No. 2.9e-314;
RESULT 636	
ID	ADH39545 standard; protein; 335 AA.
DE	Novel human secreted and transmembrane protein PRO1138.
PN	US2003180915-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 335; DB 8; Length 335;
Best Local Similarity	100.0%; Pred. No. 2.9e-314;
RESULT 637	
ID	ADH39545 standard; protein; 335 AA.
DE	Novel human secreted and transmembrane protein PRO1138.
PN	US2003180915-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 335; DB 8; Length 335;
Best Local Similarity	100.0%; Pred. No. 2.9e-314;

Query Match	100.0%;	Score 335;	DB 8;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 637				
ID ADH20032 standard; protein; 335 AA.				
DE Human secreted/transmembrane protein PRO1138.				
PN US2003219856-A1.				
PD 27-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 8;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 638				
ID ADH02543 standard; protein; 335 AA.				
DE Human PRO polypeptide #23.				
PN US2003180840-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 8;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 639				
ID ADG69037 standard; protein; 335 AA.				
DE Novel human secreted and transmembrane protein PRO1138.				
PN US2003180849-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 8;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 640				
ID ADH07640 standard; protein; 335 AA.				
DE Novel human secreted and transmembrane protein PRO1138.				
PN US2003180850-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 8;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 641				
ID ADG68162 standard; protein; 335 AA.				
DE Novel human secreted and transmembrane protein PRO1138.				
PN US2003180863-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 8;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 642				
ID ADH424758 standard; protein; 335 AA.				
DE Novel human secreted and transmembrane protein PRO1138.				
PN US2003180908-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 8;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 643				
ID ADH25806 standard; protein; 335 AA.				
DE Novel human secreted and transmembrane protein PRO1138.				
PN US2003180922-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 8;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 644				
ID ADH38372 standard; protein; 335 AA.				
DE Novel human secreted and transmembrane protein PRO1138.				
PN US2003180922-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 8;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 645				
ID ADH57211 standard; protein; 335 AA.				
DE Novel human secreted and transmembrane protein PRO1138.				
PN US2003181642-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 8;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 646				
ID ADH57211 standard; protein; 335 AA.				
DE Novel human secreted and transmembrane protein PRO1138.				
PN US2003181642-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 335;	DB 8;	Length 335;



Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 646  
ID ADH52199 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 647  
ID ADH4565 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 648  
ID ADH90527 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 649  
ID ADI11263 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 650  
ID ADH98928 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 651  
ID ADI02158 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 652  
ID ADH90697 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 653  
ID ADJ54830 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 654  
ID ADJ98572 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 655  
ID ADJ98742 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 656  
ID ADH78901 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 657  
ID ADJ99135 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 658  
ID ADJ99305 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 659  
ID ADJ98923 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 660  
ID ADH79071 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 661  
ID ADK00931 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 662  
ID ADK14452 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 663  
ID ADJ64601 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 664



ID ADM31497 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 665  
ID ADM3544 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 666  
ID ADM40349 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 667  
ID ADM80901 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 668  
ID ADN37957 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 669  
ID ADU87689 standard; protein; 335 AA.  
DE Human Csi (SLMF7) protein.  
PN WO2004100898-A2.  
PD 25-NOV-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 100.0%; Score 335; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 670  
ID ADY19131 standard; protein; 335 AA.  
DE PRO polypeptide SEQ ID NO 4937.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 671  
ID ADY77741 standard; protein; 335 AA.  
DE Neoplastic disease detection protein PRO1138.  
PN US2005059102-A1.  
PD 17-MAR-2005.  
PA (BATO) EATON D L.  
PA (FILV) FILVAROFF E.  
PA (GERR) GERRITSEN M E.  
PA (GODD) GODDARD A.  
PA (GODO) GODOWSKI P J.  
PA (GRIM) GRIMALDI J C.  
PA (GURN) GURNEY A L.  
PA (WATA) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 335; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 672  
ID AEA38506 standard; protein; 335 AA.

DE Human secreted/transmembrane protein, #139.  
PN US2005118725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 335; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 673  
ID AAB32373 standard; protein; 336 AA.  
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:59.  
PN WO200047602-A1.  
PD 17-AUG-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 100.0%; Score 335; DB 3; Length 336;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 674  
ID ADS98579 standard; protein; 340 AA.  
DE Protein factor discovery related human contig polypeptide, SEQ ID 843.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
PA (DRMA) DRMANAC R T.  
Query Match 100.0%; Score 335; DB 8; Length 340;  
Best Local Similarity 100.0%; Pred. No. 2.9e-314;  
RESULT 675  
ID AAY44610 standard; protein; 312 AA.  
DE Mature human myocardium protein-7.  
PN WO9967387-A2.  
PD 29-DEC-1999.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 93.1%; Score 312; DB 3; Length 312;  
Best Local Similarity 100.0%; Pred. No. 4.2e-292;  
RESULT 676  
ID ADS97998 standard; protein; 296 AA.  
DE Protein factor discovery related isolated human polypeptide, SEQ ID 262.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
PA (DRMA) DRMANAC R T.  
Query Match 76.7%; Score 257; DB 8; Length 296;  
Best Local Similarity 100.0%; Pred. No. 4.7e-239;  
RESULT 677  
ID ABB97473 standard; protein; 328 AA.  
DE Novel human protein SEQ ID NO: 741.  
PN WO200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 76.7%; Score 257; DB 5; Length 328;  
Best Local Similarity 100.0%; Pred. No. 5.1e-239;  
RESULT 678  
ID ADS98765 standard; protein; 328 AA.  
DE Protein factor discovery related human contig polypeptide, SEQ ID 1029.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
PA (DRMA) DRMANAC R T.  
Query Match 76.7%; Score 257; DB 8; Length 328;  
Best Local Similarity 100.0%; Pred. No. 5.1e-239;  
RESULT 679  
ID ADD16672 standard; protein; 335 AA.  
DE Human disease related protein SeqID103.  
PN WO2003018621-A2.  
PD 06-MAR-2003.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 69.9%; Score 234; DB 7; Length 335;  
Best Local Similarity 99.7%; Pred. No. 8e-217;  
RESULT 680  
ID ADU69599 standard; protein; 335 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1405.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 69.9%; Score 234; DB 7; Length 335;



Best Local Similarity 99.7%; Pred. No. 8e-217;  
RESULT 681  
ID ABR58418 standard; protein; 348 AA.  
DE Human NOV27D.  
PN WO2003029423-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 64.8%; Score 217; DB 6; Length 348;  
Best Local Similarity 100.0%; Pred. No. 2.1e-200;  
RESULT 682  
ID ADR2005 standard; protein; 165 AA.  
DE Human immune response associated protein (IRAP), seq id 15.  
PN WO2004048550-A2.  
PD 10-JUN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 37.6%; Score 126; DB 8; Length 165;  
Best Local Similarity 100.0%; Pred. No. 6.9e-113;  
RESULT 683  
ID ADN02731 standard; protein; 204 AA.  
DE Human receptor and membrane-associated protein #34.  
PN WO2004029218-A2.  
PD 08-APR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 37.6%; Score 126; DB 8; Length 204;  
Best Local Similarity 100.0%; Pred. No. 8.2e-113;  
RESULT 684  
ID AAM67811 standard; protein; 110 AA.  
DE Human secreted protein encoded by gene 5 clone HSA5AV70.  
PN WO9842738-A1.  
PD 01-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 110; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.3e-97;  
RESULT 685  
ID AAB32405 standard; protein; 110 AA.  
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:91.  
PN WO20047602-A1.  
PD 17-AUG-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 110; DB 3; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.3e-97;  
RESULT 686  
ID ADA57321 standard; protein; 110 AA.  
DE Human secreted protein #32.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 110; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.3e-97;  
RESULT 687  
ID ADA56750 standard; protein; 110 AA.  
DE Human secreted protein #32.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 110; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.3e-97;  
RESULT 688  
ID ADA40601 standard; protein; 110 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 110; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.3e-97;  
RESULT 689  
ID ADA41198 standard; protein; 110 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 110; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.3e-97;  
RESULT 690  
ID AAG00391 standard; protein; 97 AA.  
DE Human secreted protein, SEQ ID NO: 4472.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST-) GENSET.  
Query Match 29.0%; Score 97; DB 3; Length 97;  
Best Local Similarity 100.0%; Pred. No. 4.2e-85;  
RESULT 691  
ID AAV11662 standard; protein; 98 AA.  
DE Human 5' EST secreted protein SEQ ID NO:314.  
PN WO9906439-A2.  
PD 11-FEB-1999.  
PA (GEST-) GENSET.  
Query Match 29.0%; Score 97; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 4.2e-85;  
RESULT 692  
ID ABG11697 standard; protein; 684 AA.  
DE Novel human diagnostic protein #11688.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 27.5%; Score 92; DB 4; Length 684;  
Best Local Similarity 100.0%; Pred. No. 1.5e-79;  
RESULT 693  
ID ABG12169 standard; protein; 684 AA.  
DE Novel human diagnostic protein #12160.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 27.5%; Score 92; DB 4; Length 684;  
Best Local Similarity 100.0%; Pred. No. 1.5e-79;  
RESULT 694  
ID ADS98714 standard; protein; 684 AA.  
DE Protein factor discovery related human contig polypeptide, SEQ ID 978.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
PA (DRMA/) DRMANAC R T.  
Query Match 27.5%; Score 92; DB 8; Length 684;  
Best Local Similarity 100.0%; Pred. No. 1.5e-79;  
RESULT 695  
ID AAM21122 standard; protein; 91 AA.  
DE Peptide #7556 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 27.2%; Score 91; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.4e-79;  
RESULT 696  
ID ABB43438 standard; peptide; 91 AA.  
DE Peptide #10944 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 27.2%; Score 91; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.4e-79;  
RESULT 697  
ID AAM37326 standard; protein; 91 AA.  
DE Peptide #11363 encoded by probe for measuring placental gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 27.2%; Score 91; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.4e-79;  
RESULT 698  
ID ABB26408 standard; protein; 91 AA.  
DE Protein #8407 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 27.2%; Score 91; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.4e-79;



RESULT 699  
ID AAM77190 standard; protein; 91 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37496.  
PN W0200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 27.2%; Score 91; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.4e-79;  
RESULT 700  
ID AAM64367 standard; protein; 91 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36472.  
PN W0200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 27.2%; Score 91; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.4e-79;  
RESULT 701  
ID ABG58815 standard; peptide; 91 AA.  
DE Human liver peptide, SEQ ID No 37463.  
PN W0200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 27.2%; Score 91; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.4e-79;  
RESULT 702  
ID ABG46203 standard; peptide; 91 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35868.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 27.2%; Score 91; DB 5; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.4e-79;  
RESULT 703  
ID AAB32404 standard; protein; 90 AA.  
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:90.  
PN W0200047602-A1.  
PD 17-AUG-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 25.7%; Score 86; DB 3; Length 90;  
Best Local Similarity 100.0%; Pred. No. 1.6e-74;  
RESULT 704  
ID AAY12645 standard; protein; 124 AA.  
DE Human 5' EST secreted protein SEQ ID NO: 310 from WO 9906553.  
PN W09906553-A2.  
PD 11-FEB-1999.  
PA (GEST-) GENSET.  
Query Match 20.3%; Score 68; DB 2; Length 124;  
Best Local Similarity 100.0%; Pred. No. 4.9e-57;  
RESULT 705  
ID ADR20041 standard; protein; 91 AA.  
DE Human immune response associated protein (IRAP), seq id 1.  
PN W02004048550-A2.  
PD 10-JUN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 15.2%; Score 51; DB 8; Length 91;  
Best Local Similarity 100.0%; Pred. No. 9.4e-41;  
RESULT 706  
ID AAM67933 standard; protein; 33 AA.  
DE Fragment of human secreted protein encoded by gene 5.  
PN W09842738-A1.  
PD 01-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 33; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 9.2e-24;  
RESULT 707  
ID AAM67932 standard; protein; 28 AA.  
DE Fragment of human secreted protein encoded by gene 5.  
PN W09842738-A1.  
PD 01-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.1%; Score 27; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 4.9e-18;  
RESULT 708

ID AAM87990 standard; protein; 114 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:15583.  
PN W0200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.7%; Score 19; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 8.5e-10;  
RESULT 709  
ID ADC89505 standard; peptide; 11 AA.  
DE Human natural killer cell surface receptor CSI antigenic peptide #2.  
PN US2003113332-A1.  
PD 19-JUN-2003.  
PA (UNVT-) UNIV NORTH TEXAS HEALTH SCI CENT.  
Query Match 3.3%; Score 11; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0061;  
RESULT 710  
ID ADC89504 standard; peptide; 12 AA.  
DE Human natural killer cell surface receptor CSI antigenic peptide #1.  
PN US2003113332-A1.  
PD 19-JUN-2003.  
PA (UNVT-) UNIV NORTH TEXAS HEALTH SCI CENT.  
Query Match 3.3%; Score 11; DB 7; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0065;  
RESULT 711  
ID ADC89506 standard; peptide; 16 AA.  
DE Human natural killer cell surface receptor CSI antigenic peptide #3.  
PN US2003113332-A1.  
PD 19-JUN-2003.  
PA (UNVT-) UNIV NORTH TEXAS HEALTH SCI CENT.  
Query Match 3.3%; Score 11; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
RESULT 712  
ID AAG25088 standard; protein; 66 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29010.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 2.7%; Score 9; DB 3; Length 66;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
RESULT 713  
ID AAG35118 standard; protein; 66 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 42854.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 2.7%; Score 9; DB 3; Length 66;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
RESULT 714  
ID ABG25025 standard; protein; 456 AA.  
DE Novel human diagnostic protein #25016.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSR-) HYSRQ INC.  
Query Match 2.7%; Score 9; DB 4; Length 456;  
Best Local Similarity 100.0%; Pred. No. 12;  
RESULT 715  
ID AAY13308 standard; peptide; 15 AA.  
DE Naturally occurring variant of the glutenin epitope Y13221.  
PN EP905518-A1.  
PD 31-MAR-1999.  
PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.  
Query Match 2.4%; Score 8; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
RESULT 716  
ID AAB74404 standard; peptide; 26 AA.  
DE Desmoglein sequence transmembrane domain.  
PN W0200118056-A2.  
PD 15-MAR-2001.  
PA (GENE-) GENENVA LTD.  
Query Match 2.4%; Score 8; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 9.9;  
RESULT 717  
ID AAB80619 standard; protein; 105 AA.  
DE Environmental stress tolerant protein SEQ ID 24.



PN W0200106006-A1.  
PD 25-JAN-2001.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 2.4%; Score 8; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 32;  
RESULT 718  
ID AAM37871 standard; protein; 122 AA.  
DE Human protein comprising secretory signal amino acid sequence 8.  
PN W09811217-A2.  
PD 19-MAR-1998.  
PA (SAGA ) SAGAMI CHEM RES CENTRE.  
PA (PROT-) PROTEGENE INC.  
Query Match 2.4%; Score 8; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 37;  
RESULT 719  
ID ADT58961 standard; protein; 130 AA.  
DE Plant polypeptide, SEQ ID 9038.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Query Match 2.4%; Score 8; DB 8; Length 130;  
Best Local Similarity 100.0%; Pred. No. 39;  
RESULT 720  
ID AAB27244 standard; protein; 172 AA.  
DE Human EXMAD-22 SEQ ID NO: 22.  
PN W0200068380-A2.  
PD 16-NOV-2000.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 2.4%; Score 8; DB 4; Length 172;  
Best Local Similarity 100.0%; Pred. No. 49;  
RESULT 721  
ID AAM40751 standard; protein; 194 AA.  
DE Human polypeptide SEQ ID NO 5682.  
PN W0200153312-A1.  
PD 26-JUL-2001.  
PA (HYSB-) HYSBQ INC.  
Query Match 2.4%; Score 8; DB 4; Length 194;  
Best Local Similarity 100.0%; Pred. No. 55;  
RESULT 722  
ID AEA20940 standard; protein; 194 AA.  
DE Novel human polypeptide SEQ ID NO 1634.  
PN W02005049806-A2.  
PD 02-JUN-2005.  
PA (NUVE-) NUVELO INC.  
Query Match 2.4%; Score 8; DB 9; Length 194;  
Best Local Similarity 100.0%; Pred. No. 55;  
RESULT 723  
ID ADM80804 standard; protein; 259 AA.  
DE Human CADECM-33 protein SEQ ID NO:33.  
PN W02004015396-A2.  
PD 19-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 2.4%; Score 8; DB 8; Length 259;  
Best Local Similarity 100.0%; Pred. No. 70;  
RESULT 724  
ID ADT99536 standard; protein; 270 AA.  
DE Human DSG2.  
PN W02004093788-A2.  
PD 04-NOV-2004.  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
Query Match 2.4%; Score 8; DB 8; Length 270;  
Best Local Similarity 100.0%; Pred. No. 73;  
RESULT 725  
ID AAY93912 standard; protein; 289 AA.  
DE A human hyaluronan-binding protein, designated OE-HAMP.  
PN W0200039166-A1.  
PD 06-JUL-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (AMNA-) AMERICAN NAT RBD CROSS.  
Query Match 2.4%; Score 8; DB 3; Length 289;  
Best Local Similarity 100.0%; Pred. No. 77;  
RESULT 726  
ID ABU24508 standard; protein; 306 AA.

DE Protein encoded by prokaryotic essential gene #10035.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 2.4%; Score 8; DB 6; Length 306;  
Best Local Similarity 100.0%; Pred. No. 81;  
RESULT 727  
ID ADA55489 standard; protein; 310 AA.  
DE Human protein, SEQ ID 3057.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELT-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 2.4%; Score 8; DB 6; Length 310;  
Best Local Similarity 100.0%; Pred. No. 82;  
RESULT 728  
ID AAY13381 standard; protein; 360 AA.  
DE Amino acid sequence of protein PRO271.  
PN W09914328-A2.  
PD 25-MAR-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 2; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 729  
ID ADC78533 standard; protein; 360 AA.  
DE Human PRO271 protein.  
PN W0200015796-A2.  
PD 23-MAR-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 3; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 730  
ID AAB80249 standard; protein; 360 AA.  
DE Human PRO271 protein.  
PN W0200104311-A1.  
PD 18-JAN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 4; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 731  
ID AAU29037 standard; protein; 360 AA.  
DE Human PRO polypeptide sequence #14.  
PN W0200168848-A2.  
PD 20-SEP-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 4; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 732  
ID AAM38965 standard; protein; 360 AA.  
DE Human polypeptide SEQ ID NO 2110.  
PN W0200153312-A1.  
PD 26-JUL-2001.  
PA (HYSB-) HYSBQ INC.  
Query Match 2.4%; Score 8; DB 4; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 733  
ID ABU58413 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 734  
ID ABU71627 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
PN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 735  
ID ABU87961 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.



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PN US2003032127-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 736
ID ABU84276 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 737
ID ABR66150 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 738
ID ABR65540 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 739
ID ABU99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 740
ID ABU82719 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 741
ID ABU98940 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 742
ID ABU71482 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 743
ID ABR68089 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 744
ID ABU96142 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 745
ID ABU92573 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 746
ID ABO08650 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 747
ID ABO02702 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 748
ID ABR74856 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 749
ID ABR94618 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 750
ID ABU85591 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 751
ID ABU98751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003031153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 752
ID ABU97966 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 753
ID ABU91672 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 754
ID ABU71928 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 755
ID ABU89365 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
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Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 756  
ID ABU86206 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 757  
ID ABU67419 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 758  
ID ABU80447 standard; protein; 360 AA.  
DE Human PRO protein #14.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 759  
ID ABO01811 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 760  
ID ABR93365 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 761  
ID ABR98755 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 762  
ID ABO16278 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 763  
ID ABR92178 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 764  
ID ABO18619 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 765  
ID ABR78240 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 766  
ID ABU84976 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 767  
ID ABO00115 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 768  
ID ABO11447 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 769  
ID ABO02092 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 770  
ID ABU54384 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein PRO271.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 771  
ID ABU8666 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 772  
ID ABU83361 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 773  
ID ABO06162 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 774  
ID ABR59198 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 775  
ID ABO09260 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;



Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 776  
ID ABO15124 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 777  
ID ABO11142 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 778  
ID ABR66760 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 779  
ID ABO15973 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 780  
ID ABO13679 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 781  
ID ABO47399 standard; protein; 360 AA.  
DE Human secreted/transmembrane polypeptide PRO271.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 782  
ID ABU65582 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, SEQ ID 28.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 783  
ID ABO07430 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 784  
ID ABO03617 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 785  
ID ABR67065 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 786  
ID ABO15668 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 787  
ID ABU55949 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, PRO271.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 788  
ID ABU65277 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 789  
ID ABU95222 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 790  
ID ABU71125 standard; protein; 360 AA.  
DE Human PRO271 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 791  
ID ABO07735 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 792  
ID ABR69976 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 793  
ID ABR69309 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 794  
ID ABO01450 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 795  
ID ABU81252 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;



RESULT 796  
ID ABR60049 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 797  
ID ABR67784 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 798  
ID ABR65172 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 799  
ID ABR68394 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 800  
ID ABR71806 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 801  
ID ABR85286 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 802  
ID ABR88976 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 803  
ID ABR83056 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 804  
ID ABR94912 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 805  
ID ABR90460 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 806  
ID ABR83971 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 807  
ID ABR93622 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 808  
ID ABR64867 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 809  
ID ABR68699 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 810  
ID ABO06515 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 811  
ID ABR99060 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 812  
ID ABR56944 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 813  
ID ABR64536 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 814  
ID ABR85896 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 815  
ID ABR67382 standard; protein; 360 AA.  
DE Human secreted protein PRO271.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 816  
ID ABR82183 standard; protein; 360 AA.



DE	Novel human secreted and transmembrane protein PRO271.	
FN	US2003036136-A1.	
PD	20-FEB-2003.	
Query Match		
Best Local Similarity	2.4%; Score 8; DB 6; Length 360;	
PD	100.0%; Pred. No. 93;	
RESULT 817		
ID	ABU87194 standard; protein, 360 AA.	
DE	Human PRO polypeptide #14.	
FN	US2003036138-A1.	
PD	20-FEB-2003.	
Query Match		
Best Local Similarity	2.4%; Score 8; DB 6; Length 360;	
PD	100.0%; Pred. No. 93;	
RESULT 818		
ID	ABU83666 standard; protein, 360 AA.	
DE	Human secreted/transmembrane protein (PRO) #14.	
FN	US2003032109-A1.	
PD	13-FEB-2003.	
Query Match		
Best Local Similarity	2.4%; Score 8; DB 6; Length 360;	
PD	100.0%; Pred. No. 93;	
RESULT 819		
ID	ABO08040 standard; protein, 360 AA.	
DE	Human PRO polypeptide #14.	
FN	US2003040066-A1.	
PD	27-FEB-2003.	
Query Match		
Best Local Similarity	2.4%; Score 8; DB 6; Length 360;	
PD	100.0%; Pred. No. 93;	
RESULT 820		
ID	ABO14902 standard; protein, 360 AA.	
DE	Human secreted / transmembrane polypeptide PRO271.	
FN	US2003036060-A1.	
PD	20-FEB-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match		
Best Local Similarity	2.4%; Score 8; DB 6; Length 360;	
PD	100.0%; Pred. No. 93;	
RESULT 821		
ID	ABU81751 standard; protein, 360 AA.	
DE	Novel human secreted and transmembrane protein PRO271.	
FN	US2003032104-A1.	
PD	13-FEB-2003.	
Query Match		
Best Local Similarity	2.4%; Score 8; DB 6; Length 360;	
PD	100.0%; Pred. No. 93;	
RESULT 822		
ID	ABU65915 standard; protein, 360 AA.	
DE	Novel human secreted and transmembrane protein PRO271.	
FN	US2003036157-A1.	
PD	20-FEB-2003.	
Query Match		
Best Local Similarity	2.4%; Score 8; DB 6; Length 360;	
PD	100.0%; Pred. No. 93;	
RESULT 823		
ID	ABR59744 standard; protein, 360 AA.	
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.	
FN	US2003032120-A1.	
PD	13-FEB-2003.	
Query Match		
Best Local Similarity	2.4%; Score 8; DB 6; Length 360;	
PD	100.0%; Pred. No. 93;	
RESULT 824		
ID	ABU93932 standard; protein, 360 AA.	
DE	Novel human secreted and transmembrane protein PRO271.	
FN	US2003036155-A1.	
PD	20-FEB-2003.	
Query Match		
Best Local Similarity	2.4%; Score 8; DB 6; Length 360;	
PD	100.0%; Pred. No. 93;	
RESULT 825		
ID	ABU99785 standard; protein, 360 AA.	
DE	Novel human secreted and transmembrane protein PRO271.	
FN	US2003022296-A1.	
PD	30-JAN-2003.	
Query Match		
Best Local Similarity	2.4%; Score 8; DB 6; Length 360;	
PD	100.0%; Pred. No. 93;	
RESULT 826		
ID	ABR66455 standard; protein, 360 AA.	
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.	
FN	US2003027281-A1.	
PD	2.4%; Score 8; DB 6; Length 360;	
PD	100.0%; Pred. No. 93;	

[illegible]



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Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABR64562 standard; protein; 360 AA.
RESULT 837
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU79487 standard; protein; 360 AA.
RESULT 838
DE Human PRO polypeptide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU92878 standard; protein; 360 AA.
RESULT 839
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU95837 standard; protein; 360 AA.
RESULT 840
DE Human PRO polypeptide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU91057 standard; protein; 360 AA.
RESULT 841
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU90150 standard; protein; 360 AA.
RESULT 842
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABO09565 standard; protein; 360 AA.
RESULT 843
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABO10837 standard; protein; 360 AA.
RESULT 844
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABR70891 standard; protein; 360 AA.
RESULT 845
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU87499 standard; protein; 360 AA.
RESULT 846
DE Human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABO96741 standard; protein; 360 AA.
RESULT 847
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ID ABU91367 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU84581 standard; protein; 360 AA.
RESULT 848
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABR69671 standard; protein; 360 AA.
RESULT 849
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU80048 standard; protein; 360 AA.
RESULT 850
DE Human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU69659 standard; protein; 360 AA.
RESULT 851
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU93317 standard; protein; 360 AA.
RESULT 852
DE Human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABO09870 standard; protein; 360 AA.
RESULT 853
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABO09955 standard; protein; 360 AA.
RESULT 854
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU10523 standard; protein; 360 AA.
RESULT 855
DE Human secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU95532 standard; protein; 360 AA.
RESULT 856
DE Human PRO polypeptide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
PRED. NO. 93;
ID ABU96741 standard; protein; 360 AA.
RESULT 857
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DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 858  
ID ABR70586 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 859  
ID ABO04937 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003008352-A1.  
PD 09-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 860  
ID ABO08345 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 861  
ID ABO14841 standard; protein; 360 AA.  
DE Human secreted / transmembrane polypeptide PRO271.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 862  
ID ABO05552 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 863  
ID ABR73941 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 864  
ID ABR9553 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 865  
ID ABR80830 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 866  
ID ABR81135 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;

Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 867  
ID ABM00831 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 868  
ID ABR88433 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 869  
ID ABM77254 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 870  
ID ABO28738 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 871  
ID ABO31483 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 872  
ID ABM07900 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 873  
ID ABO40380 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 874  
ID ABO35805 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 875  
ID ABO43944 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;



RESULT 876  
ID ADA77780 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 877  
ID ABM24739 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 878  
ID ADB29418 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 879  
ID ABO03007 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 880  
ID ABR90263 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 881  
ID ABM17177 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 882  
ID ABR94923 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 883  
ID ABR95228 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 884  
ID ABO21466 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 885  
ID ABR97730 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 886  
ID ABR87518 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 887  
ID ABM77559 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 888  
ID ABM27789 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 889  
ID ABM06070 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 890  
ID ABR03576 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 891  
ID ABM35027 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 892  
ID ABM26264 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 893  
ID ABO48046 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 894  
ID ABR92788 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;



Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 895  
ID ABO24549 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 896  
ID ABO11560 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 897  
ID ABO2661 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 898  
ID ABO15957 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 899  
ID ABO27518 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 900  
ID ABO2909 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 901  
ID ABO06985 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 902  
ID ABO21079 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 903  
ID ABO09425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 904  
ID ABO41295 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 905  
ID ABO36110 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 906  
ID ABO43639 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 907  
ID ABO76339 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 908  
ID ABO76035 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 909  
ID ABO25654 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 910  
ID ABO25959 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 911  
ID ABO03312 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 912  
ID ABO02397 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 913  
ID ABO90568 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;



Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 914  
ID ABR73636 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 915  
ID ABO1688 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 916  
ID ABR94313 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 917  
ID ABR75820 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 918  
ID ADA18274 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003038971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 919  
ID ABO32793 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein PRO271.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 920  
ID ABR71196 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 921  
ID ABR93093 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 922  
ID ABR93398 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 923  
ID ABR87823 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 924  
ID ABO27823 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 925  
ID ABO29958 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 926  
ID ABO33167 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 927  
ID ABO4855 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 928  
ID ABO08815 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 929  
ID ABO36415 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 930  
ID ABO35500 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 931  
ID ABO39465 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 932  
ID ABO10340 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.



PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 933  
ID ABM11865 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 934  
ID ABO52011 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 935  
ID ABO52316 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 936  
ID ABO23634 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 937  
ID ABR97120 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 938  
ID ABR86908 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 939  
ID ABM10950 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 940  
ID ABM28094 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 941  
ID ABO32093 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068733-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 942  
ID ABM15220 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 943  
ID ABM06375 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 944  
ID ABM04186 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 945  
ID ABM22299 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 946  
ID ABM07595 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 947  
ID ABO40685 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 948  
ID ABM35332 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 949  
ID ABM33095 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 950  
ID ABO52621 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;



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Best Local Similarity 100.0%; Pred. No. 93;
RESULT 951
ID ABO50181 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 952
ID ABU99175 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 953
ID ABO04227 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 954
ID ABO05857 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 955
ID ABO34853 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 956
ID ABM18397 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 957
ID ADA16249 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 958
ID ABR97425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 959
ID ABR80525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 960
ID ABM01136 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PD 08-MAY-2003.
PN US2003049770-A1.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 961
ID ABR88738 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 962
ID ABM13390 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 963
ID ABM20774 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 964
ID ABO41905 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 965
ID ABO42515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 966
ID ABM10035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 967
ID ABO38550 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 968
ID ABM32790 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 969
ID ABM22604 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087373-A1.
PD 08-MAY-2003.
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Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 970  
ID ABM74815 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 971  
ID ADA79572 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 972  
ID ABR96205 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 973  
ID ABM02356 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 974  
ID ABR86298 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 975  
ID ABR86603 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 976  
ID ABM16567 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 977  
ID ABM29619 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 978  
ID ABO29043 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 979  
ID ABM23824 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 980  
ID ABM23214 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 981  
ID ABM21994 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 982  
ID ABO37635 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 983  
ID ABM28399 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 984  
ID ABM28704 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 985  
ID ABM66348 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 986  
ID ABM75730 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 987  
ID ABM34010 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 988  
ID ABM34315 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003100061-A1.  
PD 29-MAY-2003.



PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 989  
ID ABO20246 standard; protein; 360 AA.  
DE Human secreted/cranmembrane protein (PRO) #14.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 990  
ID ABO21161 standard; protein; 360 AA.  
DE Human secreted/cranmembrane protein (PRO) #14.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 991  
ID ABO22076 standard; protein; 360 AA.  
DE Human secreted/cranmembrane protein (PRO) #14.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 992  
ID ABR96510 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 993  
ID ABR8568 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 994  
ID ABR9670 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 995  
ID ABR00221 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 996  
ID ABR00526 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 997  
ID ABO29653 standard; protein; 360 AA.  
DE Human secreted/cranmembrane protein (PRO) #14.  
PN US2003068700-A1.  
PD 10-APR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 998  
ID ABR23519 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068736-A1.  
PD 10-APR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 999  
ID ABR29314 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068679-A1.  
PD 10-APR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1000  
ID ABO38245 standard; protein; 360 AA.  
DE Human secreted/cranmembrane protein (PRO) #14.  
PN US2003068767-A1.  
PD 10-APR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1001  
ID ABO45545 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003073182-A1.  
PD 17-APR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1002  
ID ABR20469 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1003  
ID ADA42394 standard; protein; 360 AA.  
DE Human secreted/cranmembrane protein, #42.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1004  
ID ADA81299 standard; protein; 360 AA.  
DE Human secreted/cranmembrane protein (PRO) #14.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1005  
ID ABO16583 standard; protein; 360 AA.  
DE Human secreted/cranmembrane protein (PRO) #14.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1006  
ID ABO18209 standard; protein; 360 AA.  
DE Human secreted/cranmembrane protein (PRO) #14.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1007  
ID ABO22636 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003027265-A1.  
PD 06-FEB-2003.



Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1008  
ID ABO22941 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1009  
ID ABR92483 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1010  
ID ABR81440 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1011  
ID ABO17531 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1012  
ID ABM77864 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1013  
ID ABR89653 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1014  
ID AMW26569 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1015  
ID ABM13695 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1016  
ID ABO28433 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1017  
ID ABO30263 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1018  
ID ABM07290 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1019  
ID ABM03881 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1020  
ID ABO37025 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1021  
ID ABO41600 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1022  
ID ABO35195 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1023  
ID ABM25044 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1024  
ID ABO47436 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1025  
ID ABO47741 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1026  
ID ABO48351 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.



PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1027  
ID ABO51401 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1028  
ID ABO51706 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1029  
ID ABO50486 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1030  
ID ABR79610 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1031  
ID ABM16872 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1032  
ID ABO17904 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1033  
ID ABO20856 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1034  
ID ABR96815 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1035  
ID ABM12170 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;

Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1036  
ID ABM16262 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1037  
ID ABM24129 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1038  
ID ABM14610 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1039  
ID ABM04491 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1040  
ID ABM06680 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1041  
ID ABM09120 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1042  
ID ABO39160 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1043  
ID ABM75425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1044  
ID ABM25349 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1045  
ID ABM19859 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.



PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1046  
ID ABO46765 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1047  
ID ABO47070 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1048  
ID ADA83097 standard; protein; 360 AA.  
DE Human secreted/cranemembrane protein (PRO) #14.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1049  
ID ABR71501 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1050  
ID ABR72111 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1051  
ID ABR98450 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1052  
ID ABO06820 standard; protein; 360 AA.  
DE Human secreted/cranemembrane protein (PRO) #14.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1053  
ID ABR84773 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1054  
ID ABR73331 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1055

ID ABR76425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1056  
ID ABR73026 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1057  
ID ABR18092 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1058  
ID ABO20551 standard; protein; 360 AA.  
DE Human secreted/cranemembrane protein (PRO) #14.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1059  
ID ABO25294 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1060  
ID ABO25599 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1061  
ID ABR94008 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1062  
ID ABR79915 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1063  
ID ABR11255 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1064  
ID ABO32862 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.



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Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1065
ID ABO30568 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1066
ID ABO30873 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1067
ID ABO27179 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1068
ID ABO29924 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1069
ID ABO05460 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1070
ID ABO15525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1071
ID ABO08510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1072
ID ABO42210 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1073
ID ABO37940 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1074
ID ABO45850 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1075
ID ABO66653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1076
ID ABO20140 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1077
ID ABO19554 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1078
ID ABO49266 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1079
ID ABO49571 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1080
ID ABO78392 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1081
ID ABO88128 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1082
ID ABO26874 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1083
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ID ABM03271 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1084  
ID ABO39770 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1085  
ID ABO49876 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003048776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1086  
ID ABO50791 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1087  
ID ABO05247 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1088  
ID ABR74551 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1089  
ID ABR77030 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1090  
ID ADA16673 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1091  
ID ABM17787 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1092  
ID ABR95838 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;

Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1093  
ID ADA13102 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1094  
ID ABO21771 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1095  
ID ABO19941 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1096  
ID ABO24244 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1097  
ID ABR85993 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1098  
ID ABM10645 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1099  
ID ABR76644 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1100  
ID ABR89348 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1101  
ID ABM12475 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1102  
ID ABM05765 standard; protein; 360 AA.



DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1103  
ID ABO34890 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PD US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1104  
ID ABO2966 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1105  
ID ABO1894 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1106  
ID ABO19249 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1107  
ID ABO46460 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PD US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1108  
ID ABO48961 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PD US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1109  
ID ADA41970 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PD US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1110  
ID ABR6904 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003027273-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1111  
ID ABR89043 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003036119-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1112  
ID ABR72416 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003036120-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1113  
ID ABR74246 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1114  
ID ABO18514 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PD US2003044921-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1115  
ID ADA17317 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PD US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1116  
ID ABR80220 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1117  
ID ABO1441 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1118  
ID ABO2051 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1119  
ID ABR87213 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1120  
ID ABO12780 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PD US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;



RESULT 1121  
ID ABO30534 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1122  
ID ABO24434 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1123  
ID ABO29348 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1124  
ID ABO31178 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1125  
ID ABO14305 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1126  
ID ABO09730 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1127  
ID ABO38855 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1128  
ID ABO34620 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1129  
ID ABO51096 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1130  
ID ADA42820 standard; protein; 360 AA.

DE Human secreted/transmembrane protein, #42.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1131  
ID ABO03922 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1132  
ID ABO10392 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1133  
ID ABR77635 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1134  
ID ABR78845 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1135  
ID ABO23939 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1136  
ID ABR93703 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1137  
ID ABO1746 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1138  
ID ABR78169 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1139  
ID ABR89958 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;



Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1140  
ID ABM27484 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1141  
ID ABM13085 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1142  
ID ABO31788 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1143  
ID ABM14000 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1144  
ID ABM08205 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1145  
ID ABO40075 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1146  
ID ABM74510 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1147  
ID ABM33705 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1148  
ID ABM20164 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1149  
ID ABO48656 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1150  
ID ABR72721 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1151  
ID ABO15363 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1152  
ID ABR85078 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1153  
ID ABO15058 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1154  
ID ABO17193 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1155  
ID ABM17482 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1156  
ID ABR85383 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1157  
ID ABO17592 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1158  
ID ABM76949 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;



RESULT 1159  
ID ABO28128 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1160  
ID ABM22909 standard; protein: 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1161  
ID ABM30229 standard; protein: 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1162  
ID ABM21689 standard; protein: 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1163  
ID ABM21384 standard; protein: 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1164  
ID ABM14915 standard; protein: 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1165  
ID ABO40990 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1166  
ID ABO36720 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1167  
ID ABO37330 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1168

ID ABM75120 standard; protein: 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1169  
ID ABM33400 standard; protein: 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1170  
ID ABO46155 standard; protein: 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1171  
ID ADA82463 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1172  
ID ABM31754 standard; protein: 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1173  
ID ABM31144 standard; protein: 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1174  
ID ADB77739 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1175  
ID ADB74875 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1176  
ID ADB85771 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1177  
ID ABM32059 standard; protein: 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.



PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1178  
ID ABM32364 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1179  
ID ABM31449 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1180  
ID ABM30839 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1181  
ID ADC28521 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1182  
ID ADC39721 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1183  
ID ADC40235 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1184  
ID ADC19059 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1185  
ID ADC34359 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1186  
ID ADC29414 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049676-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1187  
ID ADC28945 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1188  
ID ADC40830 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1189  
ID ADC19487 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1190  
ID ADC33935 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1191  
ID ADC13005 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1192  
ID ADC12457 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1193  
ID ADD05501 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1194  
ID ADD05012 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Length 360;  
RESULT 1195  
ID ADD04018 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003104381-A1.  
PD 05-JUN-2003.



PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1196  
ID ADD03594 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1197  
ID ADE34846 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1198  
ID ADG02496 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1199  
ID ADG01203 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1200  
ID ADP93578 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1201  
ID ADG12193 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1202  
ID ADH08853 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1203  
ID ADH59329 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1204  
ID ADI38108 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;

Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1205  
ID ADJ26376 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1206  
ID ADJ32634 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1207  
ID ADM30168 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 7; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1208  
ID ADE79291 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1209  
ID ADE79715 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1210  
ID ADE73391 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1211  
ID ADE74165 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1212  
ID ADE73926 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1213  
ID ADE74777 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1214  
ID ADE99480 standard; protein; 360 AA.



DE Human secreted/transmembrane protein, #42.  
PN US2003211576-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1215  
ID ADE98599 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1216  
ID ADE99026 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1217  
ID ADG40496 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODO/) GODDARD A. J.  
PA (GURN/) GURNEY A. L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1218  
ID ADF73890 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1219  
ID ADF95990 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1220  
ID ADF73466 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003166051-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1221  
ID ADG04261 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003215812-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1222  
ID ADG040421 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1223  
ID ADG82677 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1224  
ID ADG92309 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1225  
ID ADG92736 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1226  
ID ADH25958 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1227  
ID ADH32927 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1228  
ID ADH20525 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1229  
ID ADH07380 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004006211-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODO/) GODDARD A. J.  
PA (GURN/) GURNEY A. L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1230  
ID ADH59925 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003215904-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1231



ID ADH06953 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004005665-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODO/) GODDARD A.  
PA (GODD/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1232  
ID ADI18695 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003152999-A1.  
PD 14-AUG-2003.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1233  
ID ADI65415 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003148419-A1.  
PD 07-AUG-2003.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1234  
ID ADI37678 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003096340-A1.  
PD 22-MAY-2003.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1235  
ID ADH97474 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003190610-A1.  
PD 09-OCT-2003.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1236  
ID ADI65842 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003148371-A1.  
PD 07-AUG-2003.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1237  
ID ADH60585 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004023331-A1.  
PD 05-FEB-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODO/) GODDARD A.  
PA (GODD/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1238  
ID ADJ99642 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003187238-A1.  
PD 02-OCT-2003.  
PA (GERH ) GENENTECH INC.

Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1239  
ID ADL08835 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003186358-A1.  
PD 02-OCT-2003.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1240  
ID ADI54666 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1241  
ID ADM25176 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003096233-A1.  
PD 22-MAY-2003.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1242  
ID ADM29926 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003190611-A1.  
PD 09-OCT-2003.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1243  
ID ADI64437 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1244  
ID ADM31333 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1245  
ID ADM36380 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1246  
ID ADM440185 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1247  
ID ADI91793 standard; protein; 360 AA.  
DE Human PRO271 protein SEQ ID NO:14.  
PN WO2004024076-A2.  
PD 25-MAR-2004.  
PA (GERH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;



Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1248  
ID ADO06248 standard; protein: 360 AA.  
DE Human PRO polypeptide #38.  
PN US6686451-B1.  
PD 03-FEB-2004.  
PA (GERTH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1249  
ID ADN37793 standard; protein: 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GERTH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1250  
ID ADR1100 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004137561-A1.  
PD 15-JUL-2004.  
PA (GERTH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1251  
ID ADR18009 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004147017-A1.  
PD 29-JUL-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FLIV/) FLIVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1252  
ID AD574648 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein #42.  
PN US2004185531-A1.  
PD 23-SEP-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FLIV/) FLIVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1253  
ID ADR60851 standard; protein: 404 AA.  
DE Plant polypeptide, SEQ ID 10928.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Query Match 2.4%; Score 8; DB 8; Length 404;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
RESULT 1256  
ID ABO82428 standard; protein: 410 AA.  
DE Pseudomonas aeruginosa polypeptide #14603.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 2.4%; Score 8; DB 7; Length 410;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
RESULT 1257  
ID ADX75594 standard; protein: 419 AA.  
DE Plant full length insert polypeptide seqid 44960.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LTIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match 2.4%; Score 8; DB 8; Length 419;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1258  
ID AEA20028 standard; protein: 422 AA.  
DE Novel human polypeptide SEQ ID NO 722.  
PN WO2005049806-A2.  
PD 02-JUN-2005.  
PA (NOVE-) NOVELO INC.  
Query Match 2.4%; Score 8; DB 9; Length 422;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1259  
ID ADX88402 standard; protein: 438 AA.  
DE Plant full length insert polypeptide seqid 51066.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LTIU/) LIU J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEM/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1253  
ID ADT03685 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003152922-A1.  
PD 14-AUG-2003.  
PA (GERTH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1254  
ID AEA37923 standard; protein: 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GERTH ) GENENTECH INC.  
Query Match 2.4%; Score 8; DB 9; Length 360;  
Best Local Similarity 100.0%; Pred. No. 93;  
RESULT 1255  
ID ADR60851 standard; protein: 404 AA.  
DE Plant polypeptide, SEQ ID 10928.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Query Match 2.4%; Score 8; DB 8; Length 404;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
RESULT 1256  
ID ABO82428 standard; protein: 410 AA.  
DE Pseudomonas aeruginosa polypeptide #14603.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 2.4%; Score 8; DB 7; Length 410;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
RESULT 1257  
ID ADX75594 standard; protein: 419 AA.  
DE Plant full length insert polypeptide seqid 44960.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LTIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match 2.4%; Score 8; DB 8; Length 419;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1258  
ID AEA20028 standard; protein: 422 AA.  
DE Novel human polypeptide SEQ ID NO 722.  
PN WO2005049806-A2.  
PD 02-JUN-2005.  
PA (NOVE-) NOVELO INC.  
Query Match 2.4%; Score 8; DB 9; Length 422;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1259  
ID ADX88402 standard; protein: 438 AA.  
DE Plant full length insert polypeptide seqid 51066.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LTIU/) LIU J.



PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match 2.4%; Score 8; DB 8; Length 438;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1260  
ID ADY09988 standard; protein; 462 AA.  
DE Plant full length insert polypeptide seqid 65803.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUT/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match 2.4%; Score 8; DB 8; Length 462;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1261  
ID AAG74913 standard; protein; 486 AA.  
DE Human colon cancer antigen protein SEQ ID NO:5677.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCT INC.  
Query Match 2.4%; Score 8; DB 4; Length 486;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
RESULT 1262  
ID ADU02541 standard; protein; 500 AA.  
DE Novel human polypeptide seqid 1008.  
PN WO2004093804-A2.  
PD 04-NOV-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 2.4%; Score 8; DB 8; Length 500;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
RESULT 1263  
ID AAE38765 standard; protein; 585 AA.  
DE Human 69624 protein sodium sulphate symporter domain.  
PN US2002193582-A1.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.4%; Score 8; DB 7; Length 585;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
RESULT 1264  
ID ADO55650 standard; protein; 688 AA.  
DE Wheat storage protein #8.  
PN WO2004044208-A2.  
PD 27-MAY-2004.  
PA (PLAN-) PLANTECHNO SRL.  
PA (PROG-) PROGEO SCRL.  
PA (TECN-) TECNOLIMENTI SCPA.  
Query Match 2.4%; Score 8; DB 8; Length 688;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
RESULT 1265  
ID ABG10285 standard; protein; 808 AA.  
DE Novel human diagnostic protein #10276.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.4%; Score 8; DB 4; Length 808;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
RESULT 1266  
ID ABB63905 standard; protein; 868 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 18507.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 2.4%; Score 8; DB 4; Length 868;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
RESULT 1267  
ID AAM39436 standard; protein; 940 AA.  
DE Human polypeptide SEQ ID NO 2581.

PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.4%; Score 8; DB 4; Length 940;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
RESULT 1268  
ID AAV78053 standard; protein; 1117 AA.  
DE Human desmoglein 2 protein sequence.  
PN WO200210767-A2.  
PD 07-FEB-2002.  
PA (TUIA-) TULANE EDUCATIONAL FUND.  
Query Match 2.4%; Score 8; DB 5; Length 1117;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 1269  
ID ADR99232 standard; protein; 1117 AA.  
DE Clone IMAGE:4242700, SEQ ID 238.  
PN WO2004078035-A2.  
PD 16-SEP-2004.  
PA (FARB-) BAYER PHARM CORP.  
Query Match 2.4%; Score 8; DB 8; Length 1117;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 1270  
ID ADU06431 standard; protein; 1117 AA.  
DE Novel bronchial cancer-associated human protein SeqID655.  
PN DE10316701-A1.  
PD 04-NOV-2004.  
PA (HINZ/) HINZMANN B.  
PA (HERM/) HERMANN K.  
PA (CAST/) HEIDEN CASTANOS-VELEZ B.  
Query Match 2.4%; Score 8; DB 8; Length 1117;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 1271  
ID AAE20266 standard; protein; 1118 AA.  
DE Human lung specific gene (LSG) protein #4.  
PN WO200208278-A2.  
PD 31-JAN-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 2.4%; Score 8; DB 5; Length 1118;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 1272  
ID ABG10284 standard; protein; 1120 AA.  
DE Novel human diagnostic protein #10275.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.4%; Score 8; DB 4; Length 1120;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 1273  
ID AAM41222 standard; protein; 1121 AA.  
DE Human polypeptide SEQ ID NO 6153.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.4%; Score 8; DB 4; Length 1121;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 1274  
ID ADO55146 standard; protein; 1235 AA.  
DE Protein #48 with increased gene expression in renal cell carcinoma.  
PN WO2004032842-A2.  
PD 22-APR-2004.  
PA (VAND-) VAN ANDEL INST.  
Query Match 2.4%; Score 8; DB 8; Length 1235;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
RESULT 1275  
ID ABR58408 standard; protein; 1280 AA.  
DE Human NOV22a.  
PN WO2003029423-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.4%; Score 8; DB 6; Length 1280;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
RESULT 1276  
ID ADI40906 standard; peptide; 24 AA.



DE hSARS virus peptide, SEQ ID 1895.  
PN WO2004085650-A1.  
PD 07-OCT-2004.  
PA (UYHK-) UNIV HONG KONG.  
Query Match 2.1%; Score 7; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 85;  
RESULT 1277  
ID ADS80323 standard; protein; 24 AA.  
DE SARS virus complementary DNA strand reading frame 2 protein #305.  
PN WO2004085455-A1.  
PD 07-OCT-2004.  
PA (UYHK-) UNIV HONG KONG.  
Query Match 2.1%; Score 7; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 85;  
RESULT 1278  
ID ADP38436 standard; peptide; 24 AA.  
DE hSARS virus peptide, SEQ ID 1895.  
PN WO2004085633-A1.  
PD 07-OCT-2004.  
PA (UYHK-) UNIV HONG KONG.  
Query Match 2.1%; Score 7; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 85;  
RESULT 1279  
ID AAB52107 standard; peptide; 31 AA.  
DE Human secreted protein encoded by cDNA #4.  
PN WO200061624-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 3; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1280  
ID AAB19733 standard; peptide; 31 AA.  
DE Human secreted protein amino acid sequence - SEQ ID No 201.  
PN WO200277188-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 6; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1281  
ID ABP99811 standard; protein; 31 AA.  
DE Human secreted protein SEQ ID NO 755.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 6; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1282  
ID ADC20544 standard; protein; 31 AA.  
DE Human secreted protein - amino acid sequence #225.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 7; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1283  
ID ADS04547 standard; protein; 47 AA.  
DE Staphylococcus epidermis polypeptide seqid 3842.  
PN US2004147734-A1.  
PD 29-JUL-2004.  
PA (DOUC/) DOUCETTE-STAMM L.  
Query Match 2.1%; Score 7; DB 8; Length 47;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1284  
ID AAG59891 standard; protein; 64 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77517.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 64;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
RESULT 1285  
ID AAB82439 standard; protein; 65 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:10032.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 4; Length 65;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
RESULT 1286  
ID ADF04448 standard; protein; 67 AA.  
DE Bacterial polypeptide #561.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 2.1%; Score 7; DB 7; Length 67;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
RESULT 1287  
ID AAU54392 standard; protein; 72 AA.  
DE Propionibacterium acnes immunogenic protein #15288.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 2.1%; Score 7; DB 4; Length 72;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
RESULT 1288  
ID ABB34821 standard; protein; 72 AA.  
DE Human ORF3794 protein, SEQ ID NO:7588.  
PN WO200190366-A2.  
PD 29-NOV-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.1%; Score 7; DB 5; Length 72;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
RESULT 1289  
ID AAM50911 standard; protein; 72 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #15587.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 2.1%; Score 7; DB 6; Length 72;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
RESULT 1290  
ID AAG05240 standard; protein; 75 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1571.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 75;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
RESULT 1291  
ID ADM26879 standard; protein; 75 AA.  
DE Hyperthermophile Methanopyrus kandleri protein #1485.  
PN WO2003076575-A2.  
PD 18-SEP-2003.  
PA (FIDE-) FIDELITY SYSTEMS INC.  
Query Match 2.1%; Score 7; DB 7; Length 75;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
RESULT 1292  
ID AAU55764 standard; protein; 76 AA.  
DE Propionibacterium acnes immunogenic protein #16660.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 2.1%; Score 7; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
RESULT 1293  
ID AAM52283 standard; protein; 76 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #16959.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 2.1%; Score 7; DB 6; Length 76;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
RESULT 1294  
ID ADK15830 standard; protein; 76 AA.  
DE Human ABCA10 N-terminal peptide fragment SEQ ID NO:39.  
PN WO2004018633-A2.



PD 04-MAR-2004.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 2.1%; Score 7; DB 8; Length 76;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
RESULT 1295  
ID ABP32005 standard; protein; 85 AA.  
DE Human ORF978 protein, SEQ ID NO:1956.  
PN WO200190366-A2.  
PD 29-NOV-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.1%; Score 7; DB 5; Length 85;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
RESULT 1296  
ID AAG11654 standard; protein; 86 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10452.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 86;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
RESULT 1297  
ID AAG14682 standard; protein; 92 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14638.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 92;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
RESULT 1298  
ID AAG15133 standard; protein; 92 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 15546.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 92;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
RESULT 1299  
ID AAG07776 standard; protein; 93 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 5059.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 93;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
RESULT 1300  
ID AAG39872 standard; protein; 93 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49396.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 93;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
RESULT 1301  
ID AAM69995 standard; protein; 97 AA.  
DE Revised complete rodent chemokine MCP243 amino acid sequence.  
PN WO9832858-A2.  
PD 30-JUL-1998.  
PA (SCHE ) SCHERING CORP.  
Query Match 2.1%; Score 7; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1302  
ID AAV39480 standard; protein; 97 AA.  
DE Propionibacterium acnes immunogenic protein #376.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 2.1%; Score 7; DB 4; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1303  
ID ADZ58701 standard; protein; 97 AA.  
DE Mouse MCP-2 protein SEQ ID NO:29.  
PN CA2351275-A1.  
PD 20-DEC-2001.  
PA (SWIT-) SWITCH BIOTECH AG.  
Query Match 2.1%; Score 7; DB 5; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1304

ID ABM3599 standard; protein; 97 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #675.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 2.1%; Score 7; DB 6; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1305  
ID ADS85069 standard; protein; 97 AA.  
DE Mouse atopic dermatitis-related protein sequence SegID71.  
PN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES. INC.  
PA (UTUT-) UNIV UJNTENDO.  
Query Match 2.1%; Score 7; DB 8; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1306  
ID AAR93087 standard; protein; 98 AA.  
DE Human chemokine beta-10.  
PN WO9605856-A1.  
PD 29-FEB-1996.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1307  
ID AAM2670 standard; protein; 98 AA.  
DE Human chemokine beta10 or monocyte chemotactic protein 4.  
PN WO9731098-A1.  
PD 28-AUG-1997.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1308  
ID AAM30191 standard; protein; 98 AA.  
DE Monocyte chemotactic protein 5.  
PN WO9735982-A2.  
PD 02-OCT-1997.  
PA (ICOS-) ICOS CORP.  
Query Match 2.1%; Score 7; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1309  
ID AAM56087 standard; protein; 98 AA.  
DE Human monocyte chemottractant protein 4.  
PN WO9814573-A1.  
PD 09-APR-1998.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 2.1%; Score 7; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1310  
ID AAY41164 standard; protein; 98 AA.  
DE Human chemokine beta-10 (Ckbeta-10) polypeptide.  
PN US5981230-A.  
PD 09-NOV-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1311  
ID AAB15831 standard; protein; 98 AA.  
DE Human chemokine MIP1beta SEQ ID NO: 83.  
PN WO200042071-A2.  
PD 20-JUL-2000.  
PA (NEOR-) NEORX CORP.  
Query Match 2.1%; Score 7; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1312  
ID AAB15808 standard; protein; 98 AA.  
DE Human chemokine CCR-2 SEQ ID NO: 50.  
PN WO200042071-A2.  
PD 20-JUL-2000.  
PA (NEOR-) NEORX CORP.  
Query Match 2.1%; Score 7; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1313



PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 8; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1321  
ID ADO32066 standard; protein; 98 AA.  
DE Chemokine monocyte chemotactic protein (MCP-4).  
PN US6673344-B1.  
PD 06-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 8; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1322  
ID ADO20884 standard; protein; 98 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3704.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.1%; Score 7; DB 8; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1323  
ID ADM20982 standard; protein; 98 AA.  
DE Human chemokine (CK) beta-10 protein.  
PN US2004265974-A1.  
PD 30-DEC-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 9; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1324  
ID AAG26647 standard; protein; 100 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 31182.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 1325  
ID ABB42669 standard; peptide; 100 AA.  
DE Peptide #10175 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 1326  
ID AAM36482 standard; protein; 100 AA.  
DE Peptide #10519 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 1327  
ID ABB2606 standard; protein; 100 AA.  
DE Protein #8005 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 1328  
ID AAM76374 standard; protein; 100 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 36680.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 1329  
ID AAM63559 standard; protein; 100 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 35664.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 1330  
ID AAM66672 standard; protein; 98 AA.  
DE Human chemokine MCP-4.  
PN US2004037805-A1.  
PD 26-FEB-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1314  
ID AAB31795 standard; protein; 98 AA.  
DE Amino acid sequence of a human chemokine beta-10 polypeptide.  
PN US6174995-B1.  
PD 16-JAN-2001.  
PA (LIHM/) LI H.  
PA (ADAM/) ADAMS M.  
PA (LIMA/) LIMA S H.  
PA (ALDE/) ALDERSON R.  
PA (LITY/) LI Y.  
PA (PARM/) PARMELEE D.  
PA (WHIT/) WHITE J.  
PA (APPL/) APPLEBAUM R.  
Query Match 2.1%; Score 7; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1315  
ID AAO19997 standard; protein; 98 AA.  
DE Protein of human chemokine beta-10 (CKbeta-10).  
PN US2002026044-A1.  
PD 28-FEB-2002.  
PA (LIHM/) LI H.  
PA (ADAM/) ADAMS M D.  
Query Match 2.1%; Score 7; DB 5; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1316  
ID AAE15751 standard; protein; 98 AA.  
DE Human chemokine beta-10 (ckb-10) protein.  
PN WO200194557-A1.  
PD 13-DEC-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (GLAX) GLAXOSMITHKLINE.  
Query Match 2.1%; Score 7; DB 5; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1317  
ID AAU77180 standard; protein; 98 AA.  
DE Human chemokine MCP-4 (hmcp-4) polypeptide.  
PN US2002034494-A1.  
PD 21-MAR-2002.  
PA (VICA/) VICARI A P.  
PA (CAUX/) CAUX C.  
PA (LAFA/) IAFACE D.  
Query Match 2.1%; Score 7; DB 5; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1318  
ID ADD46371 standard; protein; 98 AA.  
DE Human Protein Q99616, SEQ ID NO 12051.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 2.1%; Score 7; DB 7; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1319  
ID AAD339903 standard; protein; 98 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C273.  
PN WO2003042861-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 2.1%; Score 7; DB 7; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 1320  
ID ADU66672 standard; protein; 98 AA.  
DE Human chemokine MCP-4.  
PN US2004037805-A1.  
PD 26-FEB-2004.



Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 1330  
ID ABG58080 standard; peptide; 100 AA.  
DE Human liver peptide, SEQ ID No 36728.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 1331  
ID ABG45662 standard; peptide; 100 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35327.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 5; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 1332  
ID AAB40922 standard; protein; 101 AA.  
DE Human ORFX ORF686 polypeptide sequence SEQ ID NO:1372.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.1%; Score 7; DB 3; Length 101;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 1333  
ID AAY16779 standard; protein; 104 AA.  
DE Human secreted protein (clone aeo2\_2).  
PN WO9924469-A1.  
PD 20-MAY-1999.  
PA (GBMY) GENETICS INST INC.  
Query Match 2.1%; Score 7; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
RESULT 1334  
ID AAG14713 standard; protein; 105 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14679.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 105;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
RESULT 1335  
ID ABG13572 standard; protein; 106 AA.  
DE Novel human diagnostic protein #13563.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.1%; Score 7; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
RESULT 1336  
ID AAY75273 standard; protein; 120 AA.  
DE Neisseria meningitidis ORF 628 protein sequence SEQ ID NO:2020.  
PN WO9957280-A2.  
PD 11-NOV-1999.  
PA (CHIR) CHIRON CORP.  
Query Match 2.1%; Score 7; DB 3; Length 120;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 1337  
ID ABB69393 standard; protein; 120 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 34971.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 2.1%; Score 7; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 1338  
ID AAG14712 standard; protein; 134 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14678.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 134;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1339  
ID ABO1162 standard; protein; 135 AA.  
DE Novel human diagnostic protein #1133.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.1%; Score 7; DB 4; Length 135;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1340  
ID AAG19471 standard; protein; 137 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21286.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 137;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
RESULT 1341  
ID ABW88501 standard; protein; 140 AA.  
DE Rice abiotic stress responsive polypeptide SEQ ID NO:6747.  
PN WO2003008540-A2.  
PD 30-JAN-2003.  
PA (STGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 2.1%; Score 7; DB 7; Length 140;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
RESULT 1342  
ID ADM25851 standard; protein; 145 AA.  
DE Hyperthermophile Methanopyrus kandleri protein #457.  
PN WO2003076575-A2.  
PD 18-SEP-2003.  
PA (FIDE-) FIDELITY SYSTEMS INC.  
Query Match 2.1%; Score 7; DB 7; Length 145;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 1343  
ID AAB58938 standard; protein; 153 AA.  
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 646.  
PN WO200055173-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.1%; Score 7; DB 3; Length 153;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
RESULT 1344  
ID ADI21209 standard; protein; 159 AA.  
DE Novel human protein #184.  
PN WO2003025146-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.1%; Score 7; DB 7; Length 159;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
RESULT 1345  
ID ADI214578 standard; protein; 159 AA.  
DE Human tumor associated antigenic protein MGC71744 Seg 94.  
PN WO2005030250-A2.  
PD 07-APR-2005.  
PA (GANV-) GANVYED PHARM AG.  
Query Match 2.1%; Score 7; DB 9; Length 159;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
RESULT 1346  
ID AAG19470 standard; protein; 162 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21285.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 162;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
RESULT 1347  
ID ABA49191 standard; protein; 163 AA.  
DE L. rhamosus polypeptide #55.  
PN WO2005056801-A1.  
PD 23-JUN-2005.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 2.1%; Score 7; DB 9; Length 163;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
RESULT 1348  
ID ADR09266 standard; protein; 170 AA.



DE Human protein useful for treating neurological disease Seq 2772.  
PN BPI447413-A2.  
PD 18-AUG-2004.  
PA (MOLE-) RBS ASSOC BIOTECHNOLOGY.  
Query Match 2.1%; Score 7; DB 8; Length 170;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
RESULT 1349  
ID AB023743 standard; protein; 179 AA.  
DE Protein encoded by Prokaryotic essential gene #9270.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (EITR-) EITRA PHARM INC.  
Query Match 2.1%; Score 7; DB 6; Length 179;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
RESULT 1350  
ID AB010263 standard; protein; 192 AA.  
DE Mason-Pfizer monkey virus enveloped protein gp20.  
PN US6518013-B1.  
PD 11-FEB-2003.  
PA (TRIM-) TRIMERIS INC.  
Query Match 2.1%; Score 7; DB 6; Length 192;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
RESULT 1351  
ID AAU14098 standard; peptide; 193 AA.  
DE Simian Mason-Pfizer monkey virus enveloped protein gp20.  
PN WO200151673-A2.  
PD 19-JUL-2001.  
PA (TRIM-) TRIMERIS INC.  
Query Match 2.1%; Score 7; DB 4; Length 193;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
RESULT 1352  
ID AAU33258 standard; protein; 194 AA.  
DE Novel human secreted protein #3749.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.1%; Score 7; DB 4; Length 194;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
RESULT 1353  
ID AAM17341 standard; protein; 201 AA.  
DE Peptide #3775 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1354  
ID ABB36350 standard; peptide; 201 AA.  
DE Peptide #3856 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1355  
ID AAM29848 standard; protein; 201 AA.  
DE Peptide #3885 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1356  
ID ABB31155 standard; peptide; 201 AA.  
DE Peptide #3806 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1357  
ID ABB21708 standard; protein; 201 AA.  
DE Protein #3707 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1358  
ID AAM69509 standard; protein; 201 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29815.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1359  
ID AAM57117 standard; protein; 201 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29222.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1360  
ID ABB51183 standard; peptide; 201 AA.  
DE Human liver peptide, SEQ ID No 29831.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1361  
ID AAM05030 standard; protein; 201 AA.  
DE Peptide #3712 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1362  
ID ABB39134 standard; peptide; 201 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 28799.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 2.1%; Score 7; DB 5; Length 201;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1363  
ID AD775735 standard; protein; 202 AA.  
DE Xanthomonas campestris XCCU3\_1220, SEQ ID 78.  
PN US2005100892-A1.  
PD 12-MAY-2005.  
PA (SHEA/) SHEA T P.  
PA (SLAT/) SLATER S C.  
Query Match 2.1%; Score 7; DB 9; Length 202;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1364  
ID ABB04730 standard; protein; 205 AA.  
DE Human mper3-23 protein SEQ ID NO:2.  
PN CN1311206-A.  
PD 05-SEP-2001.  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
Query Match 2.1%; Score 7; DB 5; Length 205;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1365  
ID AAM23009 standard; protein; 208 AA.  
DE Canine herpesvirus PCICP4-208 protein.  
PN WO9729772-A1.  
PD 21-AUG-1997.  
PA (HESK-) HESKA CORP.  
Query Match 2.1%; Score 7; DB 2; Length 208;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1366  
ID AAM72665 standard; protein; 208 AA.  
DE Canine herpes virus protein sequence PCICP4-208.



PN USS804197-A.  
PD 08-SEP-1998.  
PA (HESK-) HESKA CORP.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 2; Length 208;  
Pred. No. 5.4e+02;  
RESULT 1367  
ID AAB51322 standard; protein; 208 AA.  
DE Canine herpes virus protein sequence SEQ ID NO:72.  
PN US6159478-A.  
PD 12-DEC-2000.  
PA (HESK-) HESKA CORP.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 4; Length 208;  
Pred. No. 5.4e+02;  
RESULT 1368  
ID AAB39139 standard; protein; 208 AA.  
DE CHV PCICP4 208 protein.  
PN US2003049844-A1.  
PD 13-MAR-2003.  
PA (HESK-) HESKA CORP.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 7; Length 208;  
Pred. No. 5.4e+02;  
RESULT 1369  
ID ABG13573 standard; protein; 211 AA.  
DE Novel human diagnostic protein #13564.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 4; Length 211;  
Pred. No. 5.4e+02;  
RESULT 1370  
ID AAG55192 standard; protein; 220 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 70733.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 3; Length 220;  
Pred. No. 5.6e+02;  
RESULT 1371  
ID ABP29523 standard; protein; 226 AA.  
DE Streptococcus polypeptide SEQ ID NO 8222.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 5; Length 226;  
Pred. No. 5.7e+02;  
RESULT 1372  
ID ADP58027 standard; protein; 227 AA.  
DE Plant polypeptide, SEQ ID 8104.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 8; Length 227;  
Pred. No. 5.8e+02;  
RESULT 1373  
ID AAG19469 standard; protein; 228 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21284.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 3; Length 228;  
Pred. No. 5.8e+02;  
RESULT 1374  
ID AAY05733 standard; protein; 229 AA.  
DE Streptococcus pneumoniae MurB protein.  
PN EP911403-A2.  
PD 28-APR-1999.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 2; Length 229;  
Pred. No. 5.8e+02;  
RESULT 1375  
ID AAU43422 standard; protein; 230 AA.  
DE Propionibacterium acnes immunogenic protein #4318.  
PN WO200181581-A2.

PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 4; Length 230;  
Pred. No. 5.8e+02;  
RESULT 1376  
ID ABM39941 standard; protein; 230 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4617.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 6; Length 230;  
Pred. No. 5.8e+02;  
RESULT 1377  
ID AAB63119 standard; protein; 234 AA.  
DE Gene 41 human secreted protein homologous amino acid sequence #129.  
PN WO200061748-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 3; Length 234;  
Pred. No. 5.9e+02;  
RESULT 1378  
ID ABG25117 standard; protein; 235 AA.  
DE Novel human diagnostic protein #25108.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 4; Length 235;  
Pred. No. 5.9e+02;  
RESULT 1379  
ID ADX67601 standard; protein; 237 AA.  
DE Plant full length insert polypeptide seqid 38444.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TBBA/) TABASKA J E.  
PA (CMOY/) CAO Y.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 8; Length 237;  
Pred. No. 6e+02;  
RESULT 1380  
ID ADA33029 standard; protein; 244 AA.  
DE Acinetobacter Baumannii protein #190.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 6; Length 244;  
Pred. No. 6.1e+02;  
RESULT 1381  
ID ABP28316 standard; protein; 246 AA.  
DE Streptococcus polypeptide SEQ ID NO 5808.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 5; Length 246;  
Pred. No. 6.2e+02;  
RESULT 1382  
ID ABP65401 standard; protein; 246 AA.  
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:145.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST) SOC PROD NESTLE SA.  
Query Match  
Best Local Similarity 2.1%; Score 7; DB 5; Length 246;  
Pred. No. 6.2e+02;  
RESULT 1383  
ID ADV88876 standard; protein; 246 AA.  
DE Streptococcus agalactiae protein sequence, SEQ ID 1270.  
PN FR2824074-A1.  
PD 31-OCT-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.



Query Match 2.1%; Score 7; DB 8; Length 246;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1384  
ID ADV80129 standard; protein; 246 AA.  
DE Streptococcus agalactiae protein, SEQ ID 1270.  
PN W0200292818-A2.  
PD 21-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCT.  
Query Match 2.1%; Score 7; DB 8; Length 246;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1385  
ID ADV82261 standard; protein; 246 AA.  
DE Streptococcus agalactiae protein, SEQ ID 3402.  
PN W0200292818-A2.  
PD 21-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCT.  
Query Match 2.1%; Score 7; DB 8; Length 246;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1386  
ID ABU27486 standard; protein; 250 AA.  
DE Protein encoded by Prokaryotic essential gene #13013.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 2.1%; Score 7; DB 6; Length 250;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
RESULT 1387  
ID AAM47576 standard; protein; 261 AA.  
DE Drosophila cell cycle progression protein #5.  
PN W0200172774-A2.  
PD 04-OCT-2001.  
PA (CYCL-) CYCLACEL LTD.  
Query Match 2.1%; Score 7; DB 5; Length 261;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1388  
ID ADB63852 standard; protein; 262 AA.  
DE Human protein encoded by clone ASTRO20045840.  
PN EP108459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 2.1%; Score 7; DB 7; Length 262;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1389  
ID ADP94265 standard; protein; 266 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 2900.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 2.1%; Score 7; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
RESULT 1390  
ID AEA58135 standard; protein; 266 AA.  
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:2900.  
PN US2005136404-A1.  
PD 23-JUN-2005.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 2.1%; Score 7; DB 9; Length 266;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
RESULT 1391  
ID ABW92104 standard; protein; 276 AA.  
DE M. xanthus protein sequence, seq id 11303.  
PN US6833447-B1.  
PD 21-DEC-2004.  
PA (MONS) MONSANTO TECHNOLOGY LLC.  
Query Match 2.1%; Score 7; DB 9; Length 276;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
RESULT 1392  
ID ADK46429 standard; protein; 277 AA.  
DE Streptococcus pneumoniae protein, Seq ID No 2944.  
PN US6699703-B1.  
PD 02-MAR-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 2.1%; Score 7; DB 8; Length 277;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
RESULT 1393  
ID ADS41825 standard; protein; 280 AA.  
DE Bacterial polypeptide #20255.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 2.1%; Score 7; DB 8; Length 280;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
RESULT 1394  
ID AAU33365 standard; protein; 283 AA.  
DE Enterococcus faecalis cellular proliferation protein #1.  
PN W0200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 2.1%; Score 7; DB 4; Length 283;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 1395  
ID AAM80665 standard; protein; 289 AA.  
DE S. pneumoniae UDP-N-acetylglucosaminyl-3-enolpyruvate reductase.  
PN W09826072-A1.  
PD 18-JUN-1998.  
PA (ELIL) LILLY & CO ELI.  
Query Match 2.1%; Score 7; DB 2; Length 289;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1396  
ID ADN23273 standard; protein; 290 AA.  
DE Bacterial polypeptide #5926.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 2.1%; Score 7; DB 8; Length 290;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1397  
ID ADN23272 standard; protein; 290 AA.  
DE Bacterial polypeptide #5925.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 2.1%; Score 7; DB 8; Length 290;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1398  
ID ADP95627 standard; protein; 290 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 4262.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 2.1%; Score 7; DB 8; Length 290;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1399  
ID AEA59497 standard; protein; 290 AA.  
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:4262.  
PN US2005136404-A1.  
PD 23-JUN-2005.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 2.1%; Score 7; DB 9; Length 290;



Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1400  
ID AAV35025 standard; protein; 300 AA.  
DE Enterococcus faecalis cellular proliferation protein #312.  
PN W0200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 2.1%; Score 7; DB 4; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
RESULT 1401  
ID ABP28072 standard; protein; 300 AA.  
DE Streptococcus polypeptide SEQ ID NO 5320.  
PN W0200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 2.1%; Score 7; DB 5; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
RESULT 1402  
ID AAO22108 standard; protein; 300 AA.  
DE Protein of human CARD-3 SEQ ID NO 4.  
PN US6369196-B1.  
PD 09-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.1%; Score 7; DB 5; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
RESULT 1403  
ID AAV56270 standard; protein; 300 AA.  
DE Human Caspase recruitment domain protein 3, kinase domain.  
PN US6469140-B1.  
PD 22-OCT-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.1%; Score 7; DB 6; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
RESULT 1404  
ID ABU14645 standard; protein; 300 AA.  
DE Protein encoded by Prokaryotic essential gene #172.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 2.1%; Score 7; DB 6; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
RESULT 1405  
ID ADV88098 standard; protein; 300 AA.  
DE Streptococcus agalactiae protein sequence, SEQ ID 492.  
PN FR2824074-A1.  
PD 31-OCT-2002.  
PA (INSP-) INST PASTEUR.  
PA (CNRS-) CNRS CENT NAT RECH SCT.  
Query Match 2.1%; Score 7; DB 8; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
RESULT 1406  
ID ADV81529 standard; protein; 300 AA.  
DE Streptococcus agalactiae protein, SEQ ID 2670.  
PN W0200292818-A2.  
PD 21-NOV-2002.  
PA (INSP-) INST PASTEUR.  
PA (CNRS-) CNRS CENT NAT RECH SCT.  
Query Match 2.1%; Score 7; DB 8; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
RESULT 1407  
ID ADV79351 standard; protein; 300 AA.  
DE Streptococcus agalactiae protein, SEQ ID 492.  
PN W0200292818-A2.  
PD 21-NOV-2002.  
PA (INSP-) INST PASTEUR.  
PA (CNRS-) CNRS CENT NAT RECH SCT.  
Query Match 2.1%; Score 7; DB 8; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
RESULT 1408  
ID ADK47008 standard; protein; 301 AA.  
DE Streptococcus pneumoniae protein, Seq ID No 3523.  
PN US6699703-B1.

PD 02-MAR-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 2.1%; Score 7; DB 8; Length 301;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
RESULT 1409  
ID AAB46977 standard; protein; 303 AA.  
DE B. subtilis Murb protein SEQ ID 5.  
PN W020011054-A1.  
PD 15-FEB-2001.  
PA (PHAA) PHARMACIA & UPJOHN CO.  
Query Match 2.1%; Score 7; DB 4; Length 303;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
RESULT 1410  
ID ADX79238 standard; protein; 303 AA.  
DE Plant full length insert polypeptide seqid 48604.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 2.1%; Score 7; DB 8; Length 303;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
RESULT 1411  
ID ABU23861 standard; protein; 305 AA.  
DE Protein encoded by Prokaryotic essential gene #9388.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 2.1%; Score 7; DB 6; Length 305;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
RESULT 1412  
ID ABU43927 standard; protein; 307 AA.  
DE Protein encoded by Prokaryotic essential gene #29454.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 2.1%; Score 7; DB 6; Length 307;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1413  
ID ABU29984 standard; protein; 311 AA.  
DE Protein encoded by Prokaryotic essential gene #15511.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 2.1%; Score 7; DB 6; Length 311;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1414  
ID ADE63290 standard; protein; 312 AA.  
DE Rat Protein CAA28650, SEQ ID NO 9227.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 2.1%; Score 7; DB 7; Length 312;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1415  
ID ADI82102 standard; protein; 312 AA.  
DE Apolipoprotein B protein.  
PN W02004005934-A2.  
PD 15-JAN-2004.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Query Match 2.1%; Score 7; DB 8; Length 312;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1416  
ID AEA17430 standard; protein; 312 AA.  
DE Rat Apolipoprotein B protein.  
PN W02005047455-A2.  
PD 26-MAY-2005.  
PA (SEMB-) SEMBIOSIS GENETICS INC.  
Query Match 2.1%; Score 7; DB 9; Length 312;



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Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1417
ID AAM89165 standard; protein; 314 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7411.
PN W02003008540-A2.
PD 30-JUN-2003.
PA (STGN ) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 7; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1418
ID AAY05732 standard; protein; 316 AA.
DE Streptococcus pneumoniae MurB protein.
PN EP911403-A2.
PD 28-APR-1999.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
Query Match 2.1%; Score 7; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1419
ID AAN37701 standard; protein; 316 AA.
DE Streptococcus pneumoniae cellular proliferation protein #130.
PN W0200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1420
ID ABU01833 standard; protein; 316 AA.
DE S. pneumoniae type 4 strain protein from coding region #1409.
PN W0200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 2.1%; Score 7; DB 6; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1421
ID ABU46115 standard; protein; 316 AA.
DE Protein encoded by Prokaryotic essential gene #31642.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1422
ID ADZ26300 standard; protein; 316 AA.
DE Streptococcus UDP-N-acetylenolpyruvoylglycosamine reductase.
PN KR2004105416-A.
PD 16-DEC-2004.
PA (SONG/) SONG J H.
Query Match 2.1%; Score 7; DB 9; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1423
ID AAN37931 standard; protein; 317 AA.
DE Streptococcus pneumoniae cellular proliferation protein #360.
PN W0200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1424
ID ADN47056 standard; protein; 317 AA.
DE Thermococcus kodakarensis KOD1 protein sequence SeqID934.
PN W02004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 2.1%; Score 7; DB 8; Length 317;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1425
ID AAG28738 standard; protein; 318 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34069.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 318;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1426
ID AAB6957 standard; protein; 318 AA.
DE D. melanogaster peptide receptor SEQ ID 12.
PN DE10013618-A1.
PD 20-SEP-2001.
PA (FARB ) BAYER AG.
Query Match 2.1%; Score 7; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1427
ID ADC96745 standard; protein; 318 AA.
DE E. faecium protein sequence SEQ ID 6372.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.1%; Score 7; DB 7; Length 318;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1428
ID AAG28737 standard; protein; 320 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34068.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1429
ID ABU11628 standard; protein; 330 AA.
DE Human MDP1 polypeptide SEQ ID 575.
PN W0200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.1%; Score 7; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
RESULT 1430
ID ADF06337 standard; protein; 332 AA.
DE Bacterial polypeptide #2450.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.1%; Score 7; DB 7; Length 332;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1431
ID ADX71573 standard; protein; 343 AA.
DE Plant full length insert polypeptide seqid 40939.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LITU/) LIU J.
PA (ZHOV/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 2.1%; Score 7; DB 8; Length 343;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
RESULT 1432
ID ADX68254 standard; protein; 343 AA.
DE Plant full length insert polypeptide seqid 39097.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LITU/) LIU J.
PA (ZHOV/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 2.1%; Score 7; DB 8; Length 343;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
RESULT 1433
ID AAB43522 standard; protein; 344 AA.
DE Human cancer associated protein sequence SEQ ID NO:967.
PN W0200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 3; Length 344;
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Best Local Similarity 100.0%; Pred. No. 8.2e+02;
RESULT 1434
ID ABU19490 standard; protein; 344 AA.
DE Protein encoded by Prokaryotic essential gene #5017.
PN W020027183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
RESULT 1435
ID ABJ26048 standard; protein; 345 AA.
DE Aspergillus fumigatus essential gene protein #706.
PN W0200286090-A2.
PD 31-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
RESULT 1436
ID ADX90108 standard; protein; 354 AA.
DE Plant full length insert polypeptide seqid 52772.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 2.1%; Score 7; DB 8; Length 354;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
RESULT 1437
ID ADU27576 standard; protein; 357 AA.
DE Protein encoded by Prokaryotic essential gene #13103.
PN W020027183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 357;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
RESULT 1438
ID ABO83519 standard; protein; 357 AA.
DE Pseudomonas aeruginosa polypeptide #15694.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.1%; Score 7; DB 7; Length 357;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
RESULT 1439
ID AAU18004 standard; protein; 361 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 149.
PN W0200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 4; Length 361;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 1440
ID ADB31628 standard; protein; 361 AA.
DE Human novel protein SEQ ID NO 149.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 7; Length 361;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 1441
ID ADO07190 standard; protein; 362 AA.
DE Saccharomyces cerevisiae asparaginase.
PN W02004032648-A1.
PD 22-APR-2004.
PA (NOVO) NOVOZYMES AS.
Query Match 2.1%; Score 7; DB 8; Length 362;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 1442
ID AAM29662 standard; protein; 366 AA.
DE Homo sapiens CN483_2 clone secreted protein.
PN W09830695-A2.
PD 16-JUL-1998.
PA (GENY) GENETICS INST INC.
Query Match 2.1%; Score 7; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
RESULT 1443
ID ADN23206 standard; protein; 367 AA.
DE Bacterial polypeptide #5859.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.1%; Score 7; DB 8; Length 367;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
RESULT 1444
ID ADN23579 standard; protein; 369 AA.
DE Bacterial polypeptide #6232.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.1%; Score 7; DB 8; Length 369;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
RESULT 1445
ID ADY08632 standard; protein; 373 AA.
DE Plant full length insert polypeptide seqid 64447.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 2.1%; Score 7; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
RESULT 1446
ID ADH86933 standard; protein; 375 AA.
DE Enterococcus faecalis polypeptide #1413.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 2.1%; Score 7; DB 7; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
RESULT 1447
ID ABB61525 standard; protein; 376 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11367.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.1%; Score 7; DB 4; Length 376;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 1448
ID ADT61003 standard; protein; 376 AA.
DE Plant polypeptide, SEQ ID 11080.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 2.1%; Score 7; DB 8; Length 376;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 1449
ID ADN24357 standard; protein; 377 AA.
DE Bacterial polypeptide #7010.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
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PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 2.1%; Score 7; DB 8; Length 377;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
RESULT 1450  
ID AAG28736 standard; protein; 391 AA.  
DE Arbidopis chailana protein fragment SEQ ID NO: 34067.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 2.1%; Score 7; DB 3; Length 391;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
RESULT 1451  
ID ADY60859 standard; protein; 403 AA.  
DE RIPK2 isoform RIPK2v1.2, SEQ ID 4.  
PN US200505908-A1.  
PD 17-MAR-2005.  
PA (ARMO/) ARMOUR C D.  
PA (CAST/) CASTLE J C.  
PA (GAR/) GARRETT-ENGLE P W.  
PA (KANZ/) KAN Z.  
PA (LOER/) LOERCH P M.  
PA (TSIN/) TSINOREMAS N P.  
Query Match 2.1%; Score 7; DB 9; Length 403;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1452  
ID AD63997 standard; protein; 403 AA.  
DE Human cancer-linked gene RIPK2, protein, SEQ ID 38.  
PN WO2005035724-A2.  
PD 21-APR-2005.  
PA (AVAL-) AVALON PHARM INC.  
Query Match 2.1%; Score 7; DB 9; Length 403;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1453  
ID AAU51026 standard; protein; 405 AA.  
DE Propionibacterium acnes immunogenic protein #11922.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 2.1%; Score 7; DB 4; Length 405;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1454  
ID ABA47545 standard; protein; 405 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #12221.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 2.1%; Score 7; DB 6; Length 405;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1455  
ID AAW75856 standard; protein; 408 AA.  
DE Human secretory protein of clone COL39-3.  
PN WO9833916-A2.  
PD 06-AUG-1998.  
PA (GENY-) GENETICS INST INC.  
Query Match 2.1%; Score 7; DB 2; Length 408;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
RESULT 1456  
ID AA445161 standard; protein; 408 AA.  
DE Human secreted protein clone COL39\_3 protein sequence.  
PN US9565397-A.  
PD 12-OCT-1999.  
PA (GENY-) GENETICS INST INC.  
Query Match 2.1%; Score 7; DB 2; Length 408;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
RESULT 1457  
ID ABU27137 standard; protein; 410 AA.  
DE Protein encoded by Prokaryotic essential gene #12664.  
PN WO200272183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 2.1%; Score 7; DB 6; Length 410;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
RESULT 1458  
ID AAB16533 standard; protein; 415 AA.  
DE Bacteriophage 44AHD protein sequence 44HDOFR005.  
PN WO20032825-A2.  
PD 08-JUN-2000.  
PA (PHAG-) PHAGETECH INC.  
Query Match 2.1%; Score 7; DB 3; Length 415;  
Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
RESULT 1459  
ID AAM42401 standard; protein; 417 AA.  
DE TRAF2 binding protein encoded by clone 15.  
PN WO9737016-A1.  
PD 09-OCT-1997.  
PA (YEDA-) YEDA RES & DEV CO LTD.  
Query Match 2.1%; Score 7; DB 2; Length 417;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
RESULT 1460  
ID AAM60149 standard; protein; 419 AA.  
DE M. vaccae antigen GV-38B 3' amino acid sequence.  
PN WO9808542-A2.  
PD 05-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP.  
Query Match 2.1%; Score 7; DB 2; Length 419;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
RESULT 1461  
ID AAY14896 standard; protein; 419 AA.  
DE M. vaccae antigen GV-38B 3' amino acid sequence.  
PN WO9932634-A2.  
PD 01-JUL-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 2.1%; Score 7; DB 2; Length 419;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
RESULT 1462  
ID ABB73502 standard; protein; 419 AA.  
DE M vaccae GV-38B partial protein SEQ ID NO: 125.  
PN US6328978-B1.  
PD 11-DEC-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 2.1%; Score 7; DB 5; Length 419;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
RESULT 1463  
ID ADH86952 standard; protein; 427 AA.  
DE Enterococcus faecalis polypeptide #1432.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 2.1%; Score 7; DB 7; Length 427;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
RESULT 1464  
ID AAE38166 standard; protein; 431 AA.  
DE Fruit fly G protein-coupled receptor (GPCR) protein #15.  
PN WO2003052078-A2.  
PD 26-JUN-2003.  
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
Query Match 2.1%; Score 7; DB 7; Length 431;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1465  
ID ABG97421 standard; protein; 433 AA.  
DE S. macromyceticus UNBU protein.  
PN CA2387401-A1.  
PD 04-SEP-2002.  
PA (ECOP-) ECOPHA BIOSCIENCES INC.  
Query Match 2.1%; Score 7; DB 5; Length 433;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1466  
ID AEB12615 standard; protein; 433 AA.  
DE Eneidiyne related UNBU, SEQ ID 11.  
PN US2005142601-A1.  
PD 30-JUN-2005.  
PA (FARN/) FARNET C M.  
PA (STAF/) STAFPA A.



PA (ZAZO/) ZAZOPOULOS E. 2.1%; Score 7; DB 9; Length 433;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1467  
ID AEG10208 standard; protein; 433 AA.  
DE Streptomyces macromyceticus enediayne biosynthetic protein UNBU, SEQ:11.  
PN US2005170411-A1.  
PD 04-AUG-2005.  
PA (FARN/) FARNET C. M.  
PA (STAF/) STAFPA A.  
PA (ZAZO/) ZAZOPOULOS E.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1e+03; Length 433;  
RESULT 1468  
ID AAY28799 standard; protein; 439 AA.  
DE Maize histone deacetylase-3.  
PN WO9951731-A2.  
PD 14-OCT-1999.  
PA (PRON-) PRONER HI-BRED INT INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1e+03; Length 439;  
RESULT 1469  
ID ADZ6398 standard; protein; 443 AA.  
DE Human cancer-linked gene R1PK2, protein, SEQ ID 39.  
PN WO2005035724-A2.  
PD 21-APR-2005.  
PA (AVAL-) AVALON PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1e+03; Length 443;  
RESULT 1470  
ID ABB66286 standard; protein; 444 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 25650.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1e+03; Length 444;  
RESULT 1471  
ID AAU38968 standard; protein; 444 AA.  
DE Drosophila G-protein coupled receptor, GCPR #46.  
PN WO200170980-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1e+03; Length 444;  
RESULT 1472  
ID ADC35886 standard; protein; 444 AA.  
DE Drosophila G protein coupled receptor seq id 48.  
PN US2003092124-A1.  
PD 15-MAY-2003.  
PA (APPL-) APPLERA CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1e+03; Length 444;  
RESULT 1473  
ID ABU11985 standard; protein; 448 AA.  
DE M. echinospora calicheamicin biosynthesis protein CalM.  
PN WO200279465-A2.  
PD 10-OCT-2002.  
PA (SLOK-) SLOAN KETTERING INST CANCER RES.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1e+03; Length 448;  
RESULT 1474  
ID ADH71794 standard; protein; 457 AA.  
DE Human protein of the invention NOV29m SEQ ID NO:690.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1e+03; Length 457;  
RESULT 1475  
ID ADH71790 standard; protein; 457 AA.  
DE Human protein of the invention NOV29k SEQ ID NO:686.  
PN WO2003102155-A2.

PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1e+03; Length 457;  
RESULT 1476  
ID ADH71792 standard; protein; 460 AA.  
DE Human protein of the invention NOV29l SEQ ID NO:688.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Length 460;  
RESULT 1477  
ID AAU35054 standard; protein; 464 AA.  
DE Enterococcus faecalis cellular proliferation protein #341.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Length 464;  
RESULT 1478  
ID ABB49506 standard; protein; 464 AA.  
DE Listeria monocytogenes protein #210.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP-) INST PASTEUR.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Length 464;  
RESULT 1479  
ID ABU14637 standard; protein; 464 AA.  
DE Protein encoded by Prokaryotic essential gene #164.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Length 464;  
RESULT 1480  
ID ABU32474 standard; protein; 464 AA.  
DE Protein encoded by Prokaryotic essential gene #18001.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Length 464;  
RESULT 1481  
ID ABU30009 standard; protein; 465 AA.  
DE Protein encoded by Prokaryotic essential gene #15536.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Length 465;  
RESULT 1482  
ID AAU33501 standard; protein; 467 AA.  
DE Enterococcus faecalis cellular proliferation protein #137.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Length 467;  
RESULT 1483  
ID ABO64627 standard; protein; 467 AA.  
DE Klebsiella pneumoniae polypeptide seqid 11144.  
PN US610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Length 467;  
RESULT 1484  
ID ADC96490 standard; protein; 472 AA.  
DE E. faecium protein sequence SEQ ID 6117.  
PN US6583275-B1.  
PD 24-JUN-2003.



PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 2.1%; Score 7; DB 7; Length 472;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1485  
ID ADX74976 standard; protein; 472 AA.  
DE Plant full length insert polypeptide seqid 44342.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D. K.  
PA (SCRE/) SCREEN S. E.  
PA (TABA/) TABASKA J. E.  
PA (CAOY/) CAO Y.  
Query Match 2.1%; Score 7; DB 8; Length 472;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1486  
ID ADH71800 standard; protein; 473 AA.  
DE Human protein of the invention NOV29p SEQ ID NO:696.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.1%; Score 7; DB 8; Length 473;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1487  
ID ADH71798 standard; protein; 473 AA.  
DE Human protein of the invention NOV29o SEQ ID NO:694.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.1%; Score 7; DB 8; Length 473;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1488  
ID ADH71796 standard; protein; 473 AA.  
DE Human protein of the invention NOV29n SEQ ID NO:692.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.1%; Score 7; DB 8; Length 473;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1489  
ID ADH71788 standard; protein; 473 AA.  
DE Human protein of the invention NOV29j SEQ ID NO:684.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.1%; Score 7; DB 8; Length 473;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1490  
ID ADH71802 standard; protein; 473 AA.  
DE Human protein of the invention NOV29q SEQ ID NO:698.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.1%; Score 7; DB 8; Length 473;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1491  
ID AA46647 standard; protein; 474 AA.  
DE Propionibacterium acnes immunogenic protein #7743.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 2.1%; Score 7; DB 4; Length 474;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1492  
ID ABM43366 standard; protein; 474 AA.  
DE Propionibacterium acnes membrane-related polypeptide #8042.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 2.1%; Score 7; DB 6; Length 474;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1493  
ID ABB27131 standard; protein; 476 AA.  
DE Pinus radiata cell cycle protein SEQ ID NO 292.  
PN WO2005065339-A2.  
PD 21-JUL-2005.  
PA (ARBO-) ARBOGEN LLC.  
Query Match 2.1%; Score 7; DB 9; Length 476;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1494  
ID AAY59405 standard; protein; 478 AA.  
DE Human RICK protein sequence residues 54-531.  
PN WO9955134-A2.  
PD 04-NOV-1999.  
PA (UNMI) UNIV MICHIGAN.  
Query Match 2.1%; Score 7; DB 3; Length 478;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1495  
ID AM91275 standard; protein; 478 AA.  
DE M. xanthus protein sequence, seq id 10474.  
PN US6833447-B1.  
PD 21-DEC-2004.  
PA (MONS) MONSANTO TECHNOLOGY LLC.  
Query Match 2.1%; Score 7; DB 9; Length 478;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1496  
ID ABB59096 standard; protein; 487 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 4080.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 2.1%; Score 7; DB 4; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1497  
ID AAY58828 standard; protein; 493 AA.  
DE Rice histone deacetylase 1 (HD1) protein (C-terminal portion).  
PN WO200004177-A1.  
PD 27-JAN-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E. I.  
Query Match 2.1%; Score 7; DB 3; Length 493;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1498  
ID ADQ37139 standard; protein; 493 AA.  
DE Cell proliferation-related polypeptide #133.  
PN WO2004061122-A2.  
PD 22-JUL-2004.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 2.1%; Score 7; DB 8; Length 493;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1499  
ID ADQ15723 standard; protein; 493 AA.  
DE Rice stress-related protein #66.  
PN WO2004061080-A2.  
PD 22-JUL-2004.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 2.1%; Score 7; DB 8; Length 493;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1500  
ID ABB64074 standard; protein; 496 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 19014.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 2.1%; Score 7; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;



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## OM protein - protein search, using bw model

Run on: December 16, 2005, 11:18:06 ; Search time 70 Seconds

(without alignments)  
1999.612 Million cell updates/secPerfect score: 1772  
Sequence: 1 MAGSPCTCLTYILMQLTGS.....PHSLTMDPTPLPAYENVI 335Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1500 summaries

Database : Published Applications\_AA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubppaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubppaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1772	100.0	335	3	US-09-732-524-2
8	1772	100.0	335	3	US-09-745-605-4
29	1772	100.0	335	3	US-09-997-428-253
540	1772	100.0	335	4	US-10-021-741A-2
565	1772	100.0	335	4	US-10-174-587-192
629	1772	100.0	335	4	US-10-063-742-46
739	1772	100.0	335	4	US-10-262-839-110
745	1772	100.0	335	5	US-10-842-011-2
746	1772	100.0	335	5	US-10-972-317-46
748	1772	100.0	335	5	US-10-950-374-253
751	1769	99.8	335	4	US-10-104-943-5
752	1769	99.8	335	4	US-10-436-523-60
753	1769	99.8	335	4	US-10-408-765A-1405
754	1755.5	99.1	348	4	US-10-262-839-112
755	1653	93.3	312	3	US-09-732-524-4
756	933.5	52.7	684	5	US-10-450-763-42056
757	933.5	52.7	684	5	US-10-450-763-42528
758	582	32.8	110	3	US-09-984-245-125
759	582	32.8	110	3	US-09-966-262-125
760	582	32.8	110	3	US-09-983-966-125
761	582	32.8	110	4	US-10-059-395-125
762	582	32.8	110	4	US-10-143-090-125
763	582	32.8	110	4	US-10-960-251-125
764	471	26.6	91	3	US-09-864-761-41706
765	362.5	20.5	328	4	US-10-104-943-4
766	362.5	20.5	328	4	US-10-436-523-30
767	362.5	20.5	328	5	US-10-723-860-1886
768	362.5	20.5	328	5	US-10-684-206-8

769	362.5	20.5	328	5	US-10-756-149-5194	Sequence 5194, Ap
770	362.5	20.5	329	3	US-09-809-391-483	Sequence 483, App
771	362.5	20.5	329	3	US-09-882-171-483	Sequence 483, App
772	362.5	20.5	329	4	US-10-164-861-483	Sequence 111, App
773	345.5	19.5	301	5	US-10-311-829-111	Sequence 91, App
774	343	19.4	629	3	US-09-860-836B-9	Sequence 89, App
775	333.5	18.8	289	4	US-10-436-523-88	Sequence 18, App
776	330.5	18.7	289	4	US-10-220-946-18	Sequence 76, App
777	330.5	18.7	289	4	US-10-436-523-76	Sequence 91, App
778	330.5	18.7	289	4	US-10-436-523-91	Sequence 131, App
779	330.5	18.7	289	4	US-10-170-385-131	Sequence 89, App
780	327.5	18.5	289	4	US-10-436-523-89	Sequence 90, App
781	327.5	18.5	289	4	US-10-436-523-80	Sequence 77, App
782	327	18.5	270	4	US-10-436-523-77	Sequence 39, App
783	319.5	18.0	331	4	US-10-436-523-39	Sequence 48, App
784	318	17.9	615	5	US-10-659-004-48	Sequence 7, App
785	318	17.9	654	4	US-10-104-943-7	Sequence 2, App
786	318	17.9	654	4	US-10-310-612-2	Sequence 41, App
787	318	17.9	654	4	US-10-328-538-2	Sequence 2, App
788	316.5	17.9	331	4	US-10-37-413-2	Sequence 5, App
789	315.5	17.8	309	4	US-10-436-523-5	Sequence 3, App
790	315.5	17.8	331	4	US-10-104-943-2	Sequence 3, App
791	315.5	17.8	331	4	US-10-436-523-3	Sequence 3, App
792	315.5	17.8	331	4	US-10-264-227-2559	Sequence 2559, Ap
793	315.5	17.8	331	4	US-10-614-853-32	Sequence 22, App
794	315.5	17.8	331	5	US-10-484-139-2	Sequence 33, App
795	315.5	17.8	346	4	US-10-257-174-33	Sequence 40, App
796	314.5	17.7	331	4	US-10-436-523-41	Sequence 11, App
797	313.5	17.7	331	3	US-10-436-523-80	Sequence 42, App
798	312.5	17.6	610	3	US-09-860-836B-11	Sequence 10, App
799	311.5	17.6	331	5	US-10-436-523-42	Sequence 76, App
800	311	17.6	332	4	US-10-237-535-76	Sequence 41, App
809	311	17.6	332	4	US-10-239-196-76	Sequence 82, App
818	311	17.6	332	4	US-10-104-943-41	Sequence 2, App
832	311	17.6	332	4	US-10-136-574-2	Sequence 5, App
835	311	17.6	332	4	US-10-471-449-8	Sequence 100, App
851	311	17.6	332	4	US-10-471-449-8	Sequence 79, App
912	311	17.6	332	5	US-10-311-829-4	Sequence 8, App
913	307.5	17.4	285	4	US-10-436-523-100	Sequence 50, App
914	301.5	17.0	235	4	US-10-436-523-82	Sequence 48, App
915	298	16.8	217	4	US-10-436-523-79	Sequence 15, App
916	294.5	16.6	551	4	US-10-471-449-8	Sequence 16, App
917	282.5	15.9	526	5	US-10-659-004-50	Sequence 47, App
918	251	14.2	220	4	US-10-257-174-32	Sequence 47, App
919	247	13.9	310	4	US-10-258-951-88	Sequence 5, App
920	247	13.9	310	5	US-10-990-000-48	Sequence 3, App
921	245	13.8	195	4	US-10-436-523-15	Sequence 1621, Ap
922	245	13.8	203	4	US-10-436-523-16	Sequence 43, App
923	236.5	13.3	229	4	US-10-258-951-47	Sequence 48, App
924	236.5	13.3	229	5	US-10-990-000-47	Sequence 15, App
925	235.5	12.7	331	4	US-10-436-523-11	Sequence 4, App
926	225.5	12.7	351	3	US-09-745-605-5	Sequence 11, App
927	225.5	12.7	351	4	US-10-104-943-3	Sequence 8, App
928	219	12.4	168	4	US-10-264-227-1621	Sequence 20, App
929	206	11.6	220	4	US-10-104-943-33	Sequence 28, App
930	200.5	11.3	159	4	US-10-436-523-8	Sequence 3, App
931	199.5	11.3	221	4	US-10-471-449-4	Sequence 4, App
932	190.5	10.8	275	4	US-10-087-192-1485	Sequence 1485, Ap
933	182.5	10.3	335	3	US-09-731-449-10	Sequence 20, App
934	182.5	10.3	335	3	US-09-918-715-85	Sequence 28, App
935	182.5	10.3	335	3	US-09-369-248-3	Sequence 3, App
936	182.5	10.3	335	3	US-09-860-836B-1	Sequence 1, App
937	182.5	10.3	335	3	US-10-062-523-1	Sequence 20, App
938	182.5	10.3	335	4	US-10-254-426-20	Sequence 64, App
939	182.5	10.3	335	4	US-10-436-523-64	Sequence 3, App
940	182.5	10.3	335	4	US-10-464-469-3	Sequence 3, App
941	182.5	10.3	335	4	US-10-445-888A-3	Sequence 285, App
942	182.5	10.3	335	5	US-10-474-794-885	Sequence 3, App
943	182.5	10.3	335	5	US-10-892-171-3	Sequence 25, App
944	182.5	10.3	335	5	US-10-979-159-85	Sequence 25, App
945	179	10.1	278	3	US-09-731-449-25	Sequence 25, App
946	179	10.1	278	4	US-10-254-426-25	Sequence 28, App
947	177.5	10.0	258	3	US-09-731-449-28	Sequence 28, App



948	177.5	10.0	258	4	US-10-254-426-28	Sequence 28, Appl
949	175	9.9	33	3	US-09-984-245-244	Sequence 244, Appl
950	175	9.9	33	3	US-09-966-262-244	Sequence 244, Appl
951	175	9.9	33	3	US-09-983-966-244	Sequence 244, Appl
952	175	9.9	33	3	US-10-059-395-244	Sequence 244, Appl
953	175	9.9	33	4	US-10-143-090-244	Sequence 244, Appl
954	175	9.9	33	5	US-10-960-251-244	Sequence 244, Appl
955	170	9.6	355	3	US-09-860-836-5	Sequence 5, Appl1
956	170	9.6	355	4	US-10-436-923-6	Sequence 59, Appl1
957	170	9.6	351	4	US-10-264-049-2579	Sequence 2579, Ap
958	164.5	9.3	305	3	US-09-918-715-286	Sequence 286, App
959	164.5	9.3	305	4	US-10-474-794-286	Sequence 286, App
960	164.5	9.3	305	5	US-10-979-159-286	Sequence 286, App
961	158.5	8.9	329	3	US-09-860-836-3	Sequence 3, Appl1
962	152	8.6	288	3	US-09-918-715-287	Sequence 287, Appl
963	152	8.6	288	4	US-10-474-794-287	Sequence 287, App
964	152	8.6	288	5	US-10-979-159-287	Sequence 287, App
965	150.5	8.5	285	3	US-09-799-777-9	Sequence 9, Appl1
966	150.5	8.5	285	3	US-09-745-605-6	Sequence 6, Appl1
967	150.5	8.5	285	3	US-09-369-248-2	Sequence 2, Appl1
968	150.5	8.5	285	4	US-10-062-523-2	Sequence 2, Appl1
969	150.5	8.5	285	4	US-10-220-946-12	Sequence 12, Appl1
970	150.5	8.5	285	4	US-10-436-923-63	Sequence 63, Appl1
971	150.5	8.5	285	4	US-10-464-469-2	Sequence 2, Appl1
972	150.5	8.5	285	4	US-10-445-888A-2	Sequence 2, Appl1
973	150.5	8.5	285	4	US-10-755-889-158	Sequence 158, App
974	150.5	8.5	285	5	US-10-723-860-3981	Sequence 3981, Ap
975	150.5	8.5	285	5	US-10-892-171-2	Sequence 2, Appl1
976	150.5	8.5	285	5	US-10-491-997-158	Sequence 158, App
977	150.5	8.5	285	5	US-10-775-204-444	Sequence 444, Appl
978	146.5	8.3	211	3	US-09-731-449-29	Sequence 29, Appl
979	146.5	8.3	211	4	US-10-254-426-29	Sequence 29, Appl
980	146	8.2	312	4	US-09-721-449-5	Sequence 5, Appl1
981	146	8.2	312	4	US-10-254-426-5	Sequence 5, Appl1
982	146	8.2	320	3	US-09-731-449-37	Sequence 37, Appl
983	146	8.2	320	4	US-10-254-426-37	Sequence 37, Appl
984	144.5	8.2	285	3	US-09-731-449-45	Sequence 45, Appl
985	144.5	8.2	285	4	US-10-254-426-45	Sequence 45, Appl
986	144.5	8.1	358	4	US-10-087-192-1845	Sequence 1845, Ap
987	142.5	8.0	416	4	US-10-706-691-16	Sequence 16, Appl
988	142.5	8.0	416	4	US-10-706-691-11	Sequence 11, Appl
989	141	8.0	149	3	US-09-983-802-443	Sequence 443, App
990	141	8.0	149	3	US-09-984-490-443	Sequence 443, App
991	141	8.0	149	3	US-09-973-278-571	Sequence 571, App
992	140.5	7.9	142	3	US-09-973-278-252	Sequence 252, App
993	140.5	7.9	143	3	US-09-983-802-192	Sequence 192, App
994	140.5	7.9	143	3	US-09-984-490-192	Sequence 192, App
995	140.5	7.9	290	3	US-09-731-449-13	Sequence 13, Appl
996	140.5	7.9	290	4	US-10-254-426-13	Sequence 13, Appl
997	140.5	7.9	298	3	US-09-731-449-40	Sequence 40, Appl1
998	140.5	7.9	298	4	US-10-254-426-40	Sequence 40, Appl
999	139	7.8	28	3	US-09-984-245-243	Sequence 243, App
1000	139	7.8	28	3	US-09-966-262-243	Sequence 243, App
1001	139	7.8	28	3	US-09-983-966-243	Sequence 243, App
1002	139	7.8	28	4		

[illegible]



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OM protein - protein search, using sw model

Run on: December 16, 2005, 11:46:45 ; Search time 39 Seconds  
(without alignments)  
826.477 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 335  
Sequence: 1 MAGSPCTLTILYILMQLTGS ..... PHSILTWPPRRLFAVENVI 335

Scoring table: Original  
Gapop 60.0 , Gapept 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	2.7	156	2	H72621
2	9	2.7	2464	1	QMSP1
3	8	2.4	173	2	S76681
4	8	2.4	286	2	A82159
5	8	2.4	705	2	S18733
6	8	2.4	1117	2	S38673
7	7	2.1	105	2	T29918
8	7	2.1	161	2	E71866
9	7	2.1	170	2	A81817
10	7	2.1	179	2	E7283
11	7	2.1	179	2	F83305
12	7	2.1	182	2	E97499
13	7	2.1	184	2	I40220
14	7	2.1	189	2	H70416
15	7	2.1	199	2	T45543
16	7	2.1	220	2	E75285
17	7	2.1	228	2	T47847
18	7	2.1	238	2	G69820
19	7	2.1	238	2	C82884
20	7	2.1	239	2	E69966
21	7	2.1	239	2	T51270
22	7	2.1	266	2	C87367
23	7	2.1	274	2	G84218
24	7	2.1	274	2	A88616
25	7	2.1	301	2	DB3970
26	7	2.1	301	2	T52549
27	7	2.1	302	2	E75414
28	7	2.1	303	2	A43727
29	7	2.1	305	2	G96962

30	7	2.1	312	1	LPRT8	apolipoprotein B p
31	7	2.1	316	2	F98027	UDP-N-acetylmurama
32	7	2.1	316	2	G95161	UDP-N-acetylenolpy
33	7	2.1	331	2	C89469	protein F0766.1 [i
34	7	2.1	348	2	B84299	hypothetical prote
35	7	2.1	351	2	C82755	conserved hypothet
36	7	2.1	356	2	S14396	cytochrome-c oxid
37	7	2.1	362	2	S68471	asparaginase (BC 3
38	7	2.1	367	2	S41024	hypothetical prote
39	7	2.1	369	2	T21392	hypothetical prote
40	7	2.1	377	2	H89717	protein C18B12.2 [
41	7	2.1	379	2	S49614	CyH protein - Rhi
42	7	2.1	381	2	T11312	ubiquinol-cytochro
43	7	2.1	381	2	B81744	poly(A) polymerase
44	7	2.1	410	2	B81744	hypothetical prote
45	7	2.1	413	2	T48089	hypothetical prote
46	7	2.1	418	2	F64059	tryptophan transpo
47	7	2.1	428	2	AD0675	membrane transport
48	7	2.1	433	2	S45856	probable membrane
49	7	2.1	433	2	AB2719	conserved hypothet
50	7	2.1	448	2	JC2305	glucuronate permease
51	7	2.1	454	2	T19380	hypothetical prote
52	7	2.1	458	2	F69123	efflux pump antibi
53	7	2.1	463	2	A69905	conserved hypothet
54	7	2.1	464	2	AG1146	beta-glucosidase h
55	7	2.1	464	2	AG1505	beta-glucosidase h
56	7	2.1	467	2	A99498	hypothetical prote
57	7	2.1	475	2	T47480	hypothetical prote
58	7	2.1	480	2	F97500	tolerance to colic
59	7	2.1	492	2	D87606	sensor histidine k
60	7	2.1	501	2	H95859	probable ABC trans
61	7	2.1	508	2	E96804	probable thioredox
62	7	2.1	513	2	B84391	DNA damage-inducib
63	7	2.1	572	2	AB2671	cytochrome-c oxid
64	7	2.1	586	1	VCLJMP	env polypeptin -
65	7	2.1	587	1	VCLJSA	env polypeptin -
66	7	2.1	591	2	B54354	calnexin precursor
67	7	2.1	591	2	C54354	calnexin precursor
68	7	2.1	605	2	S52253	copper resistance
69	7	2.1	643	2	B72602	hypothetical prote
70	7	2.1	646	2	D82493	conserved hypothet
71	7	2.1	675	2	T22323	hypothetical prote
72	7	2.1	730	2	T13792	NMDH2 dehydrogenas
73	7	2.1	732	1	JC4655	acylaminoacyl-pept
74	7	2.1	797	2	T50072	hypothetical prote
75	7	2.1	799	2	H71255	probable cell divi
76	7	2.1	829	2	T40239	probable helicase
77	7	2.1	914	2	C97893	penicillin-binding
78	7	2.1	943	2	C97893	exonuclease ABC c
79	7	2.1	943	2	F95021	exonuclease ABC,
80	7	2.1	954	2	AF2756	glycine cleavage s
81	7	2.1	954	2	E97537	glycine cleavage s
82	7	2.1	957	2	B85946	hypothetical prote
83	7	2.1	957	2	AC0873	glycine dehydrogen
84	7	2.1	957	2	F91100	glycine decarboxyl
85	7	2.1	957	2	S36834	glycine dehydrogen
86	7	2.1	958	2	B82994	glycine cleavage s
87	7	2.1	959	2	AB0111	glycine dehydrogen
88	7	2.1	997	2	T32814	hypothetical prote
89	7	2.1	1002	2	S62035	isoleucine-tRNA 11
90	7	2.1	1020	2	JN0124	glycine dehydrogen
91	7	2.1	1032	2	T06733	hypothetical prote
92	7	2.1	1070	2	S53571	kinesin homolog F2
93	7	2.1	1085	2	S55352	IRH1 protein - yea
94	7	2.1	1166	2	T15628	hypothetical prote
95	7	2.1	1268	2	A49674	fligellin-less-1 homol
96	7	2.1	1270	2	T15109	hypothetical prote
97	7	2.1	1290	2	T00019	period protein hom
98	7	2.1	1291	2	T00019	period protein hom
99	7	2.1	1312	2	S68593	DNA-directed DNA p
100	7	2.1	1345	2	T29080	surface layer-asso
101	7	2.1	1355	2	T22552	hypothetical prote
102	7	2.1	1487	2	S15904	alpha-1 proteinase



103	7	2.1	1552	2	T05408	hypothetical prote
104	7	2.1	1560	2	T02885	peroxisome prolife
105	7	2.1	1585	2	AE2916	NAD-glutamate dehy
106	7	2.1	1585	2	H97690	NAD-glutamate dehy
107	7	2.1	1620	2	S61535	nucleotide-binding
108	7	2.1	2787	2	S45416	TRH1 protein - yea
109	7	2.1	3973	2	B71612	hypothetical prote
110	7	2.1	4545	1	S25111	alpha-2-macroglobu
111	6	1.8	30	2	S21547	ubiquinol-cytochro
112	6	1.8	32	2	S21547	T-cell receptor al
113	6	1.8	36	2	H64607	hypothetical prote
114	6	1.8	39	2	C90523	hypothetical prote
115	6	1.8	52	2	C60232	T-cell surface gly
116	6	1.8	56	2	C69044	hypothetical prote
117	6	1.8	57	2	D95852	hypothetical prote
118	6	1.8	60	2	B28918	hypothetical prote
119	6	1.8	61	2	J01086	nodulin-14 precurs
120	6	1.8	66	2	C89925	hypothetical prote
121	6	1.8	70	2	A42155	GTP-binding, regula
122	6	1.8	72	2	C83219	hypothetical prote
123	6	1.8	73	2	T13199	hypothetical prote
124	6	1.8	73	2	T26110	hypothetical prote
125	6	1.8	74	2	E95204	hypothetical prote
126	6	1.8	75	2	C95959	hypothetical prote
127	6	1.8	77	2	AG2343	hypothetical prote
128	6	1.8	82	2	C81350	hypothetical prote
129	6	1.8	83	2	JC7607	prolactin-releasin
130	6	1.8	86	2	AC2117	hypothetical prote
131	6	1.8	92	2	T64109	mercury reductase
132	6	1.8	93	2	T45245	hypothetical prote
133	6	1.8	95	2	S68231	FM22 protein prec
134	6	1.8	95	2	T49793	hypothetical prote
135	6	1.8	96	1	A42281	symblonin syms - p
136	6	1.8	96	1	ZEBPG4	gene B protein - p
137	6	1.8	96	2	A84932	10 kD chaperonin [
138	6	1.8	96	2	C92048	chaperonin, 10 kD
139	6	1.8	96	2	B64076	chaperonin groES -
140	6	1.8	96	2	JC4518	heat-shock protein
141	6	1.8	97	1	BVBCGS	chaperonin groES -
142	6	1.8	97	2	A48093	monocytic cytokine
143	6	1.8	97	2	JC5770	chaperonin groES-1
144	6	1.8	97	2	AD1045	GroES protein [imp
145	6	1.8	97	2	C91265	chaperonin GroES [
146	6	1.8	97	2	A86110	chaperonin mopB [s
147	6	1.8	97	2	E97266	glu-tRNA amidotran
148	6	1.8	98	2	S24920	NADH2 dehydrogenas
149	6	1.8	98	2	S41828	NADH2 dehydrogenas
150	6	1.8	98	2	T11488	NADH2 dehydrogenas
151	6	1.8	99	1	A32926	monocyte chemoattr
152	6	1.8	99	2	JC2336	monocyte chemoattr
153	6	1.8	99	2	A60299	monocyte chemoattr
154	6	1.8	99	2	JC5295	monocyte chemoattr
155	6	1.8	99	2	JC2136	monocyte chemoattr
156	6	1.8	99	2	JC2417	monocyte chemoattr
157	6	1.8	100	2	AE0796	NADH2 dehydrogenas
158	6	1.8	100	2	BE4999	NADH2 dehydrogenas
159	6	1.8	100	2	D85868	NADH dehydrogenase
160	6	1.8	100	2	C91024	C91024
161	6	1.8	100	2	AH0310	NADH2 dehydrogenas
162	6	1.8	100	2	BE9846	hypothetical prote
163	6	1.8	101	2	S37068	NADH2 dehydrogenas
164	6	1.8	101	2	S64222	probable membrane
165	6	1.8	102	2	F87993	protein ZC334.3 [1
166	6	1.8	103	2	S72632	probable membrane
167	6	1.8	105	2	B97734	hypothetical prote
168	6	1.8	107	2	PH0987	ig heavy chain V r
169	6	1.8	107	2	C70188	hypothetical prote
170	6	1.8	108	2	S73125	hypothetical prote
171	6	1.8	108	2	A55590	hypothetical prote
172	6	1.8	108	2	T40598	hypothetical prote
173	6	1.8	109	2	A54678	monocyte chemoact
174	6	1.8	109	2	H71142	hypothetical prote
175	6	1.8	111	2	F71940	probable ribosome-
176	6	1.8	111	2	G64650	ribosome-binding f
177	6	1.8	111	2	G75009	hypothetical prote
178	6	1.8	111	2	B83101	hypothetical prote
179	6	1.8	112	2	S48472	probable membrane
180	6	1.8	113	2	S26263	T-cell receptor be
181	6	1.8	113	2	S26262	T-cell receptor be
182	6	1.8	113	2	S17385	T-cell receptor be
183	6	1.8	113	2	S26266	T-cell receptor be
184	6	1.8	113	2	JC4143	mol-t-inhibiting ho
185	6	1.8	113	2	AD2868	hypothetical prote
186	6	1.8	114	2	AC3033	hypothetical prote
187	6	1.8	115	2	AG3279	hypothetical prote
188	6	1.8	115	2	S09751	hypothetical prote
189	6	1.8	116	2	TS1028	hypothetical prote
190	6	1.8	118	2	AB2862	conserved hypotnet
191	6	1.8	118	2	A97639	hypothetical prote
192	6	1.8	118	2	H97644	hypothetical prote
193	6	1.8	120	2	T48147	monocyte chemoattr
194	6	1.8	122	2	A05304	hemoglobin beta-1
195	6	1.8	122	2	A83283	hypothetical prote
196	6	1.8	123	2	E95940	conserved hypotnet
197	6	1.8	123	2	I48192	surface antigen -
198	6	1.8	123	2	G75336	hypothetical prote
199	6	1.8	124	2	A11647	hypothetical prote
200	6	1.8	125	2	T46857	monocyte chemoattr
201	6	1.8	125	2	T27519	hypothetical prote
202	6	1.8	126	2	S73081	hypothetical prote
203	6	1.8	126	2	AE0918	probable membrane
204	6	1.8	126	2	S30707	hypothetical 14.5K
205	6	1.8	126	2	C72650	hypothetical prote
206	6	1.8	128	2	C48552	hypothetical prote
207	6	1.8	128	2	D29504	hypothetical 14k p
208	6	1.8	128	2	C75462	hypothetical prote
209	6	1.8	128	2	AD1386	hypothetical prote
210	6	1.8	128	2	AF1761	hypothetical prote
211	6	1.8	129	2	F95987	conserved hypotnet
212	6	1.8	132	2	C87431	hypothetical prote
213	6	1.8	132	2	H75335	hypothetical prote
214	6	1.8	132	2	B83956	hypothetical prote
215	6	1.8	133	2	S57876	T cell receptor CK
216	6	1.8	133	2	C36886	hypothetical prote
217	6	1.8	134	2	D87021	probable DNA-bind
218	6	1.8	135	2	A70659	hypothetical prote
219	6	1.8	135	2	B83440	hypothetical prote
220	6	1.8	135	2	F87156	hypothetical prote
221	6	1.8	136	2	AD0630	probable exported
222	6	1.8	136	2	T22797	hypothetical prote
223	6	1.8	137	1	F64961	hypothetical prote
224	6	1.8	137	2	S03489	T-cell receptor be
225	6	1.8	137	2	D90967	hypothetical prote
226	6	1.8	137	2	C85815	hypothetical prote
227	6	1.8	137	2	A44031	probable membrane
228	6	1.8	139	2	S36296	T-cell receptor ga
229	6	1.8	140	2	C81176	hypothetical prote
230	6	1.8	140	2	A99253	hypothetical prote
231	6	1.8	141	2	E32998	chorion protein S1
232	6	1.8	141	2	D81309	probable acetyltra
233	6	1.8	142	2	T27965	hypothetical prote
234	6	1.8	143	2	D75617	response regulator
235	6	1.8	144	2	T27945	hypothetical prote
236	6	1.8	145	2	G82617	VfRk protein xR194
237	6	1.8	146	2	S26408	T-cell receptor be
238	6	1.8	146	2	T45385	ribosomal protein
239	6	1.8	146	2	T27964	hypothetical prote
240	6	1.8	149	2	AD3431	hypothetical prote
241	6	1.8	150	2	S43955	probable NADH2 deh
242	6	1.8	150	2	A87714	hypothetical prote
243	6	1.8	151	2	S48958	hypothetical prote
244	6	1.8	151	2	A83784	acetyltransferase
245	6	1.8	152	2	S21826	T-cell receptor be
246	6	1.8	152	2	F86318	protein F15H8.2 [
247	6	1.8	153	1	A28406	gastric inhibitory
248	6	1.8	153	2	E87306	hypothetical prote



249	6	1.8	153	2	C64373	hypothetical prote	322	6	1.8	205	2	S42406	protein phosphatas
250	6	1.8	157	2	S57451	cysteine proteinas	323	6	1.8	205	2	S10497	hypothetical prote
251	6	1.8	157	2	T24917	hypothetical prote	324	6	1.8	206	2	AE0891	probable membrane
252	6	1.8	158	2	H96900	probable HD superf	325	6	1.8	206	2	S61705	hypothetical prote
253	6	1.8	159	2	D90586	hypothetical prote	326	6	1.8	206	2	AE2222	hypothetical prote
254	6	1.8	161	2	B72339	hypothetical prote	327	6	1.8	207	2	A35535	23k calcium-bindin
255	6	1.8	162	1	CFKKA	C-phycocyanin alph	328	6	1.8	209	2	H69552	hypothetical prote
256	6	1.8	162	1	CFPMA	C-phycocyanin alph	329	6	1.8	209	2	I40285	outer surface prot
257	6	1.8	162	1	S30940	phycocyanin alpha	330	6	1.8	209	2	S69926	outer surface prot
258	6	1.8	162	2	H72351	phycocyanin alpha	331	6	1.8	210	2	T50713	urease accessory p
259	6	1.8	163	2	A29674	phycocyanin alpha	332	6	1.8	210	2	G97037	hypothetical prote
260	6	1.8	163	2	AH1872	phycocyanin alpha	333	6	1.8	211	2	S69932	outer surface prot
261	6	1.8	165	2	G82910	peptide methionine	334	6	1.8	211	2	CS9091	hypothetical prote
262	6	1.8	166	2	T11039	NADH2 dehydrogenas	335	6	1.8	212	2	B29010	alkylmercury lyase
263	6	1.8	170	2	T30570	hypothetical prote	336	6	1.8	212	2	S20543	outer surface prot
264	6	1.8	171	2	H87440	hypothetical prote	337	6	1.8	212	2	S69921	outer surface prot
265	6	1.8	171	2	B75562	MutT/nudix family	338	6	1.8	213	2	C70346	UDP-N-acetoenolpyr
266	6	1.8	172	1	DERIN6	NADH2 dehydrogenas	339	6	1.8	213	2	S74247	CDP diacylglycerol
267	6	1.8	172	1	H72077	ct006 hypothetical	340	6	1.8	213	2	S07573	amine oxidase (fla
268	6	1.8	172	2	C81590	conserved hypotnet	341	6	1.8	214	1	S18729	adenyl-yl-sulfate k
269	6	1.8	172	2	H86545	CT006 hypothetical	342	6	1.8	214	2	T21585	hypothetical prote
270	6	1.8	174	2	T01486	hypothetical prote	343	6	1.8	215	2	G98036	conserved hypotnet
271	6	1.8	176	2	S35949	edea protein - tre	344	6	1.8	215	2	G95170	hemolysin [importe
272	6	1.8	176	2	JC6152	orphanin FQ precur	345	6	1.8	215	2	T48789	trsl related prote
273	6	1.8	177	2	S45364	ribosomal protein	346	6	1.8	216	2	H72277	hypothetical prote
274	6	1.8	177	2	B91248	hypothetical prote	347	6	1.8	216	2	T00192	hypothetical prote
275	6	1.8	178	2	S54190	outer surface prot	348	6	1.8	217	2	S65830	alpha fucosidase p
276	6	1.8	179	2	S36295	T-cell receptor ga	349	6	1.8	217	2	S49578	tyrosin inhibitor
277	6	1.8	179	2	S54186	outer surface prot	350	6	1.8	217	2	H72390	dihydroototate deh
278	6	1.8	179	2	S54187	outer surface prot	351	6	1.8	217	2	F91246	PTS system, sorbos
279	6	1.8	179	2	S54188	outer surface prot	352	6	1.8	218	2	B83862	endonuclease III (
280	6	1.8	179	2	T35439	probable integral	353	6	1.8	218	2	G64673	DNA polymerase III
281	6	1.8	180	2	S54189	outer surface prot	354	6	1.8	218	2	B71844	probable DNA poyme
282	6	1.8	180	2	S54191	outer surface prot	355	6	1.8	218	2	S74867	hypothetical prote
283	6	1.8	181	2	G89799	hypothetical prote	356	6	1.8	219	2	S49428	hypothetical prote
284	6	1.8	181	2	I40146	outer surface prot	357	6	1.8	221	1	S24328	glutathione peroxi
285	6	1.8	181	2	AC0686	hypothetical prote	358	6	1.8	221	2	A47367	24k androgen-depen
286	6	1.8	184	2	S73640	inorganic diphosph	359	6	1.8	221	2	B42719	O-methyltransferas
287	6	1.8	185	2	AG2026	hypothetical prote	360	6	1.8	222	2	UC7697	beta-casein-like p
288	6	1.8	186	1	HHFF23	heat shock protein	361	6	1.8	222	2	AD2999	thiol:disulfide in
289	6	1.8	186	1	T11384	Arpase subunit 6 -	362	6	1.8	222	2	E98284	histone H1 - mouse
290	6	1.8	186	2	B20647	heat shock protein	363	6	1.8	223	2	S49492	conserved hypotnet
291	6	1.8	186	2	T47804	hypothetical prote	364	6	1.8	224	2	F69444	hypothetical prote
292	6	1.8	186	2	G95076	conserved hypotnet	365	6	1.8	225	2	G70721	hypothetical prote
293	6	1.8	187	2	H70450	lipoprotein nlpd h	366	6	1.8	227	2	F97276	CFSD/CAPA conserve
294	6	1.8	188	2	S50158	RER1 protein - Yea	367	6	1.8	227	2	D84775	hypothetical prote
295	6	1.8	188	2	A69880	hypothetical prote	368	6	1.8	228	2	B90369	hypothetical prote
296	6	1.8	188	2	T33366	petriplasmic nitrat	369	6	1.8	229	2	B90534	tna/rna methyltr
297	6	1.8	190	2	F82430	hypothetical prote	370	6	1.8	229	2	T18629	hypothetical prote
298	6	1.8	191	2	S70262	outer surface prot	371	6	1.8	230	2	D84215	hypothetical prote
299	6	1.8	192	2	JC4663	T-cell receptor CD	372	6	1.8	230	2	T36263	probable transcrip
300	6	1.8	192	2	S22981	T-cell surface gly	373	6	1.8	231	2	AF1798	probable N-acetylM
301	6	1.8	193	2	S70259	outer surface prot	374	6	1.8	232	2	B69392	ABC transporter. A
302	6	1.8	193	2	S70274	outer surface prot	375	6	1.8	233	2	B64525	tubi protein - Hel
303	6	1.8	193	2	S70286	conserved hypotnet	376	6	1.8	235	2	S48924	hypothetical prote
304	6	1.8	194	2	D97944	conserved hypotnet	377	6	1.8	236	2	D84961	oxidation-5'-phosp
305	6	1.8	194	2	C83312	hypothetical prote	378	6	1.8	236	2	C75516	hypothetical prote
306	6	1.8	196	2	S54196	outer surface prot	379	6	1.8	236	2	E75337	hypothetical prote
307	6	1.8	197	2	E70642	probable ribosomal	380	6	1.8	237	2	S08073	cyclic nucleotide
308	6	1.8	197	2	G85521	hypothetical prote	381	6	1.8	237	2	S34727	listeriolysin regu
309	6	1.8	197	2	C90671	hypothetical prote	382	6	1.8	237	2	AH1424	hypothetical prote
310	6	1.8	197	2	B83768	hypothetical prote	383	6	1.8	237	2	T05249	probable integral
311	6	1.8	200	2	B64756	membrane protein y	384	6	1.8	239	2	A81437	hypothetical prote
312	6	1.8	200	2	A81295	probable membrane	385	6	1.8	239	2	T31881	hypothetical prote
313	6	1.8	201	2	D86912	conserved hypotnet	386	6	1.8	240	2	AD1950	hypothetical prote
314	6	1.8	202	2	T10016	hypothetical prote	387	6	1.8	240	2	T47589	synapobrevin-like
315	6	1.8	202	2	D63046	conserved hypotnet	388	6	1.8	240	2	AG0048	hypothetical prote
316	6	1.8	202	2	B83375	hypothetical prote	389	6	1.8	241	2	T33804	hypothetical prote
317	6	1.8	203	2	AC0620	hypothetical proph	390	6	1.8	241	2	C86492	hypothetical prote
318	6	1.8	203	2	S32799	hypothetical prote	391	6	1.8	241	2	C72130	hypothetical prote
319	6	1.8	204	2	H70648	probable regulator	392	6	1.8	242	2	JC7517	caspace-14/a - hum
320	6	1.8	204	2	B72370	hypothetical prote	393	6	1.8	243	2	G81255	1-(5-phosphoribosy
321	6	1.8	204	2	T51012	hypothetical prote	394	6	1.8	244	2	T43764	Arpase chain 6 [im



395	6	1.8	245	2	B75340	transcription regu	468	6	1.8	276	2	AT0565	11poretein [impor
396	6	1.8	245	2	D36145	precortin-2 methyl	469	6	1.8	276	2	BT0591	At11 protein - yea
397	6	1.8	245	2	F83105	hypothetical prote	470	6	1.8	276	2	UT1117	hypothetical prote
398	6	1.8	246	2	T00704	hypothetical prote	471	6	1.8	276	2	F72342	conserved hypotet
399	6	1.8	247	2	A75254	conserved hypotet	472	6	1.8	276	2	T00923	hypothetical prote
400	6	1.8	247	2	E86250	protein P25C20.16	473	6	1.8	277	2	T32460	hypothetical prote
401	6	1.8	247	2	S66064	conserved hypotet	474	6	1.8	277	2	B69479	conserved hypotet
402	6	1.8	248	2	D69094	phosphoribosylamin	475	6	1.8	278	1	TDRT0X	OX-2 membrane gly
403	6	1.8	249	2	S23902	genome polypotein	476	6	1.8	279	2	E75472	ROR family protein
404	6	1.8	249	2	C75156	hypothetical prote	477	6	1.8	280	2	T02004	chitinase (EC 3.2.
405	6	1.8	250	2	B82821	NADH-ubiquinone ox	478	6	1.8	280	2	B81100	2-dehydro-3-deoxyp
406	6	1.8	250	2	H83213	hypothetical prote	479	6	1.8	280	2	G81840	2-dehydro-3-deoxyp
407	6	1.8	250	2	T40977	cdp-diacylglycerol	480	6	1.8	280	2	B45537	viral coat protei
408	6	1.8	251	2	C84036	succinate dehydrog	481	6	1.8	280	2	T32747	hypothetical prote
409	6	1.8	251	2	AC2187	phospho-2-dehydro-	482	6	1.8	280	2	B87547	transcription regu
410	6	1.8	251	2	G90810	flagellar rod prot	483	6	1.8	281	1	D69030	MW1225-related pro
411	6	1.8	251	2	C85670	flagellar rod prot	484	6	1.8	281	2	B47092	copy control prote
412	6	1.8	251	2	B64851	flagellar basal bo	485	6	1.8	281	2	B86820	conserved hypotet
413	6	1.8	251	2	B72578	hypothetical prote	486	6	1.8	282	1	SAVL64	middle surface ant
414	6	1.8	252	2	H90212	enoyl CoA hydratase	487	6	1.8	282	2	AC3084	shikimate 5-dehydr
415	6	1.8	252	2	B47188	MHC class II histo	488	6	1.8	283	2	AH0726	phosphotransferase
416	6	1.8	252	2	S05029	H+-transporting tw	489	6	1.8	283	2	AC1340	maltoedextrin ABC-t
417	6	1.8	253	2	D88427	protein R0785.15 [	490	6	1.8	283	2	A11710	UDP-N-acetylgluc
418	6	1.8	253	2	T30928	hypothetical prote	491	6	1.8	284	2	C72222	probable DMSO redu
419	6	1.8	254	1	VCCVY	coat protein - tob	492	6	1.8	284	2	H90915	probable DMSO redu
420	6	1.8	254	2	S25281	gltf protein precu	493	6	1.8	284	2	E85764	probable dimethyls
421	6	1.8	255	2	F84244	proteasome, subun	494	6	1.8	284	2	H64914	probable transpor
422	6	1.8	256	2	T22715	hypothetical prote	495	6	1.8	284	2	T36934	probable succinate
423	6	1.8	256	2	T00165	repressor - staphy	496	6	1.8	285	2	E81388	conserved hypotet
424	6	1.8	257	2	B70246	outer surface prot	497	6	1.8	285	2	B95241	hypothetical prote
425	6	1.8	257	2	AC0087	probable flagellar	498	6	1.8	285	2	C98105	phosphotransferase
426	6	1.8	259	1	OMGAOL	ovulation hormone	499	6	1.8	286	1	WQECMM	PTS enzyme IID, ma
427	6	1.8	260	2	I51544	MHC class II beta-	500	6	1.8	286	2	D85793	mannose-specific P
428	6	1.8	260	2	I51542	MHC class II beta-	501	6	1.8	286	2	A98945	murcin endopeptida
429	6	1.8	260	2	S60480	low temperature-in	502	6	1.8	286	2	H64053	probable 3-oxoacyl
430	6	1.8	260	2	T29909	hypothetical prote	503	6	1.8	287	1	A45168	xyloglucan endo-1,
431	6	1.8	260	2	T33869	hypothetical prote	504	6	1.8	287	2	T04236	cytochrome-c oxida
432	6	1.8	261	2	A83499	O-sialoglycoprotei	505	6	1.8	288	2	S36956	gene PD-1 protein
433	6	1.8	261	2	S10321	31k protein - frog	506	6	1.8	288	2	S28029	sporulation protei
434	6	1.8	261	2	D95271	hypothetical prote	507	6	1.8	288	2	S18438	probable dehydroge
435	6	1.8	262	1	CYFF3	cytochrome-c oxida	508	6	1.8	289	1	S25286	hypothetical prote
436	6	1.8	262	2	B72037	CT598 hypothetical	509	6	1.8	289	2	T41305	shikimate 5-dehydr
437	6	1.8	262	2	B66588	conserved hypotet	510	6	1.8	291	2	F98202	hypothetical prote
438	6	1.8	262	2	A81504	conserved hypotet	511	6	1.8	293	2	S04649	beta-lactamase (EC
439	6	1.8	263	1	S23009	insulin-like growt	512	6	1.8	293	2	T09171	ribosomal protein
440	6	1.8	263	2	E72675	hypothetical prote	513	6	1.8	293	2	T09170	ribosomal protein
441	6	1.8	263	2	G69064	conserved hypotet	514	6	1.8	293	2	A83623	hypothetical prote
442	6	1.8	264	2	H81720	conserved hypotet	515	6	1.8	295	2	E84336	sugar kinase [impo
443	6	1.8	265	2	S16592	chlorophyll a/b-b1	516	6	1.8	295	2	AC0214	PTS system, mannos
444	6	1.8	265	2	F69742	hypothetical prote	517	6	1.8	296	2	T45930	uracil phosphoribo
445	6	1.8	267	2	A86891	hypothetical prote	518	6	1.8	296	2	T00559	hypothetical prote
446	6	1.8	267	2	H82201	probable bax prote	519	6	1.8	296	2	A36966	probable drdp-rham
447	6	1.8	267	2	T29500	hypothetical prote	520	6	1.8	297	2	A70347	UDP-N-acetylgluc
448	6	1.8	267	2	C75131	hypothetical prote	521	6	1.8	297	2	AF0874	chromosome initiat
449	6	1.8	267	2	S70291	hypothetical prote	522	6	1.8	297	2	S22098	replication initia
450	6	1.8	268	2	A71086	hypothetical prote	523	6	1.8	297	2	F85947	replication initia
451	6	1.8	269	2	T04095	ribonuclease S hom	524	6	1.8	297	2	B91102	FLA17.4 [imported
452	6	1.8	269	2	A75397	probable signal pe	525	6	1.8	297	2	C96524	hypothetical prote
453	6	1.8	269	2	I51539	MHC class II beta-	526	6	1.8	297	2	F70572	hypothetical prote
454	6	1.8	269	2	I51540	MHC class II beta-	527	6	1.8	298	2	T36900	probable integrat
455	6	1.8	269	2	S73999	hypothetical prote	528	6	1.8	298	2	B35272	osteoblastic fac
456	6	1.8	269	2	H98273	iron(III) dicitrat	529	6	1.8	298	2	T20841	hypothetical prote
457	6	1.8	270	2	I51543	MHC class II beta-	530	6	1.8	299	2	T04669	serine O-acetyltra
458	6	1.8	270	2	S57457	formylmethanofuran	531	6	1.8	299	2	AB0609	probable membrane
459	6	1.8	271	2	D83059	phosphatidylserine	532	6	1.8	299	2	T20953	hypothetical prote
460	6	1.8	272	2	H87075	probable conserved	533	6	1.8	300	2	A84420	proteinase IV homo
461	6	1.8	273	2	B64446	formylmethanofuran	534	6	1.8	301	2	D90224	spermidine synthas
462	6	1.8	274	2	A47639	OX-2 membrane gly	535	6	1.8	301	2	T37031	hypothetical prote
463	6	1.8	274	2	D97653	hypothetical prote	536	6	1.8	302	2	AE0112	chromosome initiat
464	6	1.8	274	2	AB2877	conserved hypotet	537	6	1.8	302	2	H87476	conserved hypotet
465	6	1.8	275	2	S74417	hypothetical prote	538	6	1.8	303	2	T30737	probable DNA-dirac
466	6	1.8	275	2	S03967	intercellular adhe	539	6	1.8	303	2	AI0411	ferriochrome-bindin
467	6	1.8	276	1	PWYBAA	H+-transporting tw	540	6	1.8	303	2	S23440	hypothetical prote



541	6	1.8	304	2	C81530	614	6	1.8	338	2	AP3617	oligopeptide trans
542	6	1.8	304	2	A86614	615	6	1.8	338	2	T49998	hypothetical prote
543	6	1.8	304	2	E72010	616	6	1.8	339	2	S08981	malate dehydrogena
544	6	1.8	304	2	T40316	617	6	1.8	339	2	S73840	ribonucleotide red
545	6	1.8	304	2	T34271	618	6	1.8	340	2	C64225	ribonucleotide red
546	6	1.8	305	2	UN0647	619	6	1.8	340	2	B96661	unknown protein, 8
547	6	1.8	305	2	AF2843	620	6	1.8	340	2	T22010	hypothetical prote
548	6	1.8	305	2	G97620	621	6	1.8	341	2	S55627	hypothetical prote
549	6	1.8	305	2	D88656	622	6	1.8	341	2	C90579	hypothetical prote
550	6	1.8	305	2	C84189	623	6	1.8	342	2	S53663	hydrogenase-relate
551	6	1.8	305	2	T35344	624	6	1.8	342	2	E90772	periplasmic protei
552	6	1.8	306	2	F83348	625	6	1.8	342	2	A85635	part of regulatio
553	6	1.8	306	2	S77062	626	6	1.8	342	2	H64830	lort protein precu
554	6	1.8	307	2	B75120	627	6	1.8	343	2	A84335	chloromucinate cyc
555	6	1.8	307	2	B71011	628	6	1.8	343	2	AC3403	general L-amino ac
556	6	1.8	307	2	C81862	629	6	1.8	344	2	E84376	Na+/Ca2+-exchang
557	6	1.8	307	2	D81082	630	6	1.8	344	2	T34981	probable integrin
558	6	1.8	308	1	CRH06	631	6	1.8	345	2	S28140	gas vesicle protei
559	6	1.8	308	2	AG3317	632	6	1.8	345	2	A98251	hypothetical prote
560	6	1.8	309	2	H75113	633	6	1.8	345	2	AB3035	conserved hypotet
561	6	1.8	309	2	H89832	634	6	1.8	347	2	T11338	NADH2 dehydrogenas
562	6	1.8	310	2	T40802	635	6	1.8	347	2	T11481	NADH2 dehydrogenas
563	6	1.8	311	2	S39661	636	6	1.8	347	2	JC5788	teac-1 protein (A
564	6	1.8	311	2	D98045	637	6	1.8	347	2	B75610	probable 3-hydroxy
565	6	1.8	311	2	E95178	638	6	1.8	348	2	JC8007	N-myc downstream-x
566	6	1.8	311	2	AH3197	639	6	1.8	349	2	H95421	probable ABC trans
567	6	1.8	312	2	GH4058	640	6	1.8	350	2	B82777	conserved hypotet
568	6	1.8	312	2	H89884	641	6	1.8	350	2	JC7188	REIC protein - hum
569	6	1.8	313	2	T09670	642	6	1.8	351	2	S25480	heat shock transcr
570	6	1.8	313	2	AB3186	643	6	1.8	351	2	UQ2166	spindle body prote
571	6	1.8	313	2	H84169	644	6	1.8	352	2	S24559	Wnt-2 protein - fir
572	6	1.8	315	2	T37901	645	6	1.8	352	2	T08209	matrix protein - H
573	6	1.8	315	2	F82836	646	6	1.8	352	2	T49432	Ribonuclease III r
574	6	1.8	317	2	B83039	647	6	1.8	353	1	A45052	L-Iditol 2-dehydro
575	6	1.8	317	2	D89961	648	6	1.8	353	2	A87643	hypothetical prote
576	6	1.8	317	2	T21046	649	6	1.8	354	2	C71368	probable UDP-N-ace
577	6	1.8	317	2	A95282	650	6	1.8	354	2	A90012	hypothetical prote
578	6	1.8	317	2	S44746	651	6	1.8	354	2	B85647	hypothetical prote
579	6	1.8	319	2	A50324	652	6	1.8	354	2	B47065	phosphate starvati
580	6	1.8	323	2	A69648	653	6	1.8	354	2	B90787	ATP-binding pho re
581	6	1.8	324	2	B96606	654	6	1.8	354	2	T22274	hypothetical prote
582	6	1.8	326	2	PMWVA	655	6	1.8	355	1	S22181	gamma-1-microglobu
583	6	1.8	326	2	G70402	656	6	1.8	355	2	T03785	L-lactate dehydrog
584	6	1.8	327	2	A70871	657	6	1.8	356	2	C70249	hypothetical prote
585	6	1.8	328	2	B84545	658	6	1.8	356	2	S58529	alpha-complex prot
586	6	1.8	328	2	D69452	659	6	1.8	356	2	JQ2352	glycoprotein I - t
587	6	1.8	328	2	D69452	660	6	1.8	357	2	AD3451	hypothetical membr
588	6	1.8	328	2	C69358	661	6	1.8	358	2	D89823	hypothetical prote
589	6	1.8	328	2	D72566	662	6	1.8	359	2	H95892	probable oxidoredu
590	6	1.8	328	2	S57128	663	6	1.8	359	2	D83385	hypothetical prote
591	6	1.8	329	2	T10203	664	6	1.8	359	2	G86290	hypothetical prote
592	6	1.8	329	2	H71192	665	6	1.8	359	2	T26813	hypothetical prote
593	6	1.8	330	2	C71096	666	6	1.8	359	2	AH3465	oxidoreductase (BC
594	6	1.8	330	2	D95958	667	6	1.8	360	2	T27694	hypothetical prote
595	6	1.8	330	4	PS0079	668	6	1.8	360	2	T51870	hypothetical prote
596	6	1.8	331	2	D83480	669	6	1.8	360	2	B70863	hypothetical prote
597	6	1.8	331	2	T32168	670	6	1.8	361	2	S57182	probable polygalac
598	6	1.8	331	2	T32445	671	6	1.8	361	2	T31815	hypothetical prote
599	6	1.8	332	1	MMBP16	672	6	1.8	362	2	S29968	coat protein VPI -
600	6	1.8	332	1	MMBP26	673	6	1.8	363	2	S78515	single-stranded nu
601	6	1.8	332	2	AT1319	674	6	1.8	363	2	AC0244	conserved hypotet
602	6	1.8	332	2	AT1691	675	6	1.8	364	2	F96603	hypothetical prote
603	6	1.8	332	2	T23503	676	6	1.8	365	2	J00879	N55 protein - hepa
604	6	1.8	332	2	H82064	677	6	1.8	365	2	S42471	hnRNP protein B2 -
605	6	1.8	333	2	B86567	678	6	1.8	365	2	A12940	acetyltransferase
606	6	1.8	333	2	G72058	679	6	1.8	366	2	E87457	conserved hypotet
607	6	1.8	334	2	D83750	680	6	1.8	366	2	A55525	carboxy-cis, cis-mu
608	6	1.8	334	2	S44299	681	6	1.8	366	2	T31933	hypothetical prote
609	6	1.8	334	2	T27658	682	6	1.8	367	2	B72644	probable transketo
610	6	1.8	335	2	T25498	683	6	1.8	368	2	S71190	heat shock protein
611	6	1.8	336	2	B49683	684	6	1.8	368	2	AH2694	MFS permease [lipo
612	6	1.8	337	2	E83961	685	6	1.8	370	2	A60089	transforming prote
613	6	1.8	337	2	B88957	686	6	1.8	370	2	S29139	aggrecan - pig (fir



687	6	1.8	370	2	G90248	conserved hypotet	760	6	1.8	402	2	A83398	probable MFS trans
688	6	1.8	371	2	A90044	hypothetical prote	761	6	1.8	404	2	F71718	alanine racemase (
689	6	1.8	371	2	A53908	brevican precursor	762	6	1.8	404	2	G75152	hypothetical prote
690	6	1.8	371	2	JC5498	G protein-coupled	763	6	1.8	404	2	H71193	hypothetical prote
691	6	1.8	372	1	G84358	N2,N2-dimethylguan	764	6	1.8	405	2	T10260	patacin-like prote
692	6	1.8	372	1	QOBE88	glycoprotein I pre	765	6	1.8	405	2	T16002	hypothetical prote
693	6	1.8	372	2	P00138	dnak-type molecula	766	6	1.8	405	2	T02649	hypothetical prote
694	6	1.8	372	2	B84856	hypothetical prote	767	6	1.8	406	2	T42926	hypothetical prote
695	6	1.8	372	2	A98342	rasp protein (AP14	768	6	1.8	407	2	T34535	hypothetical prote
696	6	1.8	374	2	A40756	hypothetical prote	769	6	1.8	407	2	T08732	hypothetical prote
697	6	1.8	375	2	AH0209	probable sugar ABC	770	6	1.8	407	2	AC2721	MFS permease [lipo
698	6	1.8	375	2	A12041	hypothetical prote	771	6	1.8	407	2	G97502	probable mfs trans
699	6	1.8	376	2	AG1410	cell division prot	772	6	1.8	408	2	D83191	conserved hypotet
700	6	1.8	376	2	G83290	hypothetical prote	773	6	1.8	409	1	TS0759	membrane dipeptid
701	6	1.8	376	2	JC6535	multidrugitcin-cha	774	6	1.8	409	2	S68247	adenosine A2a rece
702	6	1.8	376	2	B71981	DNA transformation	775	6	1.8	409	2	I48095	A2 adenosine recep
703	6	1.8	377	2	S21302	succinate dehydrog	776	6	1.8	409	2	F64396	hypothetical prote
704	6	1.8	377	2	S63671	26S proteinase cha	777	6	1.8	410	2	A71481	probable poly A po
705	6	1.8	377	2	F71520	hypothetical prote	778	6	1.8	411	2	E96665	protein P22C12.16
706	6	1.8	377	2	C69758	amino acid transpo	779	6	1.8	412	2	A48978	adenosine receptor
707	6	1.8	377	2	T24186	hypothetical prote	780	6	1.8	412	2	D30341	G protein-coupled
708	6	1.8	378	2	I46268	brevican precursor	781	6	1.8	412	2	S72579	hypothetical prote
709	6	1.8	378	2	H71307	probable spore coa	782	6	1.8	413	2	C89780	probable permease
710	6	1.8	378	2	A99263	transport membrane	783	6	1.8	413	2	AC1045	conserved hypotet
711	6	1.8	380	2	H70144	ATP-binding protei	784	6	1.8	413	2	AF2728	hypothetical prote
712	6	1.8	384	2	T33762	hypothetical prote	785	6	1.8	413	2	G97509	hypothetical prote
713	6	1.8	384	2	I40867	hypothetical prote	786	6	1.8	414	2	A24872	hypothetical prote
714	6	1.8	384	2	I49528	hypothetical prote	787	6	1.8	414	2	T03996	hypothetical prote
715	6	1.8	385	2	D95350	probable transmemb	788	6	1.8	415	2	T29296	hypothetical prote
716	6	1.8	385	2	T35516	hypothetical prote	789	6	1.8	415	2	S12357	interleukin-5 rece
717	6	1.8	386	2	A42688	serotonin receptor	790	6	1.8	415	2	G64510	hypothetical prote
718	6	1.8	386	2	S18637	serotonin receptor	791	6	1.8	415	2	T09213	mRNA-binding prote
719	6	1.8	386	2	H84522	hypothetical prote	792	6	1.8	416	2	H69436	S-enolpyruvylshiki
720	6	1.8	386	2	T18890	hypothetical prote	793	6	1.8	416	2	T14554	calliculin - bee
721	6	1.8	387	2	F82998	probable iron-cont	794	6	1.8	416	2	T01159	hypothetical prote
722	6	1.8	387	2	T43140	probable heavy met	795	6	1.8	416	2	AF1127	rod shape-determ
723	6	1.8	387	2	T38252	probable zinc/cadm	796	6	1.8	417	1	MMBRHA	5SK immediate-earl
724	6	1.8	387	2	A49498	dytrophin-associ	797	6	1.8	419	2	G75252	probable brbK prot
725	6	1.8	387	2	A54746	adhalin precursor	798	6	1.8	419	2	E70489	processing protein
726	6	1.8	387	2	I48201	adhalin - golden h	799	6	1.8	420	2	H84890	hypothetical prote
727	6	1.8	387	2	JC5556	adhalin - mouse	800	6	1.8	420	2	F83494	hypothetical prote
728	6	1.8	389	2	S68422	serotonin receptor	801	6	1.8	421	2	F83400	hypothetical prote
729	6	1.8	390	1	QOBE77	glycoprotein I pre	802	6	1.8	422	1	A60503	sperm-binding glyc
730	6	1.8	390	2	JN0268	serotonin receptor	803	6	1.8	422	1	A69853	hexuronate transpo
731	6	1.8	390	2	S58126	serotonin receptor	804	6	1.8	422	1	AD2941	hypothetical prote
732	6	1.8	391	2	AH0052	Hmrt protein [lipo	805	6	1.8	424	1	S12793	modulation protein
733	6	1.8	391	2	S18666	KIN17 protein - mo	806	6	1.8	424	2	D71192	hypothetical prote
734	6	1.8	392	2	H84232	anion permease [im	807	6	1.8	424	2	E86367	protein P26R24.22
735	6	1.8	392	2	H97335	Na+ ABC transpor	808	6	1.8	424	2	G75579	branched-chain ami
736	6	1.8	393	2	UQ0461	genome polyprotein	809	6	1.8	424	2	S43560	coiled coil protei
737	6	1.8	393	2	S70637	tubulin beta chain	810	6	1.8	425	2	T39967	probable proline-t
738	6	1.8	395	2	D69779	antibiotic resista	811	6	1.8	425	2	A70394	hypothetical prote
739	6	1.8	396	1	G64313	protein-export mem	812	6	1.8	425	2	D75164	hypothetical prote
740	6	1.8	396	2	JC2313	probable nitrite h	813	6	1.8	426	1	SAVLC	large surface anti
741	6	1.8	396	2	H86675	hypothetical prote	814	6	1.8	427	1	F97476	probable integral
742	6	1.8	396	2	H84383	porphobilinogen de	815	6	1.8	428	1	SAVUS	large surface anti
743	6	1.8	396	2	B82320	membrane-bound lyl	816	6	1.8	428	2	A83005	conserved hypotet
744	6	1.8	397	2	C81851	acetylornithine tr	817	6	1.8	428	2	AF1984	hypothetical prote
745	6	1.8	398	2	H81090	acetylornithine am	818	6	1.8	430	2	G75408	probable transpor
746	6	1.8	398	2	S16721	coenzyme F420 hydr	819	6	1.8	431	1	SAVL59	large surface anti
747	6	1.8	398	2	F70695	hypothetical prote	820	6	1.8	431	1	SAVL7	large surface anti
748	6	1.8	398	2	T02161	hypothetical prote	821	6	1.8	431	1	SAVL2	large surface anti
749	6	1.8	398	2	H75043	mg2+ transport pro	822	6	1.8	431	1	SAVLW8	large surface anti
750	6	1.8	398	2	AF0049	probable membrane	823	6	1.8	431	2	T50573	probable integral
751	6	1.8	399	2	F83882	L-arabinose utiliz	824	6	1.8	431	2	B97277	probable O-antigen
752	6	1.8	399	2	D84062	S-adenosylmethioni	825	6	1.8	431	2	B81124	conserved hypotet
753	6	1.8	399	2	T21649	hypothetical prote	826	6	1.8	431	2	E81900	hypothetical prote
754	6	1.8	400	2	B64071	lysosine-specific	827	6	1.8	432	2	G71683	NADH2 dehydrogen
755	6	1.8	400	2	IS97535	ispd/ispf bifuncti	828	6	1.8	432	2	B70110	hypothetical prote
756	6	1.8	400	2	AC2754	ISPD/ISPF bifuncti	829	6	1.8	432	2	T35263	probable carboxype
757	6	1.8	401	2	T35334	probable membrane	830	6	1.8	432	2	AI0351	peptidase B [limpor
758	6	1.8	401	2	AI2255	two-component sens	831	6	1.8	433	2	AI0536	probable membrane
759	6	1.8	401	2	B69501	sugar transporter	832	6	1.8	433	2	H97846	hypothetical prote



833	6	1.8	434	2	D81743	906	6	1.8	469	2	G69267	conserved hypotnet
834	6	1.8	434	2	AG2349	907	6	1.8	470	1	A25685	hypothetical prote
835	6	1.8	435	2	G75363	908	6	1.8	470	2	T39796	negative sexual co
836	6	1.8	437	2	G34469	909	6	1.8	471	2	T43803	cytochrome-c oxida
837	6	1.8	437	2	C72570	910	6	1.8	471	2	B64099	undecaprenyl-phosp
838	6	1.8	437	2	H70918	911	6	1.8	473	1	F2LV44	photosystem II chl
839	6	1.8	438	2	T31889	912	6	1.8	473	2	G72205	hypothetical prote
840	6	1.8	440	2	C97620	913	6	1.8	473	2	B72457	probable phenylala
841	6	1.8	440	2	D95390	914	6	1.8	473	2	T04225	hypothetical prote
842	6	1.8	441	2	C45561	915	6	1.8	474	2	B83587	two-component sens
843	6	1.8	442	2	D97382	916	6	1.8	474	2	B83719	multidrug resistanc
844	6	1.8	442	2	AC2600	917	6	1.8	476	2	JC4646	bone morphogenetic
845	6	1.8	443	2	H83589	918	6	1.8	476	2	H95313	NoeA host specific
846	6	1.8	443	2	G90388	919	6	1.8	476	2	S71360	noeA protein - Rhi
847	6	1.8	444	1	F64138	920	6	1.8	476	2	T29054	probable transmemb
848	6	1.8	444	2	B82283	921	6	1.8	476	2	T23728	hypothetical prote
849	6	1.8	444	2	F98341	922	6	1.8	477	2	T47819	hypothetical prote
850	6	1.8	445	2	T31898	923	6	1.8	478	2	T38014	hypothetical zinc
851	6	1.8	446	2	T310103	924	6	1.8	480	2	D45561	merozoite surface
852	6	1.8	446	2	D64376	925	6	1.8	480	2	T36822	probable transcrip
853	6	1.8	446	2	T49149	926	6	1.8	481	2	H69275	signal-transducing
854	6	1.8	447	1	AJBCRS	927	6	1.8	482	1	JN0506	argininosuccinate
855	6	1.8	447	2	B81003	928	6	1.8	482	2	H82352	probable PTS sytle
856	6	1.8	447	2	F82025	929	6	1.8	482	2	G75483	probable leucyl am
857	6	1.8	447	2	G85980	930	6	1.8	482	2	T49079	serine-type carbox
858	6	1.8	447	2	D91135	931	6	1.8	482	2	F71969	hypothetical prote
859	6	1.8	449	1	B43698	932	6	1.8	483	2	G75392	glycosyl hydrolase
860	6	1.8	449	2	AB0889	933	6	1.8	483	2	T10552	hypothetical prote
861	6	1.8	449	2	D85962	934	6	1.8	485	2	A11696	weakly probable su
862	6	1.8	449	2	H65089	935	6	1.8	485	2	H82377	ABC transporter. A
863	6	1.8	449	2	A82597	936	6	1.8	487	1	AJSMRC	argininosuccinate
864	6	1.8	449	2	F97379	937	6	1.8	487	2	AF2692	MPS permease (limp
865	6	1.8	449	2	E71172	938	6	1.8	488	2	S27652	probable aldehyde
866	6	1.8	450	2	AC1791	939	6	1.8	488	2	B69415	group II decarboxy
867	6	1.8	450	2	AD1415	940	6	1.8	488	2	D64108	glucuronate transpor
868	6	1.8	451	2	S73433	941	6	1.8	489	2	B27657	hypothetical prote
869	6	1.8	451	2	T06090	942	6	1.8	490	2	I52410	cytochrome P450 1I
870	6	1.8	452	2	AB3222	943	6	1.8	490	2	A36122	cytochrome P450 2C
871	6	1.8	452	2	AG0326	944	6	1.8	490	2	T49096	hypothetical prote
872	6	1.8	453	2	S31313	945	6	1.8	490	2	T28382	ORF MSV221 hypot
873	6	1.8	453	2	B88040	946	6	1.8	492	2	S71245	glucose-6-phosphat
874	6	1.8	453	2	T30239	947	6	1.8	492	2	AE3033	L-xyulose kinase
875	6	1.8	453	2	AD1556	948	6	1.8	492	2	D75619	codyrlic acid synth
876	6	1.8	453	2	AP1198	949	6	1.8	492	2	T44202	hypothetical prote
877	6	1.8	454	2	JC7231	950	6	1.8	492	2	T44015	hypothetical prote
878	6	1.8	454	2	F90602	951	6	1.8	493	2	S36931	chitinase (BC 3.2.
879	6	1.8	454	2	A84148	952	6	1.8	495	2	T20038	hypothetical prote
880	6	1.8	455	2	AE0191	953	6	1.8	497	2	AD0152	probable bacteriop
881	6	1.8	455	2	A70461	954	6	1.8	498	2	B69276	hypothetical prote
882	6	1.8	456	2	C86624	955	6	1.8	501	2	T44298	sodium/proline sym
883	6	1.8	456	2	H72000	956	6	1.8	502	2	AB3203	Tn3 family transpo
884	6	1.8	458	2	B90623	957	6	1.8	503	2	T51782	hypothetical prote
885	6	1.8	458	2	S75114	958	6	1.8	503	2	A49429	interleukin-1 beta
886	6	1.8	459	2	T37704	959	6	1.8	503	2	JC5287	SHP substrate-1 pr
887	6	1.8	459	2	T43538	960	6	1.8	504	2	AB2843	hydroxylase [import
888	6	1.8	459	2	B69580	961	6	1.8	505	2	AE3168	hypothetical prote
889	6	1.8	460	2	JL0145	962	6	1.8	507	2	G72418	sugar ABC transpor
890	6	1.8	460	2	A84281	963	6	1.8	508	1	S62599	UTP-glucose-1-phos
891	6	1.8	461	1	G64537	964	6	1.8	508	1	UX0277	UTP-glucose-1-phos
892	6	1.8	461	1	I64080	965	6	1.8	508	2	B81083	cardiolipin synthe
893	6	1.8	462	1	A37986	966	6	1.8	509	2	JC5288	SHP substrate-1 pr
894	6	1.8	462	2	T26401	967	6	1.8	509	2	A96749	unknown protein T1
895	6	1.8	462	2	A86459	968	6	1.8	510	2	A71816	hypothetical prote
896	6	1.8	462	2	AH1017	969	6	1.8	510	2	A64706	lipase-like protei
897	6	1.8	463	2	JC7372	970	6	1.8	511	2	T22835	hypothetical prote
898	6	1.8	464	2	H83006	971	6	1.8	511	2	G98252	cryptic L-xyulose
899	6	1.8	466	1	KFHM7	972	6	1.8	511	2	A40110	nicotinic acetylch
900	6	1.8	467	2	T45475	973	6	1.8	513	2	T01413	probable histone d
901	6	1.8	468	2	C90599	974	6	1.8	513	2	JC5289	SHP substrate-1 pr
902	6	1.8	468	2	A13241	975	6	1.8	513	2	T31596	hypothetical prote
903	6	1.8	468	2	T41294	976	6	1.8	513	2	A82432	sodium/solute sym
904	6	1.8	469	2	AC0902	977	6	1.8	513	2	B71683	NADH2 dehydrogenas
905	6	1.8	469	2	S73404	978	6	1.8	514	2	S52771	beta-glucosidase (



979	6	1.8	514	2	TJ5371	probable Na <sup>+</sup> /H <sup>+</sup> an	1052	6	1.8	559	2	T15282	hypothetical prote
980	6	1.8	514	2	B86164	hypothetical prote	1053	6	1.8	560	2	T02404	probable beta-gluc
981	6	1.8	515	2	P96700	protein F12a21.9 [	1054	6	1.8	560	2	S46724	hexose transport p
982	6	1.8	516	2	S06443	dnak-type molecule	1055	6	1.8	561	2	T31965	hypothetical prote
983	6	1.8	517	2	AF1976	hypothetical prote	1056	6	1.8	563	2	T51348	RNA helicase RH25
984	6	1.8	518	1	B46619	Ca2+/calmodulin-de	1057	6	1.8	566	2	S42257	lamin - Caenorhabd
985	6	1.8	518	1	S43845	Ca2+/calmodulin-de	1058	6	1.8	566	2	T20380	hypothetical prote
986	6	1.8	519	2	T51367	probable PrL1 asso	1059	6	1.8	566	2	A83081	type 4 fibribrial bl
987	6	1.8	520	2	B84663	probable cytochrom	1060	6	1.8	566	2	A35384	p11B protein - pse
988	6	1.8	521	2	B64862	probable membrane	1061	6	1.8	567	2	A48895	myasthenic syndrom
989	6	1.8	521	2	B71717	hypothetical prote	1062	6	1.8	567	2	C69611	ABC transporter re
990	6	1.8	522	2	B82024	peptide methionine	1063	6	1.8	568	2	S70873	ABC transporter re
991	6	1.8	522	2	T26163	hypothetical prote	1064	6	1.8	568	2	F71614	chromatinic RING f
992	6	1.8	524	2	S44982	flagellin - Shigel	1065	6	1.8	571	2	G89123	protein K07C11.4 [
993	6	1.8	525	2	B81859	phospholipase D-fam	1066	6	1.8	575	2	B84798	probable peptide/a
994	6	1.8	525	2	T25900	hypothetical prote	1067	6	1.8	576	1	ACFP42	nicotinic acetylch
995	6	1.8	526	2	T13687	hypothetical prote	1068	6	1.8	577	2	A72283	maltose ABC transp
996	6	1.8	527	1	OBSX1	cytochrome-c oxida	1069	6	1.8	577	2	S47961	glucosyltransferas
997	6	1.8	527	1	A31908	Ca2+/calmodulin-de	1070	6	1.8	578	2	AC0119	probable OmpA-fami
998	6	1.8	527	1	S05290	cytochrome-c oxida	1071	6	1.8	578	2	AC0119	probable exported
999	6	1.8	527	2	B84483	protein-tyrosine k	1072	6	1.8	579	2	A97099	ABC-type multidrug
1000	6	1.8	527	2	I49133	protein-tyrosine k	1073	6	1.8	579	2	A27650	phosphate response
1001	6	1.8	528	2	B97474	hypothetical prote	1074	6	1.8	580	2	B82450	PTS system, fructo
1002	6	1.8	528	2	T433919	ylfB protein [impo	1075	6	1.8	581	2	H95214	ABC transporter. A
1003	6	1.8	528	2	A10359	iron(III) -transpor	1076	6	1.8	583	2	C90327	n-methylhydantoina
1004	6	1.8	530	1	B48529	ubiquinol-cytochro	1077	6	1.8	583	2	T04531	nine-cis-epoxycaro
1005	6	1.8	530	2	B89044	protein B0238.9 [i	1078	6	1.8	585	2	H83729	adenine deaminase
1006	6	1.8	531	2	D86862	hypothetical prote	1079	6	1.8	586	2	A27763	succinate dehydrog
1007	6	1.8	532	2	A75368	cysteinyI -tRNA syn	1080	6	1.8	586	2	T20816	hypothetical prote
1008	6	1.8	532	2	T49824	hypothetical prote	1081	6	1.8	587	2	B85429	hypothetical prote
1009	6	1.8	532	2	A12694	hypothetical prote	1082	6	1.8	587	2	JH0464	DM-GRASP precursor
1010	6	1.8	533	2	F75124	abc transporter in	1083	6	1.8	587	2	A84078	two-component sens
1011	6	1.8	534	2	T19951	hypothetical prote	1084	6	1.8	588	2	H89885	succinate dehydrog
1012	6	1.8	535	2	B95952	probable dipeptide	1085	6	1.8	588	2	JH0506	adhesion molecule
1013	6	1.8	536	1	POWMD	gag polypeptide -	1086	6	1.8	588	2	A45254	surface glycoprote
1014	6	1.8	537	2	T19764	hypothetical prote	1087	6	1.8	590	2	A47194	taurine and beta-a
1015	6	1.8	537	2	G85021	protoporphyritogen	1088	6	1.8	590	2	A26638	homeotic protein D
1016	6	1.8	537	2	A82454	two-component sens	1089	6	1.8	591	2	A69291	transmembrane olig
1017	6	1.8	538	2	S60645	MADH2 dehydrogenas	1090	6	1.8	591	2	B87361	flagellar hook pro
1018	6	1.8	538	2	G83653	oligopeptide ABC t	1091	6	1.8	594	2	G98078	hypothetical prote
1019	6	1.8	538	2	I51560	ribonucleoprotein	1092	6	1.8	595	2	T05087	hypothetical prote
1020	6	1.8	540	2	H88086	chaperonin GroEL [	1093	6	1.8	597	2	A32440	RNA-directed RNA p
1021	6	1.8	540	2	G95222	chaperonin, 60 kDa	1094	6	1.8	598	2	T22610	hypothetical prote
1022	6	1.8	542	2	JN0661	heat shock protein	1095	6	1.8	599	2	F87682	tykA family protei
1023	6	1.8	542	2	S32106	groEL protein - la	1096	6	1.8	599	2	T42328	hypothetical prote
1024	6	1.8	542	2	B86674	60 kD chaperonin [	1097	6	1.8	601	2	S47896	probable molybdopt
1025	6	1.8	543	2	F72071	conserved hypotet	1098	6	1.8	601	2	S56144	SH3 domain binding
1026	6	1.8	543	2	C86551	CT384 hypothetical	1099	6	1.8	603	2	A70770	hypothetical glyci
1027	6	1.8	543	2	T20964	hypothetical prote	1100	6	1.8	603	2	A84451	probable AAA-type
1028	6	1.8	543	2	T32973	hypothetical prote	1101	6	1.8	603	2	H72276	phosphoribosylform
1029	6	1.8	544	2	C86405	probable sphingosl	1102	6	1.8	603	2	T00379	KIRA0640 protein -
1030	6	1.8	545	2	T05510	hypothetical prote	1103	6	1.8	605	1	A48665	methyIamalonyl-CoA
1031	6	1.8	545	2	T47952	hypothetical prote	1104	6	1.8	605	1	T15291	sphingomyelin phos
1032	6	1.8	545	2	T02005	protoporphyritogen	1105	6	1.8	609	2	T28736	hypothetical prote
1033	6	1.8	546	2	D69679	polyketide synthas	1106	6	1.8	613	2	T51938	inositol-1',4',5'-tri
1034	6	1.8	546	2	P96562	hypothetical prote	1107	6	1.8	613	2	T16885	hypothetical prote
1035	6	1.8	546	2	F87343	ABC transporter, A	1108	6	1.8	613	2	F89801	conserved hypotet
1036	6	1.8	546	2	F84900	hypothetical prote	1109	6	1.8	617	2	T52499	ferredoxin oxidore
1037	6	1.8	548	2	JC4073	TCE-1 containing c	1110	6	1.8	618	2	H70552	probable PPR prote
1038	6	1.8	548	2	T04058	protoporphyritogen	1111	6	1.8	619	2	S29839	taurine transport
1039	6	1.8	550	2	T10564	hypothetical prote	1112	6	1.8	620	2	F83976	cytochrome-c oxida
1040	6	1.8	551	2	A80031	probable transmemb	1113	6	1.8	620	2	G01426	taurine transporte
1041	6	1.8	551	2	JC7562	glioblastoma RING	1114	6	1.8	620	2	S46487	taurine transporte
1042	6	1.8	551	2	S51941	pnnin 1 precursor	1115	6	1.8	621	2	T45936	transporter-like p
1043	6	1.8	552	2	B82633	ubiquinone biosynt	1116	6	1.8	621	1	D69295	endopeptidase Ia b
1044	6	1.8	552	2	T04653	recliver-like prot	1117	6	1.8	621	2	I57939	taurine transporte
1045	6	1.8	553	2	F86397	protein T7N9.16 [i	1118	6	1.8	622	2	E69609	cytochrome-c oxida
1046	6	1.8	556	2	JC5636	Ca2+/calmodulin-de	1119	6	1.8	622	2	B81981	probable lipopolys
1047	6	1.8	557	1	S23435	malate dehydrogena	1120	6	1.8	622	2	AB1090	bacteriophage mino
1048	6	1.8	557	2	S43231	malate dehydrogena	1121	6	1.8	622	2	A11453	bacteriophage mmo
1049	6	1.8	557	2	T07116	protoporphyritogen	1122	6	1.8	623	2	T48859	disease resistance
1050	6	1.8	559	2	AB1153	hypothetical prote	1123	6	1.8	623	2	T06674	hypothetical prote
1051	6	1.8	559	2	AC1512	hypothetical prote	1124	6	1.8	623	2	B81037	lipopolysaccharide



1125	6	1.8	624	2	T49366	1198	6	1.8	694	2	A82697	penicillin binding
1126	6	1.8	625	2	D45335	1199	6	1.8	694	2	H95012	hypothetical prote
1127	6	1.8	626	2	C72035	1200	6	1.8	696	2	E81677	conserved hypotet
1128	6	1.8	626	2	C86589	1201	6	1.8	698	2	AB3576	fusaric acid resis
1129	6	1.8	627	2	T11125	1202	6	1.8	702	2	T13708	NADH2 dehydrogenas
1130	6	1.8	630	2	S49959	1203	6	1.8	702	2	C97884	hypothetical prote
1131	6	1.8	632	2	T45471	1204	6	1.8	703	1	C48562	coat protein - San
1132	6	1.8	634	2	C81652	1205	6	1.8	704	2	T50303	hypothetical prote
1133	6	1.8	634	2	D71493	1206	6	1.8	704	2	T13127	tran protein homol
1134	6	1.8	635	2	G86589	1207	6	1.8	705	2	B75371	ABC transporter, A
1135	6	1.8	635	2	H81793	1208	6	1.8	707	1	COORJ5	phosphotransferase
1136	6	1.8	635	2	G72035	1209	6	1.8	709	2	G97337	topoisomerase B [i
1137	6	1.8	636	2	A48872	1210	6	1.8	710	1	T39865	serine/threonine-s
1138	6	1.8	636	2	S63131	1211	6	1.8	710	2	T47243	amino-acid N-acety
1139	6	1.8	637	2	B69627	1212	6	1.8	712	2	A48156	translacion regula
1140	6	1.8	639	2	T50148	1213	6	1.8	712	2	B38992	cadherin 13 precu
1141	6	1.8	640	1	HKHW7A	1214	6	1.8	713	2	B38992	DNA helicase II -
1142	6	1.8	640	2	T21394	1215	6	1.8	715	2	S73821	hypothetical prote
1143	6	1.8	640	2	T21394	1216	6	1.8	719	2	T47727	hypothetical prote
1144	6	1.8	640	2	A87606	1217	6	1.8	720	2	T02734	hypothetical prote
1145	6	1.8	641	2	S63645	1218	6	1.8	721	2	B83820	hypothetical prote
1146	6	1.8	641	2	T07668	1219	6	1.8	723	2	JC7795	epithelial calcium
1147	6	1.8	642	2	T28866	1220	6	1.8	724	2	H86427	unknown protein [i
1148	6	1.8	643	2	G64412	1221	6	1.8	725	2	JC7531	calcium transport
1149	6	1.8	643	2	H83635	1222	6	1.8	727	2	F82634	tail-specific prot
1150	6	1.8	643	2	B75055	1223	6	1.8	727	2	JC7796	epithelial calcium
1151	6	1.8	644	1	H69204	1224	6	1.8	728	1	T50719	C-Delta-1 - chicke
1152	6	1.8	644	2	S67431	1225	6	1.8	735	2	PC4225	replication licens
1153	6	1.8	645	2	T05251	1226	6	1.8	737	2	S47857	basic protein, cyt
1154	6	1.8	646	2	T51937	1227	6	1.8	739	2	G96740	hypothetical prote
1155	6	1.8	648	2	A54892	1228	6	1.8	740	1	DENTW5	NADH2 dehydrogenas
1156	6	1.8	649	2	S42488	1229	6	1.8	740	2	S61568	probable membrane
1157	6	1.8	653	2	B82872	1230	6	1.8	742	2	AH2166	hypothetical prote
1158	6	1.8	653	2	B87698	1231	6	1.8	746	2	A84800	hypothetical prote
1159	6	1.8	653	2	S52727	1232	6	1.8	751	2	S65469	DNA topoisomerase
1160	6	1.8	653	2	S11448	1233	6	1.8	753	2	T28787	hypothetical prote
1161	6	1.8	653	2	AG1190	1234	6	1.8	753	2	A86756	probable p12 prote
1162	6	1.8	654	2	S27004	1235	6	1.8	754	2	A85043	probable IRR recep
1163	6	1.8	654	2	AH2445	1236	6	1.8	755	2	T20950	hypothetical prote
1164	6	1.8	654	2	T32623	1237	6	1.8	759	2	T16368	hypothetical prote
1165	6	1.8	655	2	A46270	1238	6	1.8	761	2	B82167	5-methyltetrahydro
1166	6	1.8	655	2	G75582	1239	6	1.8	761	2	AB1848	hypothetical prote
1167	6	1.8	655	2	JC7850	1240	6	1.8	761	2	H65083	glycolate oxidase
1168	6	1.8	656	2	C71361	1241	6	1.8	762	2	G96999	hydrogenase matura
1169	6	1.8	657	2	S77543	1242	6	1.8	764	2	A49448	irregular chiasm C
1170	6	1.8	660	2	S71949	1243	6	1.8	766	2	A40258	RAS GTPase-activat
1171	6	1.8	661	2	A25398	1244	6	1.8	767	1	S77523	cdc10 start contro
1172	6	1.8	661	2	S50734	1245	6	1.8	770	2	JC4636	hypothetical prote
1173	6	1.8	662	2	T48128	1246	6	1.8	772	2	JC4636	transcription elon
1174	6	1.8	664	2	B86714	1247	6	1.8	774	2	T03919	hypothetical prote
1175	6	1.8	664	2	C71106	1248	6	1.8	775	2	S69515	replication initia
1176	6	1.8	665	2	AF0815	1249	6	1.8	777	2	T00208	transposase-like p
1177	6	1.8	667	1	A48660	1250	6	1.8	777	2	AF2410	serine/threonine k
1178	6	1.8	667	1	G91044	1251	6	1.8	779	1	S61571	suppressor protein
1179	6	1.8	667	2	B85889	1252	6	1.8	779	2	B97778	endopeptidase La (
1180	6	1.8	669	2	I38029	1253	6	1.8	782	2	A61625	tenascin-like prote
1181	6	1.8	669	2	S76474	1254	6	1.8	783	2	JC5467	cellulase (EC 3.2.
1182	6	1.8	672	2	AC0422	1255	6	1.8	784	1	A71704	endopeptidase La (
1183	6	1.8	674	2	S46092	1256	6	1.8	786	2	G85073	probable myosin-li
1184	6	1.8	676	2	D95249	1257	6	1.8	786	2	T18469	hypothetical prote
1185	6	1.8	676	2	A98114	1258	6	1.8	787	2	H70374	NADH2 dehydrogenas
1186	6	1.8	677	2	S65573	1259	6	1.8	787	2	T41974	replication origin
1187	6	1.8	677	2	JC7303	1260	6	1.8	788	2	S48191	probable ubiquinol
1188	6	1.8	682	2	JC7385	1261	6	1.8	788	2	AE3153	NADP-dependent ald
1189	6	1.8	682	2	UC0420	1262	6	1.8	790	2	S71278	DNA ligase (ATP) (
1190	6	1.8	683	2	T12127	1263	6	1.8	795	2	T34673	probable SecDF pro
1191	6	1.8	684	2	F70810	1264	6	1.8	797	2	T21487	hypothetical prote
1192	6	1.8	685	2	B96526	1265	6	1.8	798	2	D86459	probable disease r
1193	6	1.8	687	2	T02459	1266	6	1.8	798	2	F98134	hypothetical prote
1194	6	1.8	687	2	S43587	1267	6	1.8	800	2	A29003	cellulase (EC 3.2.
1195	6	1.8	690	2	B84945	1268	6	1.8	801	1	MXRXR5	RNA 5 protein - ri
1196	6	1.8	691	2	A71520	1269	6	1.8	801	2	S50660	hypothetical prote
1197	6	1.8	692	2	T12587	1270	6	1.8	802	2	T05596	probable potassium



1271	6	1.8	804	2	G64780	probable membrane	1344	6	1.8	949	2	E75352	glycine cleavage s
1272	6	1.8	804	2	A85549	probable oxidoredu	1345	6	1.8	949	2	T40330	hypothetical prote
1273	6	1.8	804	2	G90658	probable oxidoredu	1346	6	1.8	949	2	T45577	hypothetical prote
1274	6	1.8	807	2	T19836	hypothetical prote	1347	6	1.8	950	2	T25088	hypothetical prote
1275	6	1.8	809	2	T16645	probable spindle p	1348	6	1.8	954	2	S46105	glucan 1,4-alpha-g
1276	6	1.8	812	2	T19446	hypothetical prote	1349	6	1.8	958	2	S47179	hypothetical prote
1277	6	1.8	822	2	TJ0611	cellulase (EC 3.2.	1350	6	1.8	960	1	A39651	disc-large tumor
1278	6	1.8	823	2	AF3351	endopeptidase Ia (	1351	6	1.8	961	2	T03467	NADH dehydrogenase
1279	6	1.8	824	2	UC7352	cellulase (EC 3.2.	1352	6	1.8	962	2	AG2444	hypothetical prote
1280	6	1.8	827	2	S75622	hypothetical prote	1353	6	1.8	970	2	B84846	probable zinc prot
1281	6	1.8	828	2	S34695	hypothetical prote	1354	6	1.8	970	2	A13605	potassium efflux s
1282	6	1.8	834	2	S66258	glucosidase I - hu	1355	6	1.8	970	2	S63059	hypothetical prote
1283	6	1.8	835	2	S54152	sepb protein - Eme	1356	6	1.8	971	2	S54595	probable membrane
1284	6	1.8	843	2	H82352	adenylate cyclase	1357	6	1.8	973	2	B86547	polymorphic outer
1285	6	1.8	845	2	T52518	related to cytosin	1358	6	1.8	973	2	F72076	polymorphic outer
1286	6	1.8	848	2	C70203	DNA topoisomerase	1359	6	1.8	973	2	T41272	hypothetical prote
1287	6	1.8	849	2	T38728	probable trehalose	1360	6	1.8	973	2	T21069	hypothetical prote
1288	6	1.8	850	2	G70332	conserved hypotet	1361	6	1.8	978	1	RGBY13	regulatory protein
1289	6	1.8	852	2	S25359	hypothetical prote	1362	6	1.8	985	2	DJBE11	DNA-directed DNA p
1290	6	1.8	855	2	A34810	3',5'-cyclic-GMP p	1363	6	1.8	985	2	LS1672	receptor tyrosine
1291	6	1.8	855	2	T19405	hypothetical prote	1364	6	1.8	995	2	C81593	polymorphic membra
1292	6	1.8	856	2	S46750	aminopeptidase AAP	1365	6	1.8	1003	2	A39521	glycine dehydrogen
1293	6	1.8	858	2	T47223	replication licens	1366	6	1.8	1004	2	D71490	probable exodeoxyr
1294	6	1.8	862	2	A05028	ipoc protein homol	1367	6	1.8	1012	2	D86381	hypothetical prote
1295	6	1.8	863	1	S64720	replication licens	1368	6	1.8	1017	2	S62435	probable glycine d
1296	6	1.8	863	2	D88216	protein B0495.7 [1	1369	6	1.8	1018	2	T40253	hypothetical prote
1297	6	1.8	864	2	A43954	glutamate receptor	1370	6	1.8	1018	2	T22318	hypothetical prote
1298	6	1.8	868	2	T02635	D2 protein homolog	1371	6	1.8	1026	2	A89696	protein T21H8.1 [1
1299	6	1.8	869	2	S35792	glutamate receptor	1372	6	1.8	1037	2	D96786	protein P10A5.15 [
1300	6	1.8	870	2	T39731	cax2 protein - fis	1373	6	1.8	1041	2	T31097	chitin synthase (E
1301	6	1.8	874	2	H83533	alanj -rRNA synthe	1374	6	1.8	1042	2	T16169	hypothetical prote
1302	6	1.8	874	2	J00883	genome polypotein	1375	6	1.8	1045	2	F90365	hypothetical prote
1303	6	1.8	874	2	E75278	hypothetical prote	1376	6	1.8	1049	2	A27079	fibronectin recept
1304	6	1.8	880	2	AD1953	hypothetical prote	1377	6	1.8	1054	2	T01556	Ca2+-transporting
1305	6	1.8	881	2	T49279	hypothetical prote	1378	6	1.8	1056	1	GNLJG3	HIV-1 retropepsin
1306	6	1.8	881	2	T31739	hypothetical prote	1379	6	1.8	1061	2	T18085	DNA topoisomerase
1307	6	1.8	883	2	S57653	brevian precursor	1380	6	1.8	1066	2	A40265	retinoblastoma-agg
1308	6	1.8	883	2	S49126	brevian precursor	1381	6	1.8	1077	2	T38900	probable alpha-man
1309	6	1.8	883	2	T37208	hypothetical prote	1382	6	1.8	1078	2	T18352	protein p120 - Myc
1310	6	1.8	887	2	B84954	pyruvate dehydroge	1383	6	1.8	1085	2	F96712	hypothetical prote
1311	6	1.8	887	2	G88484	protein F23F12.8 [	1384	6	1.8	1085	2	JC2227	probable helicase
1312	6	1.8	888	2	A54280	cell differentiat	1385	6	1.8	1087	2	T30330	geloslin-related p
1313	6	1.8	889	2	TC7083	protein kinase (EC	1386	6	1.8	1088	2	E86312	filae.9 protein -
1314	6	1.8	890	2	T21000	hypothetical prote	1387	6	1.8	1089	2	S48244	NMD2 protein - yea
1315	6	1.8	891	2	T40137	hypothetical sefin	1388	6	1.8	1089	2	T21582	hypothetical prote
1316	6	1.8	898	2	S65474	pyruvate dehydroge	1389	6	1.8	1099	2	A55405	adenylate cyclase
1317	6	1.8	899	2	T38153	gene retII prote	1390	6	1.8	1099	2	A59300	myosin-If - mouse
1318	6	1.8	899	2	S49634	hypothetical prote	1391	6	1.8	1100	1	DBBYD1	RAD1 protein - yea
1319	6	1.8	902	1	S54495	probable carrier p	1392	6	1.8	1113	2	D86142	hypothetical prote
1320	6	1.8	902	2	D83467	probable cation-tr	1393	6	1.8	1114	2	T30819	RNA-directed RNA p
1321	6	1.8	903	2	T00358	hypothetical prote	1394	6	1.8	1123	2	T28139	PK4 protein kinase
1322	6	1.8	906	2	AD3267	protein translocas	1395	6	1.8	1127	1	E71156	endopeptidase Ia h
1323	6	1.8	906	2	T48898	disease resistance	1396	6	1.8	1136	2	T48184	hypothetical prote
1324	6	1.8	907	2	S54353	inter-alpha-trypsi	1397	6	1.8	1144	2	A81983	probable DNA-direc
1325	6	1.8	908	2	S19098	glutamate receptor	1398	6	1.8	1144	2	T27408	hypothetical prote
1326	6	1.8	908	2	T48899	disease resistance	1399	6	1.8	1148	2	AD0198	transcriptional-repa
1327	6	1.8	909	2	T00009	probable primase (	1400	6	1.8	1155	2	AC2426	adenylate cyclase
1328	6	1.8	912	2	A54423	brevian precursor	1401	6	1.8	1173	2	T25893	hypothetical prote
1329	6	1.8	922	2	S75615	exonuclease ABC c	1402	6	1.8	1174	2	A39927	RNA-directed RNA p
1330	6	1.8	923	1	MMBY7C	probable membrane	1403	6	1.8	1190	2	S21877	Pms protein - huma
1331	6	1.8	923	2	A53054	lipoxigenase (EC 1	1404	6	1.8	1194	2	T03818	apoptotic proteina
1332	6	1.8	928	1	VGBBERG	glycoprotein gi pr	1405	6	1.8	1198	2	T34340	dynein heavy chain
1333	6	1.8	928	2	T38419	Sec76 domain prote	1406	6	1.8	1201	2	F86386	hypothetical prote
1334	6	1.8	932	1	VGBBRC	glycoprotein gi pr	1407	6	1.8	1205	2	T27053	hypothetical prote
1335	6	1.8	933	2	TC6184	mismatch repair pr	1408	6	1.8	1208	2	S69015	AXI1 protein - yea
1336	6	1.8	935	2	S53608	DNA mismatch repai	1409	6	1.8	1212	2	C82834	DNA polymerase III
1337	6	1.8	937	2	C97168	glycosyltransferas	1410	6	1.8	1221	2	T25005	hypothetical prote
1338	6	1.8	940	2	D89723	protein F39D8.1b [	1411	6	1.8	1225	2	A36607	E2 glycoprotein -
1339	6	1.8	940	2	T31575	hypothetical prote	1412	6	1.8	1227	2	T48028	hypothetical prote
1340	6	1.8	943	2	B48474	glycoprotein B - f	1413	6	1.8	1245	2	G86404	probable P-glycopr
1341	6	1.8	945	2	T19943	hypothetical prote	1414	6	1.8	1247	2	A33812	interphotoreceptor
1342	6	1.8	945	2	T21998	hypothetical prote	1415	6	1.8	1272	2	C90593	hypothetical prote
1343	6	1.8	948	2	A56602	glycoprotein B hom	1416	6	1.8	1283	2	T13799	neurexin IV - fru1



1417	6	1.8	1285	2	S70582	botulinum neurotoxin
1418	6	1.8	1286	1	RJBOP	interphosphoreceptor
1419	6	1.8	1289	2	I84505	calcium-dependent
1420	6	1.8	1291	2	H71143	probable ribonucle
1421	6	1.8	1297	2	S25714	son-of-sevenless-2
1422	6	1.8	1302	2	A41249	multitrug resistanc
1423	6	1.8	1304	2	T14073	dynen 1b heavy ch
1424	6	1.8	1305	2	T18548	flax rust resistanc
1425	6	1.8	1307	2	T17453	BRG-associated pro
1426	6	1.8	1311	2	C84528	hypothetical prote
1427	6	1.8	1327	2	T14594	granidine nucleoti
1428	6	1.8	1333	2	A57488	Ras guanine nucleo
1429	6	1.8	1335	2	S07245	xanthine dehydroge
1430	6	1.8	1336	2	S25716	Ras guanine nucleo
1431	6	1.8	1336	2	T17479	hypothetical prote
1432	6	1.8	1339	2	T47841	hypothetical prote
1433	6	1.8	1388	2	A57655	tim (timeless) pro
1434	6	1.8	1400	2	T22644	hypothetical prote
1435	6	1.8	1405	2	T04426	hypothetical prote
1436	6	1.8	1416	2	T20823	hypothetical prote
1437	6	1.8	1423	1	S27941	serum albumin - se
1438	6	1.8	1423	1	A99580	hypothetical prote
1439	6	1.8	1436	2	F86904	conserved hypothec
1440	6	1.8	1436	2	A46496	antigen WCL.1 prec
1441	6	1.8	1445	2	I84505	probable gag/pol p
1442	6	1.8	1449	2	B81963	IGA-specific serin
1443	6	1.8	1449	2	D71551	hypothetical prote
1444	6	1.8	1457	2	D81019	adhesion and penet
1445	6	1.8	1460	2	T00095	hypothetical prote
1446	6	1.8	1462	1	S32437	pol polyprotein -
1447	6	1.8	1468	1	S30818	hypothetical prote
1448	6	1.8	1475	2	AD1173	hypothetical prote
1449	6	1.8	1475	2	A81530	hypothetical prote
1450	6	1.8	1485	2	T02856	probable membrane
1451	6	1.8	1509	2	B89985	hypothetical prote
1452	6	1.8	1512	2	T14883	hypothetical prote
1453	6	1.8	1513	2	S45768	mitotic spindle pr
1454	6	1.8	1534	2	S59604	DNA (cytosine-5)-
1455	6	1.8	1549	1	A40691	trichothyalin - she
1456	6	1.8	1557	2	G86419	probable reverse t
1457	6	1.8	1568	2	T09074	semaphorin recepto
1458	6	1.8	1612	2	T30805	ductil protein - mo
1459	6	1.8	1643	2	T05647	hypothetical prote
1460	6	1.8	1651	2	T14160	transmembrane rece
1461	6	1.8	1655	2	S47446	nucleoporin Np188
1462	6	1.8	1657	2	T54421	hypothetical prote
1463	6	1.8	1670	2	S71551	DNA-directed DNA p
1464	6	1.8	1682	1	C70588	probable mbtc prot
1465	6	1.8	1707	2	S77910	hypothetical prote
1466	6	1.8	1712	2	A38261	masking protein pr
1467	6	1.8	1737	2	T00209	MEGF8 protein - hu
1468	6	1.8	1737	2	T17101	probable voltage-a
1469	6	1.8	1740	2	T43215	ribonucleotide red
1470	6	1.8	1756	2	T02599	hypothetical prote
1471	6	1.8	1769	2	S53378	probable membrane
1472	6	1.8	1780	2	T17272	hypothetical prote
1473	6	1.8	1785	2	T22595	hypothetical prote
1474	6	1.8	1787	2	G97222	hypothetical prote
1475	6	1.8	1794	2	T38459	collagen alpha 1(X
1476	6	1.8	1806	1	CGHUIE	hypothetical prote
1477	6	1.8	1806	1	T23298	hypothetical prote
1478	6	1.8	1882	1	GNVYVR	genome polyprotein
1479	6	1.8	1891	2	T33262	calcium channel al
1480	6	1.8	1893	1	A40262	transcription init
1481	6	1.8	1898	1	A45973	trichothyalin - hum
1482	6	1.8	1911	2	T43048	calcium channel al
1483	6	1.8	1940	2	F75393	hypothetical prote
1484	6	1.8	1941	2	T33979	hypothetical prote
1485	6	1.8	1943	2	T23986	hypothetical prote
1486	6	1.8	1946	2	UC6032	lactocoeptin (EC 3.4
1487	6	1.8	1951	2	B43963	RNA viral polymera
1488	6	1.8	2054	2	T46612	multi PDZ domain p
1489	6	1.8	2055	2	T30259	multiple PDZ domai

1490	6	1.8	2104	2	D91286	hypothetical prote
1491	6	1.8	2104	2	H86127	hypothetical prote
1492	6	1.8	2105	2	T18968	probable serine-cy
1493	6	1.8	2124	2	A28452	proteoglycan core
1494	6	1.8	2126	2	E70522	probable polyketid
1495	6	1.8	2132	1	A55182	aggreccan precursor
1496	6	1.8	2150	2	S13553	hypothetical prote
1497	6	1.8	2150	2	F83068	hypothetical prote
1498	6	1.8	2165	1	RRNZAZ	genome polyprotein
1499	6	1.8	2167	2	AF1489	cell wall associat
1500	6	1.8	2228	2	E97942	beta-galactosidase

## ALIGNMENTS

```

RESULT 1
H72621
hypothetical protein APL1433 - Aeropyrum pernix (strain KI)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H72621
R;Kawarayashi, Y., Hino, Y., Horikawa, H., Yamazaki, S., Jit-no, K.; Takah
awa, H.; Takamaya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudon, Y.; Yamazaki, J.; K
DNA Res. 6: 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:9310339; PMID:10382966
A:Accession: H72621
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-156 <KAM>
A:Cross-references: UNIPROT:Q9YCL8; UNIPARC:UP1000005DF4B; DDBJ:AP000061; NID:G5104821;
A:Experimental source: strain KI
A:Genetics:
A:Gene: APL1433

Query Match          2.7%; Score 9; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 LTGSASGCP 25
Db      105 LTGSASGCP 113
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|

RESULT 2
Q9MSPI
microtubule-associated protein MAP1B - mouse
N:Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protei
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S07549; S44387; A33645
R;Noble, M.; Lewis, S.A.; Cowan, N.J.
J. Cell Biol. 109, 3367-3376, 1989
A:Title: The microtubule binding domain of microtubule-associated protein MAP1B contains
A:Reference number: A33645; MUID:90094539; PMID:2480963
A:Accession: S07549
A:Molecule type: mRNA
A:Residues: 1-2464 <NOB>
A:Cross-references: UNIPROT:P14873; UNIPARC:UP100000297D7; EMBL:X51396; NID:G52999; PIDN
R;Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.
Arch. Biochem. Biophys. 310, 428-432, 1994
A:Title: Binding of heat-shock protein 70 (hsp70) to tubulin.
A:Reference number: S44387; MUID:94234720; PMID:8179328
A:Accession: S44387
A:Status: preliminary
A:Molecule type: protein
A:Residues: 653-663, 'IC' <SAN>
A:Cross-references: UNIPARC:UP10000173D97
C:Superfamily: microtubule-associated protein MAP1B
C:Keywords: microtubule binding; phosphoprotein; tandem repeat
F;589-786/Domain: microtubule binding #status experimental <MTB>
F;589-592, 639-642, 649-652, 655-658, 660-663, 668-671, 674-677, 679-682, 683-686, 687-690, 691-69

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R-K-E/D-X)  
F;1861-2064/Region: 17-residue repeats  
F;91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: pH  
F;147,969,1335,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (cd  
F;1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 2.7%; Score 9; DB 1; Length 2466;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AAGPVKEL 29  
DB 812 AAGPVKEL 820

RESULT 3  
S76681  
hypothetical protein - *Synechocystis* sp. (strain PCC 6803)  
C/Species: *Synechocystis* sp.  
A/Variety: PCC 6803  
C/Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C/Accession: S76681  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yeude  
DNA Res. 3; 109-136, 1996  
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
S.  
A/Reference number: S74322; MUID:97061201; PMID:8905231  
A/Accession: S76681  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-173 <KAN>  
A/Cross-references: UNIPROT:Q55866; UNIPARC:UPI00000C0F86; EMBL:D6404; GB:AB001339; NID  
C/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C/Superfamily: cyanelle *Cyanophora paradoxa* hypothetical protein ycc36

Query Match 2.4%; Score 8; DB 2; Length 173;  
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 LLTSLFVL 243  
DB 85 LLTSLFVL 92

RESULT 4  
A82159  
hypothetical protein VC1772 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)  
C/Species: *Vibrio cholerae*  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C/Accession: A82159  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406; 477-483, 2000  
A/Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A/Reference number: A82035; MUID:20406833; PMID:10952301  
A/Accession: A82159  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-286 <HEI>  
A/Cross-references: UNIPROT:Q9KR71; UNIPARC:UPI00000C30DC; GB:AE004254; GB:AE003852; NID  
C/Experimental source: serogroup O1; strain N16961; biotype El Tor  
C/Genetics:  
A/Map position: 1

Query Match 2.4%; Score 8; DB 2; Length 286;  
Best Local Similarity 100.0%; Pred. No. 7.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 EKKRVDIC 268  
|||||

DB 134 EKKRVDIC 141

RESULT 5  
S18733  
glutenin high molecular weight chain 1B9 precursor - wheat  
C/Species: *Triticum aestivum* (common wheat)  
C/Date: 08-Jun-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
R;Halford, N.G.; Forde, J.; Anderson, O.D.; Greene, F.C.; Shewry, P.R.  
Theor. Appl. Genet. 75, 117-126, 1987  
A/Title: The nucleotide and deduced amino acid sequences of an HMW glutenin subunit gene  
A and 1D.  
A/Reference number: S18733  
A/Accession: S18733  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-705 <HML>  
A/Cross-references: UNIPROT:Q03871; UNIPARC:UPI00000A6F03; EMBL:X61026; NID:g22089; PIDN  
C/Superfamily: glutenin

Query Match 2.4%; Score 8; DB 2; Length 705;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 YSSSLQOP 115  
DB 496 YSSSLQOP 503

RESULT 6  
S38673  
desmoglein 2 - human  
N/Alternate names: desmoglein HDGC  
C/Species: *Homo sapiens* (man)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S38673; B38672  
R;Zimbelmann, R.  
submitted to the EMBL Data Library, September 1993  
A/Reference number: S38673  
A/Accession: S38673  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-117 <ZIM>  
A/Cross-references: UNIPROT:Q14126; UNIPARC:UPI000004CAAB; EMBL:Z26317; NID:g416177; PIDN  
R;Koch, P.J.; Goldschmidt, M.D.; Walsh, M.J.; Zimbelmann, R.; Franke, W.W.  
Eur. J. Cell Biol. 55, 200-208, 1991  
A/Title: Complete amino acid sequence of the epidermal desmoglein precursor polypeptide  
A/Reference number: A38672; MUID:92037656; PMID:1935985  
A/Accession: B38672  
A/Molecule type: mRNA  
A/Residues: 777-117 <KOC>  
A/Cross-references: UNIPARC:UPI0000177AF; GB:S64273  
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A/Gene: GDB:DSG2  
A/Cross-references: GDB:128808; OMIM:125671  
A/Map position: 18q12.1-18q12.2  
C/Superfamily: cadherin; cadherin repeat homology  
C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; membrane protein  
F;51-158/Domain: cadherin repeat homology <CR1>  
F;161-271/Domain: cadherin repeat homology <CR2>

Query Match 2.4%; Score 8; DB 2; Length 1117;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 LLVPLLL 238  
DB 624 LLVPLLL 631

RESULT 7  
T29918



hypothetical protein ZC449.4 - *Caenorhabditis elegans*  
C/Species: *Caenorhabditis elegans*  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T29918  
R/Latrelle, P.; Gattung, S.  
A/Description: The sequence of *C. elegans* cosmid ZC449.  
A/Reference number: Z20708  
A/Accession: T29918  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-105 <LAT>  
A/Cross-references: UNIPROT:Q23329, UNIPARC:UPI000007E7AD, EMBL:U41510, PIDD:AAA82633.1,  
C/Genetics:  
A/Gene: CESP:ZC449.4  
A/Intons: 26/3; 51/1; 87/3  
C/Superfamily: *Caenorhabditis elegans* hypothetical protein ZC449.4

Query Match 2.1%; Score 7; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 MVLLCL 232  
Db 63 MVLLCL 69

RESULT 8  
E71866  
hypothetical protein jhp0956 - *Helicobacter pylori* (strain J99)  
C/Species: *Helicobacter pylori*  
A/Variety: strain J99  
C/Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C/Accession: E71866  
R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Werberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A/Reference number: A71800; MUID:99120557; PMID:9923682  
A/Accession: E71866  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-161 <ARN>  
A/Cross-references: UNIPROT:Q9ZKH9, UNIPARC:UPI00000D72A4, GB:AE001525; GB:AE001439; NID  
C/Genetics:  
A/Gene: jhp0956  
C/Superfamily: *Helicobacter pylori* hypothetical protein jhp0956

Query Match 2.1%; Score 7; DB 2; Length 161;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 PLTSLF 241  
Db 102 PLTSLF 108

RESULT 9  
AE1817  
hypothetical protein all0085 [imported] - *Nostoc* sp. (strain PCC 7120)  
C/Species: *Nostoc* sp. PCC 7120  
A/Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C/Accession: AE1817  
R/Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriguchi,  
Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res 8, 205-213, 2001  
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*  
A/Reference number: AE1807; MUID:21595285; PMID:11759840  
A/Accession: AE1817  
A/Status: preliminary  
A/Molecule type: DNA

A/Residues: 1-170 <KUR>  
A/Cross-references: UNIPROT:Q9ZOK6, UNIPARC:UPI00000CCIC17, GB:BA000019; PIDD:BA877609.1;  
A/Experimental source: strain PCC 7120  
C/Genetics:  
A/Gene: all0085

Query Match 2.1%; Score 7; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLICLL 233  
Db 14 VLICLL 20

RESULT 10  
F97283  
ribosomal protein L6 [imported] - *Clostridium acetobutylicum*  
C/Species: *Clostridium acetobutylicum*  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: F97283  
R/Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J. Bacteriol. 183, 4823-4838, 2001  
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clo*  
A/Reference number: A96900; MUID:21359325; PMID:21359325  
A/Accession: F97283  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-179 <KUR>  
A/Cross-references: UNIPROT:Q97EJ3, UNIPARC:UPI00000CA72A, GB:AE001437; PIDD:AAK01057.1;  
A/Experimental source: *Clostridium acetobutylicum* ATCC824  
C/Genetics:  
A/Gene: CAC3118  
C/Superfamily: ribosomal protein L6/L9

Query Match 2.1%; Score 7; DB 2; Length 179;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KELVGSV 33  
Db 139 KELVGSV 145

RESULT 11  
F83305  
hypothetical protein PA2724 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C/Species: *Pseudomonas aeruginosa*  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C/Accession: F83305  
R/Stover, C.K.; Pham, X.Q.; Ervin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardis, K.; Lim,  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathoc  
A/Reference number: A82950; MUID:20437337; PMID:10984043  
A/Accession: F83305  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-179 <STD>  
A/Cross-references: UNIPROT:Q910B8, UNIPARC:UPI00000C57D0, GB:AE004700; GB:AE004091; NID  
C/Genetics:  
A/Gene: PA2724

Query Match 2.1%; Score 7; DB 2; Length 179;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 RVDPFDG 86  
Db 42 RVDPFDG 48



## RESULT 12

F97499

hypothetical protein AGR\_C\_2123 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
C/Species: Agrobacterium tumefaciens

C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 31-Dec-2004

C/Accession: F97499

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: F97499

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-182 <KUR>

A/Cross-references: UNIPROT:Q8UG92; UNIPARC:UPI00000D1A64; GB:AE007869; P1DN:AAK6951.1;

C/Genetics:

A/Gene: AGR\_C\_2123

A/Map position: circular chromosome

C/Superfamily: Bacillus subtilis hypothetical protein yung

Query Match 2.1%; Score 7; DB 2; Length 182;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 LLSLFVL 243

Db 34 LLSLFVL 40

## RESULT 13

I40220

hypothetical protein 2 - Bacillus licheniformis (fragment)

C/Species: Bacillus licheniformis

C/Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 12-Jul-2004

C/Accession: I40220

R/Harry, E.J.; Partridge, S.R.; Weiss, A.S.; Wake, R.G.

Gene 147, 85-89, 1994

A/Title: Conservation of the 168 divB gene in Bacillus subtilis W23 and B. licheniformi

A/Reference number: I40220; MUID:94374713; PMID:8088553

A/Accession: I40220

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-184 <RES>

A/Cross-references: UNIPROT:Q45305; UNIPARC:UPI000012P92D; EMBL:U01958; NID:g404008; P1D

C/Superfamily: UDP-N-acetylmuramate dehydrogenase

Query Match 2.1%; Score 7; DB 2; Length 184;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GSVGAV 37

Db 9 GSVGAV 15

## RESULT 14

H70416

hypothetical protein aq\_1348 - Aquifex aeolicus

C/Species: Aquifex aeolicus

C/Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004

C/Accession: H70416

R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy

V. Nature 392, 353-358, 1998

A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A/Reference number: A70300; MUID:98196666; PMID:9537320

A/Accession: H70416

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-189 <ACQ>

A/Cross-references: UNIPROT:O67363; UNIPARC:UPI00000565CC; GB:AE00736; NID:g2983763; P1I  
A/Experimental source: strain VF5  
C/Genetics:  
A/Gene: aq\_1348  
C/Superfamily: Aquifex aeolicus hypothetical protein aq\_1348

Query Match 2.1%; Score 7; DB 2; Length 189;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 GLFLMFL 250

Db 142 GLFLMFL 148

## RESULT 15

T45543

hypothetical protein 2 [imported] - Klebsiella pneumoniae transposon Tn5711

C/Species: Klebsiella pneumoniae

C/Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 09-Jul-2004

C/Accession: T45543

R/Albiger, B.; Hubert, J.C.; Lett, M.C.

Submitted to the EMBL Data Library, October 1998

A/Description: Composite transposons Tn5708 and Tn5709 are based on a Tn3-like element Tr

A/Reference number: Z23003

A/Accession: T45543

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-199 <ALB>

A/Cross-references: UNIPROT:O87756; UNIPARC:UPI00000BA6E5; EMBL:AJ011907; P1DN:CAA09858.1

A/Experimental source: strain K11A

C/Genetics:

A/Mobile element: transposon Tn5711

C/Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match 2.1%; Score 7; DB 2; Length 199;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 LLSLFVL 242

Db 132 LLSLFVL 138

Search completed: December 16, 2005, 11:53:49

Job time : 41 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 16, 2005, 11:46:50 ; Search time 231 Seconds  
(without alignments)  
1023.169 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 335  
Sequence: 1 MAGSPCTCLTLYIMQLTGS.....PMSLLTMPDTPRLPAYENV1 335

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

Database : UniProt\_05.80:\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335	100.0	335	1	SLAF7 HUMAN
2	156	2.7	335	1	O9YC18 ABRPE
3	9	2.7	333	1	SLAF7 MOUSE
4	9	2.7	572	1	O5NS1 CRYNE
5	9	2.7	2464	1	MAP1B MOUSE
6	9	2.4	83	2	O884T6 PSESM
7	8	2.4	129	2	O81V10 HUMAN
8	8	2.4	136	2	O54WZ7 DICDI
9	8	2.4	139	2	O5YY9 NCCPA
10	8	2.4	155	2	O6ERB1 ORYSA
11	8	2.4	173	2	O55866 SYNY3
12	8	2.4	202	2	O7V2B6 PROMP
13	8	2.4	211	2	O9S488 PROS9
14	8	2.4	230	2	O5VID5 HALMA
15	8	2.4	240	2	O5V4S6 HALMA
16	8	2.4	279	2	O7MJC1 VIBRV
17	8	2.4	284	2	O6LP53 PHOBV
18	8	2.4	286	2	O9KR71 VIBCB
19	8	2.4	317	2	O9TPE7 MONDO
20	8	2.4	328	2	O9BDP0 ACTTR
21	8	2.4	343	2	O6MDM3 BDBRA
22	8	2.4	346	2	O4R6C4 MACFA
23	8	2.4	347	2	O9TPK7 MONDO
24	8	2.4	348	2	O7USC6 RHOB
25	8	2.4	360	1	HEPLN3 HUMAN
26	8	2.4	362	2	O9TPI0 MONDO
27	8	2.4	364	2	O5WSU5 MONDO
28	8	2.4	364	2	O5WSU5 MONDO
29	8	2.4	412	2	O6SRV6 BRAJA
30	8	2.4	421	2	O6F8F7 ACTAD
31	8	2.4	439	2	O6SHV3_BACLD
32	8	2.4	467	2	O8D7P9 VIBVU
33	8	2.4	469	2	O7MERO_VIBVY
34	8	2.4	533	1	LNT_CHLRE
35	8	2.4	551	2	O5P4J3 AZOSE
36	8	2.4	653	2	O58D55 BOVIN
37	8	2.4	669	1	BGAL_FELCA
38	8	2.4	671	2	O829F0 STRAM
39	8	2.4	705	2	O03871_WHEAT
40	8	2.4	720	2	O84TG6 TRITV
41	8	2.4	720	2	O941U6 WHEAT
42	8	2.4	728	2	O4SDX7 TETNG
43	8	2.4	801	2	O4T2D9 TETNG
44	8	2.4	868	2	O9VH63 DROME
45	8	2.4	1053	2	O81A08 PLAF7
46	8	2.4	1117	1	DSG2_HUMAN
47	8	2.4	1118	2	O4KKU6 HUMAN
48	8	2.4	1122	1	DSG2_MOUSE
49	8	2.4	1235	2	O9S4Z8 HUMAN
50	7	2.1	31	2	O4QTH0_LEIMA
51	7	2.1	64	2	O4Y596 PLACH
52	7	2.1	66	2	O9WME3 JMURI
53	7	2.1	69	2	O64U72 BACPR
54	7	2.1	71	2	O6MNM5_BDBRA
55	7	2.1	72	2	O5D864_PREEN
56	7	2.1	75	1	MTRF_METKA
57	7	2.1	75	2	O4WE52 ASPFU
58	7	2.1	76	2	O233Z9 CAEBL
59	7	2.1	82	2	O4UBR2 SULAC
60	7	2.1	82	2	O6Z5Z6 ORYSA
61	7	2.1	83	2	O4ZOK3_PSEST
62	7	2.1	90	2	O9GK67_RABIT
63	7	2.1	91	2	O4HG64_9DEIO
64	7	2.1	93	2	O4P200 USTMA
65	7	2.1	93	2	O5BRQ7_SCHJA
66	7	2.1	96	2	O83R08_COXBU
67	7	2.1	97	1	CCL8_MOUSE
68	7	2.1	97	1	O64DH5_9ARCH
69	7	2.1	97	2	O9TTS6 BOVIN
70	7	2.1	97	2	O5SR19_MOUSE
71	7	2.1	97	2	O9Z318_CAVPO
72	7	2.1	98	1	CCL13_HUMAN
73	7	2.1	98	2	O6IC06_HUMAN
74	7	2.1	99	2	O4Q4G7_LEIMA
75	7	2.1	101	1	PHS_STRAW
76	7	2.1	104	2	O4J1R8_AZOV1
77	7	2.1	115	2	O8KX15 SYNP2
78	7	2.1	117	2	O8HXK4_MACPA
79	7	2.1	120	2	O9VNS7_DROME
80	7	2.1	122	2	O6NMK3_DROME
81	7	2.1	124	2	O9BNJ9_MYTRI
82	7	2.1	126	2	O9BB60_MACFA
83	7	2.1	132	2	O5RTZ6_BRARE
84	7	2.1	132	2	O6GQ49_XENLA
85	7	2.1	135	2	O5UX16_HALMA
86	7	2.1	144	2	O8GMH4_ARATH
87	7	2.1	145	2	O5D863_CALNA
88	7	2.1	145	2	O8TY49_METKA
89	7	2.1	146	2	O4TR06_9SPRN
90	7	2.1	149	2	O5NK16_AZOSE
91	7	2.1	150	2	O9RFN9_MYCFE
92	7	2.1	153	2	O9XK65_KLEOB
93	7	2.1	156	2	O9EMQ1_AMEPV
94	7	2.1	159	2	O6PEY1_HUMAN
95	7	2.1	159	2	O8BR62_MOUSE
96	7	2.1	159	2	O9DON8_MOUSE
97	7	2.1	160	2	O5SB67_DICDI
98	7	2.1	160	2	O7TUK7_PROWMA
99	7	2.1	161	2	O4HUB0_GIBZE
100	7	2.1	161	2	O9ZKH9_HELPJ
101	7	2.1	162	2	O67LKL1_SYMTM
102	7	2.1	162	2	O98P38_HRILO
103	7	2.1	165	2	O7YXD5_GILORO
104	7	2.1	165	2	O98J36_RHILLO
105	8	2.4	467	2	O8D7P9 VIBVU
106	8	2.4	469	2	O7MERO_VIBVY
107	8	2.4	533	1	LNT_CHLRE
108	8	2.4	551	2	O5P4J3 AZOSE
109	8	2.4	653	2	O58D55 BOVIN
110	8	2.4	669	1	BGAL_FELCA
111	8	2.4	671	2	O829F0 STRAM
112	8	2.4	705	2	O03871_WHEAT
113	8	2.4	720	2	O84TG6 TRITV
114	8	2.4	720	2	O941U6 WHEAT
115	8	2.4	728	2	O4SDX7 TETNG
116	8	2.4	801	2	O4T2D9 TETNG
117	8	2.4	868	2	O9VH63 DROME
118	8	2.4	1053	2	O81A08 PLAF7
119	8	2.4	1117	1	DSG2_HUMAN
120	8	2.4	1118	2	O4KKU6 HUMAN
121	8	2.4	1122	1	DSG2_MOUSE
122	8	2.4	1235	2	O9S4Z8 HUMAN
123	8	2.4	31	2	O4QTH0_LEIMA
124	8	2.4	64	2	O4Y596 PLACH
125	8	2.4	66	2	O9WME3 JMURI
126	8	2.4	69	2	O64U72 BACPR
127	8	2.4	71	2	O6MNM5_BDBRA
128	8	2.4	72	2	O5D864_PREEN
129	8	2.4	75	1	MTRF_METKA
130	8	2.4	75	2	O4WE52 ASPFU
131	8	2.4	76	2	O233Z9 CAEBL
132	8	2.4	82	2	O4UBR2 SULAC
133	8	2.4	82	2	O6Z5Z6 ORYSA
134	8	2.4	83	2	O4ZOK3_PSEST
135	8	2.4	90	2	O9GK67_RABIT
136	8	2.4	91	2	O4HG64_9DEIO
137	8	2.4	93	2	O4P200 USTMA
138	8	2.4	93	2	O5BRQ7_SCHJA
139	8	2.4	96	2	O83R08_COXBU
140	8	2.4	97	1	CCL8_MOUSE
141	8	2.4	97	1	O64DH5_9ARCH
142	8	2.4	97	2	O9TTS6 BOVIN
143	8	2.4	97	2	O5SR19_MOUSE
144	8	2.4	97	2	O9Z318_CAVPO
145	8	2.4	98	1	CCL13_HUMAN
146	8	2.4	98	2	O6IC06_HUMAN
147	8	2.4	99	2	O4Q4G7_LEIMA
148	8	2.4	101	1	PHS_STRAW
149	8	2.4	104	2	O4J1R8_AZOV1
150	8	2.4	115	2	O8KX15 SYNP2
151	8	2.4	117	2	O8HXK4_MACPA
152	8	2.4	120	2	O9VNS7_DROME
153	8	2.4	122	2	O6NMK3_DROME
154	8	2.4	124	2	O9BNJ9_MYTRI
155	8	2.4	126	2	O9BB60_MACFA
156	8	2.4	132	2	O5RTZ6_BRARE
157	8	2.4	132	2	O6GQ49_XENLA
158	8	2.4	135	2	O5UX16_HALMA
159	8	2.4	144	2	O8GMH4_ARATH
160	8	2.4	145	2	O5D863_CALNA
161	8	2.4	145	2	O8TY49_METKA
162	8	2.4	146	2	O4TR06_9SPRN
163	8	2.4	149	2	O5NK16_AZOSE
164	8	2.4	150	2	O9RFN9_MYCFE
165	8	2.4	153	2	O9XK65_KLEOB
166	8	2.4	156	2	O9EMQ1_AMEPV
167	8	2.4	159	2	O6PEY1_HUMAN
168	8	2.4	159	2	O8BR62_MOUSE
169	8	2.4	159	2	O9DON8_MOUSE
170	8	2.4	160	2	O5SB67_DICDI
171	8	2.4	160	2	O7TUK7_PROWMA
172	8	2.4	161	2	O4HUB0_GIBZE
173	8	2.4	161	2	O9ZKH9_HELPJ
174	8	2.4	162	2	O67LKL1_SYMTM
175	8	2.4	162	2	O98P38_HRILO
176	8	2.4	165	2	O7YXD5_GILORO
177	8	2.4	165	2	O98J36_RHILLO
178	8	2.4	467	2	O8D7P9 VIBVU
179	8	2.4	469	2	O7MERO_VIBVY
180	8	2.4	533	1	LNT_CHLRE
181	8	2.4	551	2	O5P4J3 AZOSE
182	8	2.4	653	2	O58D55 BOVIN
183	8	2.4	669	1	BGAL_FELCA
184	8	2.4	671	2	O829F0 STRAM
185	8	2.4	705	2	O03871_WHEAT
186	8	2.4	720	2	O84TG6 TRITV
187	8	2.4	720	2	O941U6 WHEAT
188	8	2.4	728	2	O4SDX7 TETNG
189	8	2.4	801	2	O4T2D9 TETNG
190	8	2.4	868	2	O9VH63 DROME
191	8	2.4	1053	2	O81A08 PLAF7
192	8	2.4	1117	1	DSG2_HUMAN
193	8	2.4	1118	2	O4KKU6 HUMAN
194	8	2.4	1122	1	DSG2_MOUSE
195	8	2.4	1235	2	O9S4Z8 HUMAN
196	8	2.4	31	2	O4QTH0_LEIMA
197	8	2.4	64	2	O4Y596 PLACH
198	8	2.4	66	2	O9WME3 JMURI
199	8	2.4	69	2	O64U72 BACPR
200	8	2.4	71	2	O6MNM5_BDBRA
201	8	2.4	72	2	O5D864_PREEN
202	8	2.4	75	1	MTRF_METKA
203	8	2.4	75	2	O4WE52 ASPFU
204	8	2.4	76	2	O233Z9 CAEBL
205	8	2.4	82	2	O4UBR2 SULAC
206	8	2.4	82	2	O6Z5Z6 ORYSA
207	8	2.4	83	2	O4ZOK3_PSEST
208	8	2.4	90	2	O9GK67_RABIT
209	8	2.4	91	2	O4HG64_9DEIO
210	8	2.4	93	2	O4P200 USTMA
211	8	2.4	93	2	O5BRQ7_SCHJA
212	8	2.4	96	2	O83R08_COXBU
213	8	2.4	97	1	CCL8_MOUSE
214	8	2.4	97	1	O64DH5_9ARCH
215	8	2.4	97	2	O9TTS6 BOVIN
216	8	2.4	97	2	O5SR19_MOUSE
217	8	2.4	97	2	O9Z318_CAVPO
218	8	2.4	98	1	CCL13_HUMAN
219	8	2.4	98	2	O6IC06_HUMAN
220	8	2.4	99	2	O4Q4G7_LEIMA
221	8	2.4	101	1	PHS_STRAW
222	8	2.4	104	2	O4J1R8_AZOV1
223	8	2.4	115	2	O8KX



105	7	2.1	167	2	Q46295_CLOPE	Q46295_clostridium	178	7	2.1	215	2	Q7Q1S1_ANOGA	Q7q1s1_anopheles g
106	7	2.1	167	2	Q8XPC3_CLOPE	Q8xpc3_clostridium	179	7	2.1	215	2	Q6J1F4_GCAUD	Q6j1f4_bacterioph
107	7	2.1	169	2	Q94S06_ZENNE	Q94s06_zenopsis ne	180	7	2.1	215	2	Q8W6N4_GCAUD	Q8w6n4_bacterioph
108	7	2.1	170	2	Q6ZSF8_HUMAN	Q6zsf8_homo sapien	181	7	2.1	215	2	Q9FGS6_ARATH	Q9fgs6_arabidopsis
109	7	2.1	170	2	Q8ZOK6_ANASP	Q8zok6_anabaena sp	182	7	2.1	216	2	Q72M18_LEPIC	Q72m18_leptospira
110	7	2.1	171	2	Q85DH2_9TELE	Q85dh2_corydoras r	183	7	2.1	216	2	Q8EZS4_LEPIN	Q8ezs4_leptospira
111	7	2.1	173	2	Q6D693_ERWCT	Q6d693_ervinia car	184	7	2.1	217	2	Q4HTQ4_DBERO	Q4htq4_deinococcus
112	7	2.1	173	2	Q94YR3_9TELE	Q94yr3_engraulis j	185	7	2.1	217	2	Q566V2_BRARE	Q566v2_bacchydantio
113	7	2.1	173	2	Q6T233_AMICA	Q6t233_ama calva	186	7	2.1	220	2	Q94BC4_ARATH	Q94bc4_arabidopsis
114	7	2.1	173	2	Q8HQLO_AMICA	Q8hqlo_ama calva	187	7	2.1	220	2	Q4L8S9_STALT	Q4l8s9_staphylococ
115	7	2.1	173	2	Q7IBEL4_EUDEL	Q7ibel4_eudromia el	188	7	2.1	220	2	Q9RRZ0_DEIRA	Q9rrz0_deinococcus
116	7	2.1	174	2	Q870Y3_NEUCR	Q870y3_neurospora	189	7	2.1	221	2	Q7TPT2_RHOCB	Q7tpt2_rhensu cyto
117	7	2.1	174	2	Q8H162_SYNMA	Q8h162_synthbranchus	190	7	2.1	224	2	Q8W6X2_GCAUD	Q8w6x2_cyanophage
118	7	2.1	175	2	NU6M_UROTA	Q7Y8d2_urotichus	191	7	2.1	224	2	Q93NK7_YEREN	Q93nk7_yersinia en
119	7	2.1	175	2	Q7Y8B4_MOGMO	Q7Y8e4_mogera wogu	192	7	2.1	224	2	Q9KKH2_YEREN	Q9kkh2_yersinia en
120	7	2.1	175	2	Q9MJAS_TALEU	Q9mjas_talpa europ	193	7	2.1	224	2	Q62DW8_BURMA	Q62dw8_burkholderi
121	7	2.1	175	2	Q5P663_AZOSE	Q5p663_azarcus sp	194	7	2.1	224	2	Q62JDI1_BURPS	Q62jdi1_burkholderi
122	7	2.1	175	2	Q4RYN1_TETNG	Q4rynl_tetradodon n	195	7	2.1	225	2	Q61JYC2_DROME	Q61jyc2_drosophila
123	7	2.1	177	1	RL18A_SPOFR	Q8uq17_epidoptera	196	7	2.1	225	2	Q68BQ4_ORYSA	Q68bq4_oryza sativ
124	7	2.1	177	2	Q6F445_PLOXY	Q6f445_plutella xy	197	7	2.1	225	2	Q4LIS0_9BURK	Q4lis0_burkholderi
125	7	2.1	179	2	Q910B8_PSEAB	Q910b8_pseudomonas	198	7	2.1	226	2	Q5VON8_ORYSA	Q5von8_oryza sativ
126	7	2.1	179	2	Q97BJ3_CIOAB	Q97bj3_clostridium	199	7	2.1	226	2	Q4NAV5_9MICC	Q4nav5_arthrobacte
127	7	2.1	182	2	Q7CZV8_AGRTS	Q7czv8_agrobacteri	200	7	2.1	226	2	Q5XAB3_STRP6	Q5xab3_streptococc
128	7	2.1	182	2	Q8Y365_RALSO	Q8y365_ralstonia s	201	7	2.1	226	2	Q601H5_MYCHY	Q601h5_mycoplasm
129	7	2.1	183	2	Q57UZ6_9TRYP	Q57uz6_trypanosoma	202	7	2.1	226	2	Q99YAB8_STRPY	Q99yab8_streptococ
130	7	2.1	183	2	Q8UH31_CHICK	Q8uh31_gallus gal1	203	7	2.1	226	2	Q8NZL3_STRP3	Q8nzl3_streptococ
131	7	2.1	184	1	MURB_BACLI	Q45305_bacillus 11	204	7	2.1	226	2	Q8K607_STRP3	Q8k607_streptococ
132	7	2.1	185	2	Q7ZH77_SHIV1	Q7zh77_human immun	205	7	2.1	228	1	UTP11_ARATH	Q54E70_DICDI
133	7	2.1	185	2	Q7ZH80_SHIV1	Q7zh80_human immun	206	7	2.1	229	2	Q54E70_DICDI	Q54e70_dicystoseli
134	7	2.1	186	2	Q80UC0_MOUSE	Q80uc0_mus musculu	207	7	2.1	233	2	Q82DQ3_STRAW	Q82dq3_streptomyce
135	7	2.1	187	2	Q9EUY8_SALTY	Q9euj8_salmonella	208	7	2.1	233	2	Q63A70_BACCZ	Q63a70_bacillus ce
136	7	2.1	187	2	Q7DAN4_SALTY	Q7dan4_salmonella	209	7	2.1	235	2	Q6STF8_9GOBI	Q6stf8_gymnogobius
137	7	2.1	187	2	Y1348_AQUAE	Q514a2_salmonella	210	7	2.1	235	2	Q6STG5_9GOBI	Q6stg5_gymnogobius
138	7	2.1	189	1	Q534A2_SALCH	Q53463_aquilex aeo	211	7	2.1	235	2	Q6J109_9GOBI	Q6j109_gymnogobius
139	7	2.1	189	2	Q4LIU2_SENTR	Q4liu2_salmonella	212	7	2.1	235	2	Q6J102_9GOBI	Q6j102_gymnogobius
140	7	2.1	189	2	Q7ZH66_SHIV1	Q7zh66_human immun	213	7	2.1	235	2	Q6J101_9GOBI	Q6j101_gymnogobius
141	7	2.1	189	2	Q7ZH70_SHIV1	Q7zh70_human immun	214	7	2.1	235	2	Q6U100_9GOBI	Q6u100_gymnogobius
142	7	2.1	189	2	Q7ZH75_SHIV1	Q7zh75_human immun	215	7	2.1	235	2	Q6J128_9GOBI	Q6j128_gymnogobius
143	7	2.1	190	2	Q7ZH67_SHIV1	Q7zh67_human immun	216	7	2.1	235	2	Q6J126_9GOBI	Q6j126_gymnogobius
144	7	2.1	190	2	Q7ZH68_SHIV1	Q7zh68_human immun	217	7	2.1	235	2	Q6J123_9GOBI	Q6j123_gymnogobius
145	7	2.1	190	2	Q7ZH71_SHIV1	Q7zh71_human immun	218	7	2.1	235	2	Q6J107_9GOBI	Q6j107_gymnogobius
146	7	2.1	190	2	Q7ZH72_SHIV1	Q7zh72_human immun	219	7	2.1	235	2	Q6J105_9GOBI	Q6j105_gymnogobius
147	7	2.1	190	2	Q7ZH73_SHIV1	Q7zh73_human immun	220	7	2.1	235	2	Q6J103_9GOBI	Q6j103_gymnogobius
148	7	2.1	190	2	Q7ZH74_SHIV1	Q7zh74_human immun	221	7	2.1	235	2	Q6S9Z6_9GOBI	Q6s9z6_gymnogobius
149	7	2.1	191	2	Q9J4B8_9BETA	Q9j4b8_baboon cyto	222	7	2.1	235	2	Q6STH2_9GOBI	Q6sth2_gymnogobius
150	7	2.1	193	2	Q8U0S5_PYRFU	Q8u0s5_pyrococcus	223	7	2.1	235	2	Q6J124_9GOBI	Q6j124_gymnogobius
151	7	2.1	195	2	Q7ZH48_SHIV1	Q7zh48_human immun	224	7	2.1	235	2	Q6STG6_9GOBI	Q6stg6_gymnogobius
152	7	2.1	195	2	Q7ZH51_SHIV1	Q7zh51_human immun	225	7	2.1	236	2	Q5GYR5_XANOR	Q5gyr5_xanthomonas
153	7	2.1	195	2	Q7ZH52_SHIV1	Q7zh52_human immun	226	7	2.1	236	2	Q7PMX3_ANOGA	Q7pmx3_anopheles g
154	7	2.1	195	2	Q7ZH53_SHIV1	Q7zh53_human immun	227	7	2.1	238	2	Q610H9_BACAN	Q610h9_bacillus an
155	7	2.1	195	2	Q7ZH57_SHIV1	Q7zh57_human immun	228	7	2.1	238	2	P97032_BACSV	P97032_bacillus su
156	7	2.1	195	2	Q7ZH58_SHIV1	Q7zh58_human immun	229	7	2.1	238	2	Q9PZP8_UREPA	Q9ppz8_ureaplaasma
157	7	2.1	195	2	Q7ZH61_SHIV1	Q7zh61_human immun	230	7	2.1	239	1	YTM1_BACSU	Ytm1_bacillus su
158	7	2.1	196	2	Q9AG89_BDEBA	Q9ag89_bellioleibri	231	7	2.1	239	2	Q9LBS6_ARATH	Q9lbs6_arabidopsis
159	7	2.1	199	2	Q87756_KUEBN	Q87756_klebsiella	232	7	2.1	241	2	Q4J9S6_SULAC	Q4j9s6_sulfatobac
160	7	2.1	199	2	Q74JH7_LACCO	Q74jh7_lactobacilli	233	7	2.1	243	2	Q6K7K8_ORYSA	Q6k7k8_oryza sativ
161	7	2.1	204	2	Q66087_9ALPH	Q66087_canine hepr	234	7	2.1	244	2	Q4JW49_CORJK	Q4jw49_corynebacte
162	7	2.1	205	2	Q5Y3C1_SHIV1	Q5y3c1_human immun	235	7	2.1	244	2	Q35892_9CHON	Q35892_squatinia ne
163	7	2.1	208	2	Q4LIJH8_9BURK	Q4lijh8_burkholderi	236	7	2.1	246	2	Q4WC42_ASPTU	Q4wc42_aspergillus
164	7	2.1	210	1	MATA1_CANAL	Q9uw23_candida alb	237	7	2.1	246	2	Q8L655_ORYSA	Q8l655_oryza sativ
165	7	2.1	211	2	Q5K273_GUTTH	Q5k273_gulliardia	238	7	2.1	246	2	Q8E7M3_STRAS	Q8e7m3_streptococ
166	7	2.1	212	2	Q4RVC0_TETNG	Q4rvco_tetradodon n	239	7	2.1	246	2	Q8G7M3_BIFLO	Q8g7m3_bifidobacte
167	7	2.1	212	2	Q8LWK7_9GOBI	Q8lwk7_gymnogobius	240	7	2.1	246	2	Q8E263_STRAS	Q8e263_streptococ
168	7	2.1	212	2	Q8LWML_9GOBI	Q8lwm1_gymnogobius	241	7	2.1	248	2	Q886J4_PSEEM	Q886j4_pseudomonas
169	7	2.1	212	2	Q8LWK8_9GOBI	Q8lwk8_gymnogobius	242	7	2.1	255	2	Q4K6Q1_PSEES	Q4k6q1_pseudomonas
170	7	2.1	212	2	Q8LWU0_9GOBI	Q8lw10_gymnogobius	243	7	2.1	258	2	Q5RBG0_PONXY	Q5rbg0_pongo pygma
171	7	2.1	212	2	Q8LWU2_9GOBI	Q8lw12_gymnogobius	244	7	2.1	262	2	Q5T1P5_HUMAN	Q5t1p5_homo sapien
172	7	2.1	212	2	Q8LWKR9_9GOBI	Q8lwkr9_gymnogobius	245	7	2.1	266	1	FLIP_CANCR	Q45980_caulobacter
173	7	2.1	212	2	Q8LWKR6_9GOBI	Q8lwkr6_gymnogobius	246	7	2.1	266	2	Q8A871_BACTN	Q8a871_bacteroides
174	7	2.1	212	2	Q8LWV2_9GOBI	Q8lwv2_gymnogobius	247	7	2.1	266	2	Q67N79_SYMTN	Q67n79_symblabacte
175	7	2.1	212	2	Q8LWV0_9GOBI	Q8lwv0_gymnogobius	248	7	2.1	267	2	Q5J3Z6_PYRKO	Q5j3z6_pyrococcus
176	7	2.1	212	2	Q8LWV1_9GOBI	Q8lwv1_gymnogobius	249	7	2.1	274	2	Q9HRP3_HALSA	Q9hrp3_haloabacteri
177	7	2.1	212	2	Q8LWU5_9GOBI	Q8lwu5_gymnogobius	250	7	2.1	274	2	Q9L2E8_STRCO	Q9l2e8_streptomyce



251	7	2.1	279	2	Q73ZR3_MYCPA	Q73zr3 mycobacteri	324	7	2.1	344	2	Q8VJG4_SWPV	Q8vjg4 sheenepox vi
252	7	2.1	282	2	Q7ORC6_GIALA	Q7orc6 giardia lam	325	7	2.1	345	1	Q116I1_HELHP	Q1vth6 helicobacte
253	7	2.1	284	2	Q4SPD6_TETNG	Q4spd6 tetraodon n	326	7	2.1	345	2	Q4X117_ASFPV	Q4x117 aspergillus
254	7	2.1	286	2	Q7O1J0_AMOGA	Q7o1j0 amophles g	327	7	2.1	346	2	Q51M00_SILPO	Q51m00 silicibacte
255	7	2.1	287	2	Q7M5E7_VIBHY	Q7mj57 vibrio vuln	328	7	2.1	347	2	Q50UK3_ENTHI	Q50uk3 entamoeba h
256	7	2.1	290	2	Q986W0_RHIL0	Q986w0 rhizobium 1	329	7	2.1	347	2	Q81WB8_GIACA	Q81wb8 glaucidium
257	7	2.1	291	2	Q6FE32_ACIAD	Q6fe32 acinetobact	330	7	2.1	347	2	Q8H1V9_BUBAB	Q8h1v9 bubo aescala
258	7	2.1	292	2	Q6UP77_ALCEU	Q6up77 alcaligenes	331	7	2.1	347	2	Q8H1V7_BUBAB	Q8h1v7 bubo bubo (
259	7	2.1	293	1	CEXQ_GUTTH	Q78450 giardiadia	332	7	2.1	347	2	Q8H1V6_BUBAB	Q8h1v6 bubo bubo (
260	7	2.1	295	2	Q515A3_CHIAB	Q515a3 chlamydomph	333	7	2.1	347	2	Q8H1E5_OTUAT	Q8h1e5 otus atrica
261	7	2.1	296	2	Q728V0_DBSVH	Q728v0 desulfovibr	334	7	2.1	347	2	Q8HC11_BUBAB	Q8hc11 bubo bubo (
262	7	2.1	300	1	MURB_ENTPA	Q830p3 enterococcu	335	7	2.1	347	2	Q8HCG3_BUBAB	Q8hcg3 bubo bubo (
263	7	2.1	300	1	MURB_STRAS	PS5465 streptococc	336	7	2.1	347	2	Q8HRS5_BUBAB	Q8hcr5 bubo bubo (
264	7	2.1	300	1	MURB1_STRAS	PS5465 streptococc	337	7	2.1	347	2	Q8HAS5_BUBAB	Q8had5 bubo bubo (
265	7	2.1	301	1	MURB1_BACAN	Q81wd1 bacillus an	338	7	2.1	347	2	Q8H4S5_BUBAB	Q8h4s5 bubo bubo (
266	7	2.1	301	1	MURB1_BACCR	Q819g4 bacillus ce	339	7	2.1	347	2	Q81M43_BUBVI	Q81m43 bubo vitigin
267	7	2.1	301	1	MURB1_BACHD	Q819g4 bacillus ha	340	7	2.1	348	2	Q9HPV6_HAUSA	Q9hpv6 halobacteri
268	7	2.1	301	1	Q8TES8_HUMAN	Q8tes8 homo sapien	341	7	2.1	348	2	Q6XR98_9BACT	Q6xr98 uncultured
269	7	2.1	301	2	Q93FJ1_9ENTR	Q93fj1 citrobacter	342	7	2.1	349	2	Q5WK14_BACBK	Q5wk14 bacillus cl
270	7	2.1	301	2	Q50573_BACPF	Q50573 bacillus ps	343	7	2.1	349	2	Q98N17_RHIL0	Q98n17 rhizobium 1
271	7	2.1	301	2	Q4MT93_BACCE	Q4mt93 bacillus th	344	7	2.1	351	2	Q87AJ8_XYLEPT	Q87aj8 xylella fas
272	7	2.1	301	2	Q6HROS_BACCH	Q6hros bacillus ce	345	7	2.1	351	2	Q9PF30_XYLEPA	Q9pf30 xylella fas
273	7	2.1	301	2	Q732F9_BACCI	Q732f9 bacillus th	346	7	2.1	353	2	Q4IXD4_XANCP	Q4uxd4 xanthomonas
274	7	2.1	301	2	Q74K66_IACCO	Q74k66 lactobacill	347	7	2.1	353	2	Q8PES6_XANCP	Q8pes6 xanthomonas
275	7	2.1	301	2	Q636B7_BACCC	Q636b7 bacillus ce	348	7	2.1	355	2	Q70CV9_9SOLA	Q70cv9 nicotiana s
276	7	2.1	301	2	Q5R019_IDILO	Q5r019 idiomarina	349	7	2.1	355	2	Q70CW2_9SOLA	Q70cw2 nicotiana s
277	7	2.1	302	2	Q9RUM6_DBRRA	Q9rue6 deinococcus	350	7	2.1	356	1	COX2_BACSU	P24012 bacillus su
278	7	2.1	303	1	MURB_BACSU	P18579 bacillus nu	351	7	2.1	356	2	Q4KE36_PSEBS	Q4ke36 pseudomonas
279	7	2.1	303	2	Q5QNJ1_ORYSA	Q5qnj1 oryza sativ	352	7	2.1	356	2	Q6FAZ7_ACTID	Q6faz7 acinetobact
280	7	2.1	303	2	Q65UX9_BACLD	Q65ux9 bacillus li	353	7	2.1	356	2	Q9TBP0_BUBVI	Q9tbp0 bubo vitigin
281	7	2.1	304	2	Q89E11_BRAJA	Q89e11 bradyrhizob	354	7	2.1	357	2	Q75DH7_ASHGO	Q75dh7 ashya goss
282	7	2.1	305	1	MURB_CIOAB	Q971p4 clostridium	355	7	2.1	357	2	Q5BJW9_RAT	Q5bjw9 ratulus norv
283	7	2.1	306	2	Q82BN1_STRAW	Q82bn1 streptococc	356	7	2.1	360	2	Q8VIF0_RAT	Q8vif0 ratulus norv
284	7	2.1	307	2	Q414G3_STRAU	Q414g3 streptococc	357	7	2.1	362	1	ASPG2_YEAST	P1163 saccharomyc
285	7	2.1	308	2	Q5NW79_AZOSE	Q5nw79 azoarcus sp	358	7	2.1	362	2	Q9VRF5_DROME	Q9vrf5 drosophila
286	7	2.1	309	2	Q8DJ14_SYNEL	Q8dj14 synechococc	359	7	2.1	367	1	GLN4_CABEL	P3447 caenorhabdi
287	7	2.1	309	2	Q91T37_LSDV	Q91t37 lumby skin	360	7	2.1	367	2	Q60S77_CABER	Q60s77 caenorhabdi
288	7	2.1	311	2	Q5MDX4_BACSK	Q5mdx4 bacillus cl	361	7	2.1	367	2	Q88QG3_PSEBK	Q88qg3 pseudomonas
289	7	2.1	312	1	APOR_RAT	P02650 rectus norv	362	7	2.1	368	2	Q6SDP5_BACLD	Q6sdp5 bacillus li
290	7	2.1	312	1	Q6FAH0_RAT	Q6fah0 rectus norv	363	7	2.1	369	2	Q9XVU2_CABEL	Q9xvu2 caenorhabdi
291	7	2.1	315	2	Q88H04_PSEPK	Q88h04 pseudomonas	364	7	2.1	370	2	Q4TKZ3_9SPFN	Q4tkz3 erythrobact
292	7	2.1	316	1	MURB_STRPN	PS5466 streptococc	365	7	2.1	374	2	Q6MDU7_PARUV	Q6md7 parachlamyd
293	7	2.1	316	1	MURB_STR6	PS5467 streptococc	366	7	2.1	375	2	Q4LRM0_9BDRK	Q4lrmo burkholderi
294	7	2.1	317	2	Q5JGS4_PYRKO	Q5jgs4 pyrococcus	367	7	2.1	378	2	Q859J4_9CAUD	Q859j4 staphylococ
295	7	2.1	317	2	Q86915_PPOXY	Q86915 sheenepox vi	368	7	2.1	378	2	Q859L5_9CAUD	Q859l5 staphylococ
296	7	2.1	319	2	Q5WR24_BUBBB	Q5wr24 bubo bubo k	369	7	2.1	379	2	Q85DZ8_9TELE	Q85dz8 eigemannia
297	7	2.1	320	2	Q4W9M8_ASPPU	Q4w9m8 aspergillus	370	7	2.1	379	2	Q4RMT0_TETNG	Q4rmt0 tetradodon n
298	7	2.1	322	2	Q7M968_WOLISU	Q7m968 wolucella s	371	7	2.1	380	2	Q9XKJ7_HIMSI	Q9xkj7 himantusa s
299	7	2.1	323	2	Q8LK49_LEUGL	Q8lk49 leucaena gl	372	7	2.1	381	1	CYB_ISUPA	P34871 isurus pauc
300	7	2.1	323	2	Q73RJ5_TREDE	Q73rj5 treponema d	373	7	2.1	381	1	CYB_SCYCA	Q79443 scyliorhinu
301	7	2.1	325	2	Q5FUV7_LACAC	Q5fuv7 lactobacill	374	7	2.1	381	1	CYB_RHIME	P45400 rhizobium m
302	7	2.1	325	2	Q98B70_RHIL0	Q98b70 rhizobium 1	375	7	2.1	381	2	Q8PL48_XANNC	Q8pl48 xanthomonas
303	7	2.1	328	2	Q8JU20_LSDV	Q8ju20 lumby skin	376	7	2.1	381	2	Q79571_9CHON	Q79571 muscelus ma
304	7	2.1	329	2	Q986Z1_RHIL0	Q986z1 rhizobium 1	377	7	2.1	382	2	Q41ZG7_AZOVY	Q41zg7 azotobacter
305	7	2.1	331	2	Q54H04_DICDI	Q54h04 dictyosteli	378	7	2.1	383	2	Q41ID8_GIBZE	Q41id8 gibberella
306	7	2.1	331	2	Q19173_CABER	Q19173 caenorhabdi	379	7	2.1	383	2	Q41VP1_AZOVY	Q41vp1 azotobacter
307	7	2.1	331	2	Q7NEU0_GLOVI	Q7neu0 gloeobacter	380	7	2.1	386	2	Q6AYH0_RAT	Q6ayh0 ratulus norv
308	7	2.1	332	2	Q86UT8_HUMAN	Q86ut8 homo sapien	381	7	2.1	388	2	Q8VOV8_9ACTO	Q8vov8 9ACTO
309	7	2.1	333	1	Y2204_WOLISU	Q7mq14 wolincella s	382	7	2.1	390	2	Q5LRR8_SILPO	Q5lrr8 silicibacte
310	7	2.1	333	2	Q4N0U6_9DELT	Q4n0u6 anaeromyxob	383	7	2.1	392	2	Q8K1N8_THRSM	Q8k1n8 thryonomyx
311	7	2.1	334	2	Q56D13_TRIMO	Q56d13 triticum mo	384	7	2.1	392	2	Q8K1Q8_9HYST	Q8k1q8 petromys ty
312	7	2.1	334	2	Q4QV85_9TELE	Q4qv85 prochloridus	385	7	2.1	393	2	Q6AAV1_PROAC	Q6aav1 propionibac
313	7	2.1	335	2	Q4QV83_9TELE	Q4qv83 acestrorhyn	386	7	2.1	394	2	Q8KNC8_MICROC	Q8knc8 micromonas
314	7	2.1	336	2	Q7XVK0_ORYSA	Q7xvk0 oryza sativ	387	7	2.1	394	2	Q8VIE8_RAT	Q8vie8 ratulus norv
315	7	2.1	337	2	Q511B9_GEOGA	Q511b9 geobacillus	388	7	2.1	395	2	Q8VIE9_RAT	Q8vie9 ratulus norv
316	7	2.1	339	2	Q7Q286_ANOGA	Q7q286 anophelies g	389	7	2.1	399	2	Q8N772_HUMAN	Q8n772 homo sapien
317	7	2.1	341	2	Q8A703_BACTN	Q8a703 bacteroides	390	7	2.1	400	2	Q6LEB3_YEAST	Q6leb3 saccharomyc
318	7	2.1	341	2	Q73IK1_MOLPM	Q73ik1 wolbachia p	391	7	2.1	401	2	Q63M80_BURPS	Q63m80 burkholderi
319	7	2.1	341	2	Q8JTX8_LSDV	Q8jtx8 lumby skin	392	7	2.1	401	2	Q62D43_BURMA	Q62d43 burkholderi
320	7	2.1	341	2	Q91MZ1_LSDV	Q91mz1 lumby skin	393	7	2.1	404	2	Q821H5_STRAW	Q821h5 streptomyce
321	7	2.1	343	2	Q61HB4_CABER	Q61hb4 caenorhabdi	394	7	2.1	406	2	Q9AUD8_ORYSA	Q9aud8 oryza sativ
322	7	2.1	343	2	Q6NMB7_ARATH	Q6nmb7 arabidopsis	395	7	2.1	408	2	Q4J0Z5_AZOVY	Q4j0z5 azotobacter
323	7	2.1	343	2	Q8R0W2_MOUSE	Q8r0w2 mus musculu	396	7	2.1	410	2	Q9PLM2_CHILMU	Q9plm2 chlamydia m



397	7	2.1	411	2	Q9N81_LEIMA	Q9Nf81 leishmania	470	7	2.1	480	2	Q7CZV1_AGRIS	Q7CZV1 agrobacteri
398	7	2.1	413	2	Q9LYC2_ARATH	Q9LYc2 arabidopsis	471	7	2.1	486	2	Q7SIF4_ORISA	Q7SIF4 oryza sativ
399	7	2.1	415	2	Q4ZE47_GCAUD	Q4ze47 bacterioph	487	7	2.1	487	2	Q9VZ97_DROME	Q9VZ97 drosophila
400	7	2.1	415	2	Q6A6B9_PROAC	Q6a6b9 propionibac	473	7	2.1	487	2	Q6Y154_9ASTR	Q6Y154 lactuca sal
401	7	2.1	418	1	MTR_HABIN	P44614 haemophilus	474	7	2.1	490	2	Q4KCP0_PSEFS	Q4KCP0 pseudomonas
402	7	2.1	418	2	Q4ONQ4_HABE18	Q4onq4 haemophilus	475	7	2.1	492	2	Q4HN36_CAMLA	Q4hn36 campylobact
403	7	2.1	419	2	Q55XU1_CRYNE	Q55xui cryptococcu	476	7	2.1	492	2	Q9A4P0_CAUCR	Q9A4P0 caulobacter
404	7	2.1	419	2	Q5KM51_CRYNE	Q5km51 cryptococcu	477	7	2.1	493	2	Q9A4P0_ORISA	Q9A4P0 oryza sativ
405	7	2.1	419	2	Q89M64_BRAJA	Q89m64 bradyrhizob	478	7	2.1	493	2	Q4V912_BRARE	Q4V912 brachydanio
406	7	2.1	427	2	Q83410_ENTFA	Q83410 enterococcu	479	7	2.1	495	2	Q75A18_ASHCO	Q75a18 ashyba goss
407	7	2.1	428	2	Q52DX6_MAGGR	Q52dx6 magickarthe	480	7	2.1	496	2	Q96119_DROME	Q96119 drosophila
408	7	2.1	428	2	Q4UMA6_RICPE	Q4ume6 rickettsia	481	7	2.1	496	2	Q9VX74_DROME	Q9VX74 drosophila
409	7	2.1	428	2	Q8Z716_SALT1	Q8z716 salmonella	482	7	2.1	500	2	Q91KG1_MESCR	Q91kg1 mesembryant
410	7	2.1	428	2	Q8ZPG6_SALTY	Q8zpg6 salmonella	483	7	2.1	501	2	Q9BU25_HUMAN	Q9bu25 homo sapien
411	7	2.1	429	2	Q5BBT7_EMENT	Q5bbt7 aspergillus	484	7	2.1	501	2	Q92X18_RHIME	Q92x18 rhizobium m
412	7	2.1	430	2	Q88NK6_PSEPK	Q88nk6 pseudomonas	485	7	2.1	504	2	Q951K5_MACPA	Q951k5 macaca fasc
413	7	2.1	431	2	Q4RT15_TETNG	Q4rt15 tetradomonas	486	7	2.1	504	2	Q5GZL9_XANOR	Q5gzl9 xanthomonas
414	7	2.1	433	1	YHL4_YEAST	P38211 saccharomyc	487	7	2.1	505	2	Q8IM14_DROME	Q8im14 drosophila
415	7	2.1	433	2	Q84H74_STRMA	Q84h74 streptomyce	488	7	2.1	505	2	Q8UG64_CHICK	Q8ug64 gallus gall
416	7	2.1	434	2	Q7NVT0_CHRVO	Q7nvt0 chromobacte	489	7	2.1	506	2	Q4SIC8_TETNG	Q4sic8 tetradodon n
417	7	2.1	437	2	Q4MP77_ASPFU	Q4mp77 aspergillus	490	7	2.1	507	1	AL7A1_MALDO	Q9zp77 malus domes
418	7	2.1	438	2	Q65RAB_MANSM	Q65rab mannheimia	491	7	2.1	507	2	Q8VIF1_RAT	Q8vif1 rattus norv
419	7	2.1	439	2	Q8AAJ1_BACTN	Q8aaaj1 bacteroides	492	7	2.1	508	1	PD12_ARATH	Q9er93 arabidopsis
420	7	2.1	442	2	Q8H0O9_THRTM	Q8h0o9 thripes imag	493	7	2.1	509	2	Q8IOQ3_DROME	Q8ioq3 drosophila
421	7	2.1	443	2	Q9V6N4_DROME	Q9ven4 dirosophila	494	7	2.1	509	2	Q4HA39_9DEIO	Q4ha39 deinococcus
422	7	2.1	443	2	Q8UG85_AGRIS	Q8ug85 agrobacteri	495	7	2.1	513	2	Q9HMS7_HALSA	Q9hms7 halobacteri
423	7	2.1	445	2	Q4Q482_LEIMA	Q4q482 leishmania	496	7	2.1	513	2	Q5LTA7_SILPO	Q5lta7 silicibacte
424	7	2.1	445	2	P97001_STRPN	P97001 streptococc	497	7	2.1	513	2	Q8K052_MOUSE	Q8k052 mus musculu
425	7	2.1	448	1	GNTP_BACCI	P46832 bacillus li	498	7	2.1	514	2	Q872D0_NEUCR	Q872d0 neuropept
426	7	2.1	448	2	Q455T3_BACST	Q455t3 bacillus su	499	7	2.1	515	1	SIR2_CANAL	Q59923 candida alb
427	7	2.1	448	2	Q4MUX8_BACCE	Q4mux8 bacillus ce	500	7	2.1	516	2	Q5UKJ1_ORISA	Q5ukj1 oryza sativ
428	7	2.1	448	2	Q6HPK7_BACHK	Q6hpk7 bacillus th	501	7	2.1	517	2	Q4WFK6_ASPFU	Q4wfk6 aspergillus
429	7	2.1	448	2	Q81VN2_BACAN	Q81vn2 bacillus an	502	7	2.1	517	2	Q8KY45_STRCU	Q8ky45 streptomyce
430	7	2.1	448	2	Q63H39_BACCZ	Q63h39 bacillus ac	503	7	2.1	518	2	Q7Y0Y8_ORISA	Q7y0y8 oryza sativ
431	7	2.1	448	2	Q65CW3_BACLD	Q65cw3 bacillus li	504	7	2.1	518	2	Q6DG87_BRARE	Q6dgr7 brachydanio
432	7	2.1	450	2	Q75AOT7_ASHGO	Q75aot7 ashyba goss	505	7	2.1	522	2	Q8NP67_CORGL	Q8np67 corynebacte
433	7	2.1	451	2	Q67NE1_SYMTM	Q67ne1 eymbiobacte	506	7	2.1	524	2	Q6OSY5_CAEBR	Q6osy5 caenorhabdi
434	7	2.1	452	2	Q7YF45_9BIVA	Q7yef45 venerupis (	507	7	2.1	524	2	Q86385_9RHAB	Q86385 rabies viru
435	7	2.1	452	2	Q7YF47_9BIVA	Q7yef47 venerupis (	508	7	2.1	524	2	Q86393_9RHAB	Q86393 rabies viru
436	7	2.1	452	2	Q7YF50_9BIVA	Q7yef50 venerupis (	509	7	2.1	524	2	Q86404_9RHAB	Q86404 rabies viru
437	7	2.1	452	2	Q7YF51_9BIVA	Q7yef51 venerupis (	510	7	2.1	524	2	Q9DKD1_9RHAB	Q9dkd1 rabies viru
438	7	2.1	452	2	Q7YF52_9BIVA	Q7yef52 venerupis (	511	7	2.1	524	2	Q6DPL0_XENTLA	Q6dpl0 xenopus lae
439	7	2.1	452	2	Q8WF40_9BIVA	Q8wf40 venerupis (	512	7	2.1	525	2	Q4ZYF1_PSEBY	Q4zyf1 pseudomonas
440	7	2.1	453	2	Q756A3_ASHGO	Q756a3 ashyba goss	513	7	2.1	525	2	Q5P8K4_AZOSE	Q5p8k4 azoacus sp
441	7	2.1	453	2	Q61P95_CAEBR	Q61p95 caenorhabdi	514	7	2.1	526	2	Q6M477_CORGL	Q6m477 corynebacte
442	7	2.1	454	2	Q9U3P6_CAEBL	Q9u3p6 caenorhabdi	515	7	2.1	527	2	Q65XT8_ORISA	Q65xrt8 oryza sativ
443	7	2.1	458	2	Q26297_METTH	Q26297 methanobact	516	7	2.1	528	2	Q4ZXZ6_PSEBY	Q4zxz6 pseudomonas
444	7	2.1	459	2	Q4S6L5_METTH	Q4s6l5 tetradodon n	517	7	2.1	530	2	Q691M5_ORISA	Q691m5 oryza sativ
445	7	2.1	460	2	Q5VP94_ORISA	Q5vp94 oryza sativ	518	7	2.1	532	1	LGPI_MOUSE	Q99j23 mus musculu
446	7	2.1	460	2	Q803K4_BRARE	Q803k4 brachydanio	519	7	2.1	532	2	Q6FRE9_CANGA	Q6fre9 candida gla
447	7	2.1	462	2	Q70JW8_BACAM	Q70jw8 bacillus am	520	7	2.1	532	2	Q9VCQ0_DROME	Q9vcq0 drosophila
448	7	2.1	463	2	Q34474_BACST	Q34474 bacillus su	521	7	2.1	532	2	Q9ACQ5_ORISA	Q9acq5 oryza sativ
449	7	2.1	464	2	Q722X6_LISMF	Q722x6 listeria mo	522	7	2.1	534	2	Q73BG1_BACCI	Q73bg1 bacillus ce
450	7	2.1	464	2	Q836T7_ENTPA	Q836t7 enterococcu	523	7	2.1	537	1	Q4XBN9_PSEFS	Q4xbn9 pseudomonas
451	7	2.1	464	2	Q819F4_LISMO	Q819f4 listeria mo	524	7	2.1	539	1	R1PK2_MOUSE	Q58h91 mus musculu
452	7	2.1	464	2	Q92E77_LISIN	Q92e77 listeria in	525	7	2.1	539	2	Q991L2_MOUSE	Q991l2 mus musculu
453	7	2.1	465	2	Q4ZYM6_PSEBY	Q4zym6 pseudomonas	526	7	2.1	540	1	Q547H1_MOUSE	Q547h1 mus musculu
454	7	2.1	467	2	Q97UB1_SULSO	Q97ub1 sulfolobus	527	7	2.1	540	1	R1PK2_HUMAN	Q43333 h receptor-
455	7	2.1	468	2	Q5PAM0_NANMM	Q5pam0 anaplasma m	528	7	2.1	540	2	Q88BX4_PSEEM	Q88bx4 pseudomonas
456	7	2.1	469	1	NUZM_YAKLI	Q9b6c8 yarowia li	529	7	2.1	541	2	Q9WU61_RAT	Q9wu61 rattus norv
457	7	2.1	469	2	Q4MUD4_BACCE	Q4mud4 bacillus ce	530	7	2.1	541	2	Q6H05_RAT	Q6h05 rattus norv
458	7	2.1	469	2	Q6HKH3_BACHK	Q6hkh3 bacillus th	531	7	2.1	546	2	Q5B860_EMENT	Q5b860 aspergillus
459	7	2.1	469	2	Q81F82_BACCH	Q81f82 bacillus ce	532	7	2.1	549	2	Q4SNZ3_TETNG	Q4snz3 tetradodon n
460	7	2.1	469	2	Q73AD4_BACCI	Q73ad4 bacillus ac	533	7	2.1	550	2	Q6FX45_CANCA	Q6fx45 candida gla
461	7	2.1	469	2	Q81NB5_BACAN	Q81nb5 bacillus an	534	7	2.1	550	2	Q4KKU3_HUMAN	Q4kku3 homo sapien
462	7	2.1	469	2	Q639G8_BACCZ	Q639g8 bacillus ce	535	7	2.1	551	2	Q96S66_HUMAN	Q96s66 homo sapien
463	7	2.1	469	2	Q63D32_BACCZ	Q63d32 bacillus ce	536	7	2.1	551	2	Q7R3Y0_GITALA	Q7r3y0 gardia lam
464	7	2.1	470	2	Q9N4U9_CAEBL	Q9n4u9 caenorhabdi	537	7	2.1	556	2	Q6P9H7_HUMAN	Q6p9h7 homo sapien
465	7	2.1	470	2	Q50510_XENTR	Q50510 xenopus tro	538	7	2.1	556	2	Q6AXD5_MOUSE	Q6axd5 mus musculu
466	7	2.1	472	2	Q4UIP3_THEAN	Q4uif3 theileria a	539	7	2.1	558	2	Q6YNN4_LACCI	Q6ynn4 lactobacillu
467	7	2.1	474	2	Q4IAW9_GIBZE	Q4iaw9 gibberella	540	7	2.1	572	2	Q8UBH4_AGRIS	Q8ubh4 agrobacteri
468	7	2.1	475	2	Q9M3D9_ARATH	Q9m3d9 arabidopsis	541	7	2.1	574	2	Q6FKX3_CANCA	Q6fkx3 candida gla
469	7	2.1	477	2	Q4WAQ5_ASPFU	Q4waq5 aspergillus	542	7	2.1	577	2	Q8KAB6_CHLTE	Q8kab6 chlorobium



543	7	2.1	577	2	Q8K38_CHLRE	Q8K38_chlorobium	616	7	2.1	742	2	Q4H347_CIOIN	Q4h347_ciona_intes
544	7	2.1	578	2	Q6PV2_MOUSE	Q6pv2_mus_musculu	617	7	2.1	750	2	Q5A2H1_CANAL	Q5a2h1_candida_alb
545	7	2.1	579	2	Q8T7M1_PHYPO	Q8t7m1_physarum_po	618	7	2.1	757	2	Q6T6T7_ERWAM	Q6t6t7_erwinia_amy
546	7	2.1	582	2	Q8PRA6_XANAC	Q8pra6_xanthomonas	619	7	2.1	759	2	Q5INS3_MAGGR	Q5ins3_magnaporthe
547	7	2.1	585	2	ENV_MPMV	P07575 simian maso	620	7	2.1	765	2	Q20479_CAEEL	Q20479_caenorhabdi
548	7	2.1	586	2	Q77G6_MPMV	Q77g6_simian maso	621	7	2.1	769	2	Q4PHM4_USTMA	Q4phm4_ustilago_ma
549	7	2.1	587	1	ENV_SRV1	P04027 simian retr	622	7	2.1	775	2	Q5VS39_ORYSA	Q5vs39_oryza_sativ
550	7	2.1	588	2	Q01465_CAEEL	P01465 caenorhabdi	623	7	2.1	777	2	Q6PK58_HUMAN	Q6pk58_homo_sapien
551	7	2.1	591	1	CALX_MOUSE	P35565 ratu musculu	624	7	2.1	786	2	Q6BGH4_PARTB	Q6bgh4_parmectium
552	7	2.1	591	1	CALX_MOUSE	P35565 ratu musculu	625	7	2.1	789	2	Q6FUT6_CANGA	Q6fut6_candida_gla
553	7	2.1	591	2	Q5SUC3_MOUSE	Q5suc3_mus_musculu	626	7	2.1	790	2	Q6BU29_DEBBA	Q6bu29_debaryomyce
554	7	2.1	591	2	Q8K38_CRIGR	Q8k38_cricetulus	627	7	2.1	791	2	Q5W199_BACSK	Q5w199_bacillus_cl
555	7	2.1	593	2	Q64DP8_GAMPH	Q64dp8_scolecocorp	628	7	2.1	797	2	Q9UTK6_SCHPO	Q9utk6_schizosacch
556	7	2.1	597	2	Q54X44_DICDI	Q54x44_dicyosteli	630	7	2.1	799	1	FTSK_TREPA	Q83b64_lypdonema_p
557	7	2.1	600	2	Q8FPD5_CORER	Q8fpd5_corynebacte	631	7	2.1	801	2	Q9LWV8_ORYSA	Q9lwv8_oryza_sativ
558	7	2.1	602	2	Q86VY9_HUMAN	Q86vy9_homo_sapien	632	7	2.1	803	2	Q8S808_ORYSA	Q8s808_oryza_sativ
559	7	2.1	604	1	PGH2_CAYPO	P70682 cavia porce	633	7	2.1	814	2	Q6NUT7_BRARE	Q6nut7_brachydanio
560	7	2.1	605	1	PCOA_ECOLI	Q47452 escherichia	634	7	2.1	814	2	Q6NUT7_BRARE	Q6nut7_brachydanio
561	7	2.1	605	2	Q71M97_KLEBP	Q71m97_klebsiella	635	7	2.1	815	2	Q72K11_THRT2	Q72k11_thermus_the
562	7	2.1	605	2	Q6MKP4_SBRMA	Q6mkp4_serratia_ma	636	7	2.1	818	2	Q5SK21_THRT8	Q5sk21_thermus_the
563	7	2.1	607	2	Q6USP5_KLEBP	Q6usp5_klebsiella	637	7	2.1	819	2	Q7OB30_ANOGA	Q7qb30_aspergillus_g
564	7	2.1	613	2	Q5IKC8_MAGGR	Q5ikc8_magnaporthe	638	7	2.1	835	2	Q4MKK7_ASPPU	Q4mkk7_aspergillus_g
565	7	2.1	613	2	Q98C87_RHILLO	Q98c87_rhizodium_1	639	7	2.1	842	2	Q4T648_TERNNG	Q4t648_tetradodon_n
566	7	2.1	615	2	Q5N0S8_SYNP6	Q5n0s8_synechococc	640	7	2.1	845	2	Q5BRG8_EMENI	Q5brg8_aspergillus_g
567	7	2.1	616	2	Q4R7A7_MACPA	Q4r7a7_macaca_fasc	641	7	2.1	847	2	Q95KP7_CANPA	Q95kp7_canis_famil
568	7	2.1	617	2	Q8VDQ7_MOUSE	Q8vdq7_mus_musculu	642	7	2.1	855	2	Q54R00_DICDI	Q54r00_dicyosteli
569	7	2.1	619	2	Q51PM8_MAGGR	Q51pm8_magnaporthe	643	7	2.1	856	2	Q5BR45_PONPY	Q5br45_pongo_pygma
570	7	2.1	619	2	Q4PPO5_USTMA	Q4pfo5_ustilago_ma	644	7	2.1	870	1	GP155_HUMAN	Q723f1_homo_sapien
571	7	2.1	619	2	Q9VUK5_DROME	Q9vuk5_drosophila	645	7	2.1	870	2	Q4G0Y6_HUMAN	Q4g0y6_homo_sapien
572	7	2.1	622	2	Q5A120_CANAL	Q5a120_candida_alb	646	7	2.1	872	1	GP155_FONPY	Q5r3a7_pongo_pygma
573	7	2.1	623	2	Q6T448_LEIMA	Q6t448_leishmania	647	7	2.1	873	2	Q5AXH0_EMENI	Q5axh0_aspergillus_g
574	7	2.1	624	2	Q6BNO2_9MYRI	Q6bn2_abaction_mag	648	7	2.1	878	2	Q9USU3_SCHPO	Q9usu3_schizosacch
575	7	2.1	624	2	Q4SRN5_TERNNG	Q4srn5_tetradodon_n	649	7	2.1	890	2	Q5VUB5_HUMAN	Q5vub5_homo_sapien
576	7	2.1	634	2	Q4UC10_THEAN	Q4uc10_theileria_a	650	7	2.1	890	2	Q5RDU3_PONPY	Q5rd34_pongo_pygma
577	7	2.1	643	2	Q9YCH6_ABRER	Q9ych6_aetopyrum_p	651	7	2.1	892	2	Q9Y438_HUMAN	Q9y438_homo_sapien
578	7	2.1	643	2	Q7UVL7_RHOBA	Q7uvl7_rhodopirell	652	7	2.1	900	2	Q6AX42_XENLA	Q6ax42_xenopus_lae
579	7	2.1	646	2	Q9KMZ5_VIBCH	Q9kms5_vibrio_chol	653	7	2.1	912	2	Q61KT4_CABER	Q61kt4_caenorhabdi
580	7	2.1	648	2	Q55RR9_CRYNE	Q55rr9_cryptococcu	654	7	2.1	914	1	PBPA_BACSV	P39793_bacillus_su
581	7	2.1	648	2	Q5KES1_CRYNE	Q5kes1_cryptococcu	655	7	2.1	929	1	Q5PYG6_SALPA	Q5pyg6_salmonella
582	7	2.1	650	1	LIRB1_HUMAN	Q6nh16_h leukocyte	656	7	2.1	941	2	Q73Z06_MYCPA	Q73z06_mycobacteri
583	7	2.1	650	2	Q8NAB4_HUMAN	Q8nab4_homo sapien	657	7	2.1	941	2	Q5H722_FUGRU	Q5h722_fugu_rubrip
584	7	2.1	650	2	Q4V729_XENLA	Q4v729_xenopus lae	658	7	2.1	943	1	UVRA_STRPN	P63384_streptococc
585	7	2.1	656	2	Q9Y114_DROME	Q9y114_drosophila	659	7	2.1	946	2	Q44825_CAEEL	P63385_streptococc
586	7	2.1	660	2	Q8ZNM7_SALTY	Q8znm7_salmonella	660	7	2.1	946	2	Q5A825_CAEEL	Q44825_caenorhabdi
587	7	2.1	675	1	HPBA_XANAC	Q6ph20_xanthomonas	661	7	2.1	946	2	Q827G6_STRAW	Q827g6_streptomyce
588	7	2.1	675	1	HPBA_XANAC	Q6ph20_xanthomonas	662	7	2.1	947	2	Q9B1A3_CAEEL	Q9b1a3_caenorhabdi
589	7	2.1	675	2	Q4UYB5_XANCP	Q4uyb5_xanthomonas	663	7	2.1	951	2	Q72268_HELAM	Q72268_helicoverpa
590	7	2.1	679	2	Q6C335_YARLI	Q6c335_yarrowia_1i	664	7	2.1	951	2	Q86Q16_HELAM	Q86q16_helicoverpa
591	7	2.1	694	2	Q4MOR4_ASPPU	Q4mqr4_aspergillus	665	7	2.1	951	2	Q8MUT9_HELAM	Q8mut9_helicoverpa
592	7	2.1	694	2	Q7JUN23_RHOBA	Q7jun23_rhodopirell	666	7	2.1	951	2	Q8MUT9_HELAM	Q8mut9_helicoverpa
593	7	2.1	695	2	Q7S5Z3_NEUCR	Q7s5z3_neurospora	667	7	2.1	953	2	Q5NOD4_SYNP6	Q5nod4_synechococc
594	7	2.1	695	2	Q55XL5_CRYNE	Q55xl5_cryptococcu	668	7	2.1	954	1	GCSP_AGRTS	Q8uff6_agrobacteri
595	7	2.1	695	2	Q5KMC0_CRYNE	Q5kmc0_cryptococcu	669	7	2.1	954	1	GCSP_RHIME	Q92q11_rhizobium_m
596	7	2.1	695	2	Q32508_LYCCR	Q32508_lycium_cest	670	7	2.1	954	1	GCSP_SYNEL	Q8dl13_synechococc
597	7	2.1	695	2	Q32700_NOLSP	Q32700_nolana spat	671	7	2.1	954	1	GCSP_VIBPA	Q87l05_vibrio_para
598	7	2.1	695	2	Q33168_BSOLA	Q33168_salpinglosi	672	7	2.1	954	1	GCSP_VIBVU	Q8d797_vibrio_vuln
599	7	2.1	696	2	Q17479_HYACE	Q17479_hyalophora	673	7	2.1	954	1	GCSP_VIBVY	Q7meb9_vibrio_vuln
600	7	2.1	701	2	Q4R6H5_MACPA	Q4r6h5_macaca fasc	674	7	2.1	955	2	Q5DZM3_VIBP1	Q4k416_pseudomonas
601	7	2.1	701	2	Q6J2B2_PSEYM	Q6j2b2_pseudomonas	675	7	2.1	955	2	GCSP_ECO57	Q5dzm3_vibrio_fisc
602	7	2.1	708	2	Q8ZMU4_PYPAR	Q8zmu4_pyrobaculum	676	7	2.1	956	1	GCSP_ECOL6	Q8xd33_escherichia
603	7	2.1	711	2	Q6LWF5_LACP1	Q6lwf5_lactobacill	677	7	2.1	956	1	GCSP_ECOLI	Q8f673_escherichia
604	7	2.1	715	2	Q8WSS5_9TROC	Q8wss5_olkopleura	678	7	2.1	956	1	GCSP_SALTY	P33195_escherichia
605	7	2.1	716	2	Q87CY5_XYLP1	Q87cy5_xyella_fas	679	7	2.1	956	1	GCSP_SALTY	Q82k30_salmonella
606	7	2.1	717	2	Q8VLC6_DROME	Q8vlc6_drosophila	680	7	2.1	956	1	GCSP_SHIFL	Q8zm76_salmonella
607	7	2.1	719	2	Q5YTH1_NOCFA	Q5yth1_nocardiella fa	681	7	2.1	957	1	GCSP2_PSEBP	Q83q42_singella_fi
608	7	2.1	719	2	Q7Q858_ANOGA	Q7q858_anopheles g	682	7	2.1	957	1	Q6D974_ERWCT	Q88c19_pseudomonas
609	7	2.1	724	2	Q4RMA0_TERNNG	Q4rma0_tetradodon n	683	7	2.1	958	1	GCSP2_PSEAR	Q6d974_erwinia_car
610	7	2.1	726	2	Q8GFR4_CITFR	Q8gfr4_citrobacter	684	7	2.1	958	1	GCSP_PHOIL	Q9hct7_pseudomonas
611	7	2.1	728	2	Q81EM1_PLAF7	Q81em1_plasmodium	685	7	2.1	958	1	GCSP_YERPR	Q7n139_phocorhabdu
612	7	2.1	730	2	Q98698_EXAAF	Q98698_exacium affi	686	7	2.1	958	2	Q6MPZ6_BDBBA	Q8zn19_yersinia_pe
613	7	2.1	730	2	Q6PFN2_BRARE	Q6pfm2_brachydanio	687	7	2.1	959	1	GCSP_STNPK	Q6mpz6_bdellovibri
614	7	2.1	730	2	Q802D0_BRARE	Q802d0_brachydanio	688	7	2.1	959	1	Q666R7_YERPS	Q7n335_synechococc
615	7	2.1	732	1	ACPH_HUMAN	P13798_homo sapien	688	7	2.1	959	1	Q666R7_YERPS	Q666r7_yersinia_ps



689	7	2.1	963	1	TRES_THETH	066458	thermus the	762	7	2.1	1398	2	06E2N4_BRARE	06e2n4	brachydanio
690	7	2.1	963	2	Q8BX19_MOUSE	Q8bx19	mus musculus	763	7	2.1	1415	2	08A9R6_BACTN	08a9r6	bacteroides
691	7	2.1	964	1	GCSP_ROMA	Q7v9k4	prochloroco	764	7	2.1	1422	2	Q95KU4_CANPA	095ku4	caneis famil
692	7	2.1	965	2	Q7WU15_THETH	Q7wu15	thermus the	765	7	2.1	1447	2	Q4WPJ3_ASPPU	04wpj3	aspergillus
693	7	2.1	965	2	Q9RA59_THETH	Q9ras9	thermus the	766	7	2.1	1471	2	Q413J9_GIBZE	0413j9	gibberella
694	7	2.1	965	2	Q4FTK9_GGAMM	Q4fte9	thermus cal	767	7	2.1	1487	2	Q036Z6_RAT	0036z6	rattus norv
695	7	2.1	965	2	Q5SL15_THETH	Q5sl15	thermus the	768	7	2.1	1510	2	Q4S9X7_TETNG	04s9x7	tetradodon n
696	7	2.1	969	2	Q7W47_HORER	Q7w47	bordelella	769	7	2.1	1533	2	Q7Z2I9_HUMAN	07z2i9	homo sapien
697	7	2.1	969	2	Q7U2J5_PROMP	Q7u2j5	prochloroco	770	7	2.1	1543	2	Q8WMZ4_HUMAN	08wmz4	homo sapien
698	7	2.1	972	2	Q4VAK4_HUMAN	Q4vak4	homo sapien	771	7	2.1	1552	2	Q49370_ARATH	049370	arabidopsis
699	7	2.1	972	2	Q5NZ93_AZOSZ	Q5nz93	azotarcus sp	772	7	2.1	1560	2	Q883Z3_MOUSE	0883z3	mus musculus
700	7	2.1	975	1	GCSP_XANCP	Q8pbk7	xanthomonas	773	7	2.1	1560	2	Q925J9_MOUSE	0925j9	mus musculus
701	7	2.1	975	2	Q4URZ4_XANCP	Q4urz4	xanthomonas	774	7	2.1	1560	2	Q925K0_MOUSE	0925k0	mus musculus
702	7	2.1	975	2	Q4LZ94_SBURK	Q4l294	xanthomonas	775	7	2.1	1581	1	PPRB_HUMAN	PPRB	homo
703	7	2.1	975	2	Q6ZFN1_BURMA	Q6zfn1	burkholderi	776	7	2.1	1581	2	Q5RES4_PONPY	05res4	pongo pygma
704	7	2.1	975	2	Q63PL2_BURPS	Q63pl2	burkholderi	777	7	2.1	1585	2	Q8UBT4_AGRY5	08ubt4	agrobacteri
705	7	2.1	977	1	GCSP_XANAC	Q8p512	xanthomonas	778	7	2.1	1620	2	Q24984_GIALA	024984	giardia lam
706	7	2.1	977	1	Q8WRU7_9TRYP	Q8wru7	theileria a	779	7	2.1	1630	1	Q7QXB2_GIALA	07qxb2	giardia lam
707	7	2.1	979	1	PPRPN_BOVIN	P56722	bos taurus	780	7	2.1	1630	1	NHS_HUMAN	NHS	homo
708	7	2.1	979	2	Q4PGJ9_USITMA	Q4pgj9	usellago ma	781	7	2.1	1704	2	Q4IZD0_GIBZE	04izd0	gibberella
709	7	2.1	982	1	GCSP_RALSO	Q8xue8	raisteconia s	782	7	2.1	1781	2	Q86KX8_DICDI	086kx8	dictyosteli
710	7	2.1	984	2	Q6CHEO_YARLI	Q6cheo	yarrowia li	783	7	2.1	1785	1	Q7YYR5_CRYPV	07yyr5	cryptospori
711	7	2.1	994	2	Q57K62_SALCH	Q57k62	salmonella	784	7	2.1	1821	2	Q7PSP2_AMOGA	07psp2	anopheles g
712	7	2.1	996	2	Q4UHT9_THEAN	Q4uht9	theileria a	785	7	2.1	1868	2	Q6BNV2_DEBNA	06bnv2	debaromyce
713	7	2.1	1002	1	SYIM_YEAST	P48526	saccharomyc	786	7	2.1	2025	2	Q4Q534_LEIMA	04q534	leishmania
714	7	2.1	1009	2	Q7SE77_NEUCR	Q7sey7	neurospora	787	7	2.1	2055	2	Q7XSV2_ARATH	07xsv2	arabidopsis
715	7	2.1	1009	2	Q5GWX0_XANOR	Q5gwxc0	xanthomonas	788	7	2.1	2061	2	Q91TV5_ARATH	091tv5	arabidopsis
716	7	2.1	1012	2	QFPI_HUMAN	Q75665	homo sapien	789	7	2.1	2087	2	Q8MXL2_LEIMA	08mxl2	leishmania
717	7	2.1	1019	2	Q8BJQ7_MOUSE	Q8bjq7	mus musculus	790	7	2.1	2301	2	Q5L196_GEOGA	05l196	geobacillus
718	7	2.1	1020	1	GCSP_HITMAN	P23378	homo sapien	791	7	2.1	2378	2	Q5OXT0_ENTHI	05oxt0	entamoeba h
719	7	2.1	1025	1	GCSP_MOUSE	Q91w43	mus musculus	792	7	2.1	2623	2	Q6WR10_HUMAN	06wr10	homo sapien
720	7	2.1	1031	2	Q51ZM7_FELCA	Q51zm7	felis silve	793	7	2.1	2747	2	Q9LB00_AERSA	09lb00	aeromonas s
721	7	2.1	1032	1	Q8HZ52_FELCA	Q8hz52	felis silve	794	7	2.1	2787	1	TELI_YEAST	TELI	yeast
722	7	2.1	1031	2	MET18_YEAST	P40469	saccharomyc	795	7	2.1	2961	2	Q7P3B9_FUSNV	07p3b9	fusarium
723	7	2.1	1036	2	Q5VYQ3_HUMAN	Q5vyq3	homo sapien	796	7	2.1	3322	2	Q6BBQ3_CAEEL	06bbq3	caenorhabdi
724	7	2.1	1057	2	Q7SAD5_NEUCR	Q7sad5	neurospora	797	7	2.1	3405	2	Q6BRQ5_CAEEL	06brq5	caenorhabdi
725	7	2.1	1057	2	Q8MR53_DROME	Q8mr53	dirosophila	798	7	2.1	3436	2	Q86NPF_CAEEL	086nfp	caenorhabdi
726	7	2.1	1057	2	Q869U6_DICDI	Q869u6	dictyosteli	799	7	2.1	3436	2	Q86NPF_CAEEL	086nfp	caenorhabdi
727	7	2.1	1066	2	Q5SFC4_STRBI	Q5sfc4	streptomyce	800	7	2.1	3436	2	Q18290_CAEEL	018290	caenorhabdi
728	7	2.1	1067	2	Q6CSG8_KLULA	Q6csg8	kluyveromyc	801	7	2.1	3522	2	Q86N7F_CAEEL	086n7f	caenorhabdi
729	7	2.1	1070	2	Q9SVJ6_ARATH	Q9svj6	arabidopsis	802	7	2.1	3821	2	Q7NUJ3_CHRYO	07nuj3	chrysothab
730	7	2.1	1084	2	Q51KZ9_MAGGR	Q51kz9	magnaporthe	803	7	2.1	4091	2	Q96Z04_PLAF7	096z04	plasmodium
731	7	2.1	1085	1	IFPH1_YEAST	P39520	saccharomyc	804	7	2.1	4340	2	Q30764_PACTO	030764	pactro
732	7	2.1	1100	2	Q7SG89_NEUCR	Q7sg89	neurospora	805	7	2.1	4410	2	Q6EUT7_CAEEL	06eut7	caenorhabdi
733	7	2.1	1101	2	Q59H95_HUMAN	Q59h95	homo sapien	806	7	2.1	4545	2	Q61291_MOUSE	061291	mus musculus
734	7	2.1	1128	2	Q9DFU8_XENILA	Q9dfu8	xenopus lae	807	7	2.1	4862	2	Q5R1Z7_BRARE	05r1z7	brachydanio
735	7	2.1	1134	2	Q6ZPU0_MOUSE	Q6zpu0	mus musculus	808	7	2.1	4944	2	Q7K7B6_CAEEL	07k7b6	caenorhabdi
736	7	2.1	1141	2	Q4Q5K4_LEIMA	Q4q5k4	leishmania	809	7	2.1	4955	2	Q867D9_CAEEL	0867d9	caenorhabdi
737	7	2.1	1142	2	Q7SZV2_XENILA	Q7szv2	xenopus lae	810	7	2.1	5359	2	Q5VXR4_SACER	05vxr4	saccharopol
738	7	2.1	1161	2	Q7KQV5_DROME	Q7kqv5	dirosophila	811	7	2.1	6145	2	Q93H84_STRAM	093h84	streptomyce
739	7	2.1	1185	2	Q5BJJ0_MOUSE	Q5bjj0	mus musculus	812	7	2.1	6239	2	Q9S0R7_STRAM	09s0r7	streptomyce
740	7	2.1	1186	2	Q4PI08_USITMA	Q4pi08	usellago ma	813	7	2.1	8402	2	Q4R8B9_TETNG	04r8b9	tetradodon n
741	7	2.1	1201	1	PER3_HUMAN	P56645	homo sapien	814	7	2.1	8402	2	Q9UMU6_HUMAN	09umu6	homo sapien
742	7	2.1	1210	2	Q5H8X5_HUMAN	Q5h8x5	homo sapien	815	7	1.8	22	2	Q9T2R5_SOLTV	09t2r5	solanum tub
743	7	2.1	1244	1	PER1_RAT	Q8ch15	ratleus norv	816	7	1.8	25	2	Q6U782_HUMAN	06u782	homo sapien
744	7	2.1	1254	1	Q4QAP3_LEIMA	Q4qap3	leishmania	817	7	1.8	26	2	Q9QVZ8_9MURI	09qvz8	mus sp. b c
745	7	2.1	1269	2	FLI1_HUMAN	Q13045	homo sapien	818	7	1.8	29	2	Q88224_MOUSE	088224	mus musculus
746	7	2.1	1269	2	Q5RA49_PONPY	Q5ra49	pongo pygma	819	7	1.8	30	2	Q34897_9MEYA	034897	lasiorhinus
747	7	2.1	1271	2	Q8CHRI_MOUSE	Q8chri	mus musculus	820	7	1.8	32	2	Q4YM48_PLABE	04ym48	plasmodium
748	7	2.1	1277	2	Q17517_CAEEL	Q17517	caenorhabdi	821	7	1.8	35	2	Q6QNA6_HUMAN	06qna6	homo sapien
749	7	2.1	1281	2	Q7RFM4_PLAYO	Q7rfm4	plasmodium	822	7	1.8	35	2	Q8M1N3_PDIYT	08m1n3	limbodesus
750	7	2.1	1285	2	Q8K3T3_SPAJD	Q8k3t3	spalax juda	823	7	1.8	36	2	Q25409_HELPY	025409	helpy
751	7	2.1	1290	1	PER1_HUMAN	Q15534	homo sapien	824	7	1.8	37	2	Q8FPD8_LEPIN	08fpd8	leptocbacta
752	7	2.1	1291	1	PER1_MOUSE	Q35973	mus musculus	825	7	1.8	39	2	Q4Z7A6_PLABE	04z7a6	plasmodium
753	7	2.1	1291	2	Q5CWZ4_CRYPV	Q5cwz4	cryptospori	826	7	1.8	39	2	Q98RB8_MYCPU	098rb8	mycoplasma
754	7	2.1	1291	2	Q5NCG2_MOUSE	Q5ncg2	mus musculus	827	7	1.8	40	2	Q6XYV1_SPTCV	06xyv1	spiroplasma
755	7	2.1	1312	1	DPOL_PYRSD	Q51334	pyrococcus	828	7	1.8	41	2	Q5BKX2_SCHPA	05bkx2	schistosoma
756	7	2.1	1331	2	Q6A060_MOUSE	Q6a060	mus musculus	829	7	1.8	41	2	Q93ILM0_HELPY	093ilm0	helicobacte
757	7	2.1	1345	2	Q54437_STAMA	Q54437	staphyloche	830	7	1.8	41	2	Q93LM5_HELPY	093lm5	helicobacte
758	7	2.1	1345	2	Q51242_MAGGR	Q51242	magnaporthe	831	7	1.8	41	2	Q5BVU2_SCHPA	05bv2	schistosoma
759	7	2.1	1365	2	Q76DY4_CYNPY	Q76dy4	cynops pyrr	832	7	1.8	42	2	Q82949_CHRYA	082949	chriatogoma
760	7	2.1	1383	2	Q89232_SALPH	Q89232	canine hecp	833	7	1.8	43	2	Q82949_CHRYA	082949	chriatogoma
761	7	2.1	1398	2	Q6UV33_BRARE	Q6uv33	brachydanio	834	7	1.8	44	2	Q93U23_CHRYA	093u23	chriatogoma



835	6	1.8	46	2	093LS1_HELPY	0931st helicobacte	908	6	1.8	66	2	08NMN2_STAMM	08nmn2 staphylococ
836	6	1.8	46	2	093LS3_HELPY	0931se helicobacte	909	6	1.8	66	2	09NU22_STAMM	09nu22 staphylococ
837	6	1.8	46	2	093LS6_HELPY	0931se helicobacte	910	6	1.8	67	2	07Y8G4_9ETHH	07y8g4 hemiechlar s
838	6	1.8	46	2	093LT0_HELPY	0931to helicobacte	911	6	1.8	67	2	086132_9RHAB	086132 vesicular s
839	6	1.8	46	2	093LT1_HELPY	0931ti helicobacte	912	6	1.8	68	2	093LL6_NOSPU	093116 nostoc punc
840	6	1.8	46	2	093LT2_HELPY	0931t2 helicobacte	913	6	1.8	68	2	08DX22_STRAS	08dx22 staphylococ
841	6	1.8	46	2	093LUD_HELPY	0931ud helicobacte	914	6	1.8	68	2	05OWM8_IDILIO	05owm8 idiomarina
842	6	1.8	46	2	093LUT_HELPY	0931ut helicobacte	915	6	1.8	68	2	071OT1_JACJA	0710t1 jaculus jac
843	6	1.8	48	2	08G233_BRUSU	08g233 helicobacte	916	6	1.8	68	2	098SP3_BRARB	098sp3 brachydanio
844	6	1.8	49	1	LHA7_RHOAC	P35093 rhodopendo	917	6	1.8	70	1	GBG1_DROME	P38040 drosophila
845	6	1.8	49	2	057C16_BRUBA	057c16 bruceella ab	918	6	1.8	70	2	0540Y8_DROME	0540y8 drosophila
846	6	1.8	49	2	08G004_BRUSU	08g004 bruceella su	919	6	1.8	72	2	08T1A1_DICD1	08t1a1 dictyostelli
847	6	1.8	50	2	057OK9_ARATH	057ok9 arabidopsis	920	6	1.8	72	2	081YF6_BACRC	081y76 bacillus ce
848	6	1.8	51	2	09UDD2_HUMAN	09udd2 homo sapien	921	6	1.8	72	2	09HYJ4_PSEAR	09hyj4 pseudomonas
849	6	1.8	51	2	05BZ15_SCHJA	05bz15 schistosoma	922	6	1.8	72	2	071BL6_GRETR	071bl6 simian retr
850	6	1.8	52	1	CD3E_BOVIN	028073 bos taurus	923	6	1.8	73	2	09XVG6_CAEBL	09xvg6 caenorhabdi
851	6	1.8	52	2	05EJRO_CEPNE	05ejro cepaea nemo	924	6	1.8	73	2	003922_GCAUD	003922 bacterioph
852	6	1.8	52	2	05EJH3_CEPNE	05ejh3 cepaea nemo	925	6	1.8	73	2	085WY1_PINKO	085wy1 pinus korai
853	6	1.8	52	2	05EJH7_CEPNE	05ejh7 cepaea nemo	926	6	1.8	73	2	032310_BACTV	032310 bacillus th
854	6	1.8	52	2	05EJH8_CEPNE	05ejh8 cepaea nemo	927	6	1.8	74	2	06JCJ3_BORBU	06jcj3 borelia bu
855	6	1.8	52	2	05EJH9_CEPNE	05ejh9 cepaea nemo	928	6	1.8	74	2	05P284_AZOSE	05p284 azoarcus sp
856	6	1.8	52	2	05EJH0_CEPNE	05ejh0 cepaea nemo	929	6	1.8	74	2	097PB7_STRPN	097pb7 streptococ
857	6	1.8	52	2	05EJH1_CEPNE	05ejh1 cepaea nemo	930	6	1.8	75	2	05RJ63_HUMAN	05rj63 homo sapien
858	6	1.8	52	2	05EJH2_CEPNE	05ejh2 cepaea nemo	931	6	1.8	75	2	09TTO1_HORSE	09tt01 equus cabal
859	6	1.8	52	2	05EJH3_CEPNE	05ejh3 cepaea nemo	932	6	1.8	75	2	094IC7_ARATH	094ic7 arabidopsis
860	6	1.8	52	2	05EJH4_CEPNE	05ejh4 cepaea nemo	933	6	1.8	75	2	057OK8_ARATH	057ok8 arabidopsis
861	6	1.8	52	2	05EJH5_CEPNE	05ejh5 cepaea nemo	934	6	1.8	75	2	04V213_BACC2	04v213 bacillus ce
862	6	1.8	52	2	05EJH6_CEPNE	05ejh6 cepaea nemo	935	6	1.8	75	2	0920Z5_RHIME	092u5 thryzobium m
863	6	1.8	52	2	05EJH7_CEPNE	05ejh7 cepaea nemo	936	6	1.8	76	2	06BUB6_DEBHA	06bub6 debaryomyce
864	6	1.8	52	2	05EJH7_CEPNE	05ejh7 cepaea nemo	937	6	1.8	76	2	024505_DROSOPH	024505 drosophila
865	6	1.8	52	2	05EJH7_CEPNE	05ejh7 cepaea nemo	938	6	1.8	76	2	0618M2_CAEBR	0618m2 caenorhabdi
866	6	1.8	52	2	091G27_IRAV6	091g27 chilo iride	939	6	1.8	76	2	04YX67_FLABE	04yx67 plasmodium
867	6	1.8	53	2	05BY58_SCHJA	05by58 schistosoma	940	6	1.8	77	2	05NVV9_9ARCH	05nv9 uncultured
868	6	1.8	53	2	04XTL3_PLACH	04xtl3 plasmodium	941	6	1.8	77	2	08YP97_9ARCH	08yp97 anabena sp
869	6	1.8	53	2	06N0X3_RHOPA	06n0x3 rhodopende	942	6	1.8	77	2	05RL04_MOUSE	05rl04 mus musculu
870	6	1.8	53	2	082EM7_STRAM	08em7 streptomyce	943	6	1.8	78	2	080OK6_METMA	080ok6 methanosarc
871	6	1.8	53	2	08VA91_POVBK	08va91 polyomaviru	944	6	1.8	78	2	05HYU8_HUMAN	05hyu8 homo sapien
872	6	1.8	54	2	0592S5_LYMST	0592s5 lymphaea sta	945	6	1.8	78	2	07Y2E7_9CAUD	07y2e7 bacterioph
873	6	1.8	54	2	067JH5_SYMTJ	067jhs symbiacte	946	6	1.8	78	2	05DKS6_9NOCA	05dks6 rhodococcus
874	6	1.8	54	2	082AA3_STRAM	082aa3 streptomyce	947	6	1.8	79	2	05TVF8_9NOCA	05tvf8 anopheles g
875	6	1.8	56	2	0273B8_METTH	0273b8 methanobact	948	6	1.8	79	2	06PFM8_ACTIAD	06pfm8 actinobact
876	6	1.8	56	2	092X78_RHIME	092x78 rhizobium m	949	6	1.8	80	2	06XHU6_DROYA	06xhu6 drosophila
877	6	1.8	57	2	05QUV3_IDILIO	05quv3 idiomarina	950	6	1.8	80	2	04YX8_FLABE	04yx8 plasmodium
878	6	1.8	58	2	05C7L1_SCHJA	05c7l1 schistosoma	951	6	1.8	81	2	06RH77_HUMAN	06rh77 homo sapien
879	6	1.8	58	2	0517S1_PSEFL	0517s1 pseudomonas	952	6	1.8	81	2	07OPT5_GIALA	07qps5 giardia lam
880	6	1.8	58	2	04KG24_PSEFL	04kg24 pseudomonas	953	6	1.8	81	2	09TTO2_HORSE	09tt02 equus cabal
881	6	1.8	59	2	05C5K2_SCHJA	05c5k2 schistosoma	954	6	1.8	81	2	04HT87_CAMCO	04ht87 campylobact
882	6	1.8	59	2	05OMQ7_ORYSA	05omq7 oryza sativ	955	6	1.8	81	2	05HYU5_CAMJR	05hyu5 campylobact
883	6	1.8	60	2	06BS48_ORYSA	06bs48 oryza sativ	956	6	1.8	81	2	06LTJ9_PHOPR	06ltj9 photobacter
884	6	1.8	60	2	057L03_SALCH	057l03 salmonella	957	6	1.8	81	2	04JUN1_9HEPC	04jun1 hepatitis c
885	6	1.8	60	2	04HGRT_CAMCO	04hgtr campylobact	958	6	1.8	81	2	04JUN3_9HEPC	04jun3 hepatitis c
886	6	1.8	60	2	059131_9GAMA	059131 human herpe	959	6	1.8	81	2	04JUN4_9HEPC	04jun4 hepatitis c
887	6	1.8	61	2	004361_9GAMA	004361 human herpe	960	6	1.8	81	2	04JUN5_9HEPC	04jun5 hepatitis c
888	6	1.8	61	1	NO14_PEA	P26415 plsum sativ	961	6	1.8	81	2	04JUN7_9HEPC	04jun7 hepatitis c
889	6	1.8	61	2	05NKB7_AZOSE	05nkb7 azoarcus sp	962	6	1.8	82	2	09PPD2_CAMBE	09ppd2 campylobact
890	6	1.8	61	2	0836K7_ENTPA	0836k7 enterococcu	963	6	1.8	82	2	07ZIT8_BRARB	07zit8 brachydanio
891	6	1.8	61	2	037321_HABPV	037321 heliochris a	964	6	1.8	83	1	PRRP_RAT	P91278 ratius norv
892	6	1.8	62	2	07PEX8_9NOGA	07pex8 anopheles g	965	6	1.8	83	2	097BH2_THEVO	097bh2 theloplasm
893	6	1.8	62	2	067S86_SYMTJ	067s86 symbiobacte	966	6	1.8	83	2	05DBE6_PPRTM	05dbe6 gorilla gor
894	6	1.8	63	2	096374_MANSE	096374 manduca sex	967	6	1.8	83	2	05XIF6_BORGA	05xif6 borrelia ga
895	6	1.8	63	2	04XB71_PLACH	04xbt1 plasmodium	968	6	1.8	83	2	05P2E9_AZOSE	05p2e9 azoarcus sp
896	6	1.8	63	2	0940T4_ARATH	0940t4 arabidopsis	969	6	1.8	84	1	070182_MOUSE	070182 mus musculu
897	6	1.8	63	2	0519S1_BACPN	0519s1 bacterioides	970	6	1.8	84	1	RL27_CHLTR	08k72 chlorobium
898	6	1.8	64	2	05TFP9_BRUBA	05tf94 bruceella ab	971	6	1.8	84	2	04H1E2_LEIMA	04h1e2 leishmania
899	6	1.8	64	2	08G2O6_BRUSU	08g2q6 bruceella su	972	6	1.8	84	2	06KIT0_ORYSA	06kit0 oryza sativ
900	6	1.8	65	2	05T7A4_9NOGA	05t7a4 anopheles g	973	6	1.8	84	2	05YD52_9NOSO	05y52 nostoc sp.
901	6	1.8	65	2	05DBE7_PPRTM	05dbe7 gorilla gor	974	6	1.8	84	2	04NSE8_9DELT	04nse8 anaeromyxob
902	6	1.8	65	2	06K7K9_ORYSA	06k7k9 oryza sativ	975	6	1.8	84	2	08Q540_9BETA	08q540 pongine her
903	6	1.8	66	2	06T5T5_HRLPY	06t5t5 heliobacte	976	6	1.8	85	2	07RIG8_PLAYO	07rig8 plasmodium
904	6	1.8	66	2	06G995_STRAS	06g995 staphylococ	977	6	1.8	85	2	09TUE8_SHEEP	09tue8 ovis aries
905	6	1.8	66	2	05HFV6_STAAC	05hfve staphylococ	978	6	1.8	85	2	04ZCB7_VVIRU	04zcb7 bacterioph
906	6	1.8	66	2	07ASJ5_STAPHN	07asj5 streptococc	979	6	1.8	85	2	04NV04_9DELT	04nv04 anaeromyxob
907	6	1.8	66	2	08K6N7_STRP3	08k6n7 streptococc	980	6	1.8	85	2	04MVJ1_BACBE	04mvj1 bacillus ce



981	6	1.8	85	2	Q738K8_BACCI	Q738K8 bacillus ce	1054	6	1.8	96	1	VGE_BPG4	P03640 bacterioph
982	6	1.8	85	2	Q4RAX0_TETNG	Q4RAX0 tetradon n	1055	6	1.8	96	2	Q715B8_9ECHI	Q715B8 ophiophis
983	6	1.8	86	2	Q5D218_VEST	Q5D218 halictie as	1056	6	1.8	96	2	Q8W6C5_BPG4	Q8W6C5 bacterioph
984	6	1.8	86	2	Q4TT97_CABEL	Q4TT97 caenorhabdi	1057	6	1.8	96	2	Q5GRR2_WOLFR	Q5GRR2 wolbachia s
985	6	1.8	86	2	Q84YJ6_ARATH	Q84YJ6 arabidopsis	1058	6	1.8	96	2	Q5E8E7_VIBF1	Q5E8E7 vibrio fisc
986	6	1.8	86	2	Q53845_SPICI	Q53845 spiroplasma	1059	6	1.8	96	2	Q8XIM6_9ENTR	Q8XIM6 buchiera ap
987	6	1.8	86	2	Q9EUC4_SRRMA	Q9EUC4 serratia ma	1060	6	1.8	96	2	Q8XIM6_9ENTR	Q8XIM6 buchiera ap
988	6	1.8	86	2	Q9EXM6_9ENTR	Q9EXM6 enterobacte	1061	6	1.8	96	2	Q4QNO6_HAE18	Q4QNO6 haemophilus
989	6	1.8	86	2	Q9EXM8_9ENTR	Q9EXM8 enterobacte	1062	6	1.8	96	2	Q83DL6_COXBU	Q83DL6 coxiella bu
990	6	1.8	86	2	Q8YU64_ANASP	Q8YU64 anabeena sp	1063	6	1.8	96	2	Q5QVY3_IDILIO	Q5QVY3 idiomarina
991	6	1.8	87	2	Q527N3_MAGSR	Q527N3 magnaporthe	1064	6	1.8	96	2	Q65LY8_BACLD	Q65LY8 bacillus li
992	6	1.8	87	2	Q79P19_BAGSR	Q79P19 bacillus su	1065	6	1.8	97	1	CC17_MOUSE	CC17 mus musculu
993	6	1.8	88	2	Q4X1Y5_PLACH	Q4X1Y5 plasmodium	1066	6	1.8	97	1	CH10_BUCBP	CH10_BUCBP
994	6	1.8	88	2	Q4TZ19_SFABA	Q4TZ19 vigna radia	1067	6	1.8	97	1	CH10_BUCBP	CH10_BUCBP
995	6	1.8	88	2	Q6189_ENTTAS	Q6189 enterobacte	1068	6	1.8	97	1	CH10_BUCPS	CH10_BUCPS
996	6	1.8	88	2	Q66191_ENTT	Q66191 enterobacte	1069	6	1.8	97	1	CH10_BUCTT	CH10_BUCTT
997	6	1.8	88	2	Q66193_ENTTGE	Q66193 enterobacte	1070	6	1.8	97	1	CH10_BUCTS	CH10_BUCTS
998	6	1.8	88	2	Q66195_ENTTAM	Q66195 enterobacte	1071	6	1.8	97	1	CH10_BUCTT	CH10_BUCTT
999	6	1.8	88	2	Q66197_ENTTAE	Q66197 enterobacte	1072	6	1.8	97	1	CH10_BUCTT	CH10_BUCTT
1000	6	1.8	88	2	Q66201_SRRU	Q66201 serratia ru	1073	6	1.8	97	1	CH10_EC057	CH10_EC057
1001	6	1.8	88	2	Q66203_SRRF1	Q66203 serratia fi	1074	6	1.8	97	1	CH10_EC016	CH10_EC016
1002	6	1.8	88	2	Q66205_SRRMA	Q66205 serratia ma	1075	6	1.8	97	1	CH10_EC011	CH10_EC011
1003	6	1.8	88	2	Q66207_KLEPN	Q66207 klebsiella	1076	6	1.8	97	1	CH10_ENTAB	CH10_ENTAB
1004	6	1.8	88	2	Q66209_KLEFX	Q66209 klebsiella	1077	6	1.8	97	1	CH10_ERMCT	CH10_ERMCT
1005	6	1.8	88	2	Q66211_KLEPL	Q66211 klebsiella	1078	6	1.8	97	1	CH10_SALTI	CH10_SALTI
1006	6	1.8	88	2	Q66213_KLEOR	Q66213 klebsiella	1079	6	1.8	97	1	CH10_SALTI	CH10_SALTI
1007	6	1.8	88	2	Q66217_PANAN	Q66217 pantoea ana	1080	6	1.8	97	1	CH10_SHIFL	CH10_SHIFL
1008	6	1.8	88	2	Q66219_ERWCA	Q66219 erwina car	1081	6	1.8	97	1	CH10_WIGBR	CH10_WIGBR
1009	6	1.8	88	2	Q66221_ERWAP	Q66221 erwina aph	1082	6	1.8	97	1	CH10_XANMA	CH10_XANMA
1010	6	1.8	88	2	Q31217_DESVU	Q31217 desulfovibr	1083	6	1.8	97	1	GATC2_CLOAB	GATC2 cloab
1011	6	1.8	88	2	Q66199_ENTTAC	Q66199 enterobacte	1084	6	1.8	97	2	Q6TUT1_ASCSV	Q6TUT1 asciscu
1012	6	1.8	88	2	Q66215_ENTTAC	Q66215 enterobacte	1085	6	1.8	97	2	Q8MXM8_DICDI	Q8MXM8 dicodi
1013	6	1.8	88	2	Q72EL6_DESVH	Q72EL6 desulfovibr	1086	6	1.8	97	2	Q70XF1_DROAV	Q70XF1 droav
1014	6	1.8	88	2	Q4T082_TETNG	Q4T082 tetradon n	1087	6	1.8	97	2	Q6ASV5_ORYSA	Q6ASV5 oryza
1015	6	1.8	89	2	Q81E81_PLAF7	Q81E81 plasmydia	1088	6	1.8	97	2	Q9FAB9_9BACT	Q9FAB9 bacilli ma
1016	6	1.8	89	2	Q8L1J37_ORYSA	Q8L1J37 oryza sativ	1089	6	1.8	97	2	Q7BGB6_RCOLI	Q7BGB6 rcoli
1017	6	1.8	89	2	Q33687_9ENTR	Q33687 primary end	1090	6	1.8	97	2	Q6LXK1_PHOFR	Q6LXK1 phofr
1018	6	1.8	89	2	Q73NM2_TREDE	Q73NM2 treponema d	1091	6	1.8	97	2	Q5FL63_SALPA	Q5FL63 salpa
1019	6	1.8	89	2	Q8DJNC2_SYNEL	Q8DJNC2 synechococc	1092	6	1.8	97	2	Q7U349_CANBP	Q7U349 canbp
1020	6	1.8	90	2	Q6ZD73_ORYSA	Q6ZD73 oryza sativ	1093	6	1.8	97	2	Q5SVU0_MOUSE	Q5SVU0 mouse
1021	6	1.8	90	2	Q6NFP3_CORDI	Q6NFP3 corynebacte	1094	6	1.8	97	2	Q4PIY1_9Z2ZZ	Q4PIY1 z2zzz
1022	6	1.8	90	2	Q5LZX4_SRR1	Q5LZX4 streptococc	1095	6	1.8	98	1	CC1A3_CANPA	CC1A3 canpa
1023	6	1.8	91	2	Q86BD7_DROME	Q86BD7 dirosophila	1096	6	1.8	98	1	NU4LM_BALMU	NU4LM balmu
1024	6	1.8	91	2	Q9N038_MACFA	Q9N038 macaca fasc	1097	6	1.8	98	1	NU4LM_BALPH	NU4LM balph
1025	6	1.8	91	2	Q56ZHO_ARATH	Q56ZHO arabidopsis	1098	6	1.8	98	1	NU4LM_MUNFE	NU4LM munfe
1026	6	1.8	92	1	Y1050_HAEIN	Y1050 haemophilus	1099	6	1.8	98	1	NU4LM_MUNGO	NU4LM mungo
1027	6	1.8	92	2	Q4QUN3_HAE18	Q4QUN3 haemophilus	1100	6	1.8	98	1	NU4LM_MUNVU	NU4LM munvu
1028	6	1.8	92	2	Q64UJ73_BACFR	Q64UJ73 bacteroides	1101	6	1.8	98	1	NU4LM_RABIT	NU4LM rabbit
1029	6	1.8	93	2	Q64BM1_PARCA	Q64BM1 uncultured	1102	6	1.8	98	1	PRRP_BOVIN	PRRP bovin
1030	6	1.8	93	2	Q9X7B6_MYCLE	Q9X7B6 mycobacteri	1103	6	1.8	98	2	PRRP_SHEEP	PRRP sheep
1031	6	1.8	93	2	Q6MJN7_BDEBA	Q6MJN7 bdellovibri	1104	6	1.8	98	2	Q556E0_DICDI	Q556E0 dicodi
1032	6	1.8	93	2	Q4SDK3_TETNG	Q4SDK3 tetradon n	1105	6	1.8	98	2	Q679A3_9CARN	Q679A3 carn
1033	6	1.8	94	2	Q65SH8_MANSM	Q65SH8 manheimia	1106	6	1.8	98	2	Q69B62_BALAC	Q69B62 balac
1034	6	1.8	95	1	CH10_ALTHA	CH10 alteromonas	1107	6	1.8	98	2	Q69B66_BALBN	Q69B66 balbn
1035	6	1.8	95	2	Q7RUJ73_NEUCR	Q7RUJ73 neurospora	1108	6	1.8	98	2	Q69B76_DELIS	Q69B76 delis
1036	6	1.8	95	2	Q5SMZ7_ORYSA	Q5SMZ7 oryza sativ	1109	6	1.8	98	2	Q69B78_EUBAS	Q69B78 eubas
1037	6	1.8	95	2	Q57B59_BRUBA	Q57B59 pseudocalt	1110	6	1.8	98	2	Q69B80_9CERA	Q69B80 cera
1038	6	1.8	95	2	Q9AJB6_9GAMM	Q9AJB6 pseudocalt	1111	6	1.8	98	2	Q69B84_MEGNO	Q69B84 megn
1039	6	1.8	95	2	Q8FTN4_BRUSU	Q8FTN4 brucella su	1112	6	1.8	98	2	Q69B86_ZIPCA	Q69B86 zipca
1040	6	1.8	95	2	Q61EB1_ORYSLA	Q61EB1 oryzias lat	1113	6	1.8	98	2	Q70RZ3_BALAC	Q70RZ3 balac
1041	6	1.8	96	1	CH101_VIBCH	CH101 vibrio chol	1114	6	1.8	98	2	Q70S06_ESCGI	Q70S06 escgi
1042	6	1.8	96	1	CH101_VIBPA	CH101 vibrio para	1115	6	1.8	98	2	Q70S32_BALMU	Q70S32 balmu
1043	6	1.8	96	1	CH101_VIBVU	CH101 vibrio vuln	1116	6	1.8	98	2	Q71VU7_MUNMU	Q71VU7 munmu
1044	6	1.8	96	1	CH101_VIBVY	CH101 vibrio vuln	1117	6	1.8	98	2	Q71VU9_MUNMU	Q71VU9 munmu
1045	6	1.8	96	1	CH10_ACTAC	CH10 actinobacil	1118	6	1.8	98	2	Q71VU0_MUNMU	Q71VU0 munmu
1046	6	1.8	96	1	CH10_ACTPL	CH10 actinobacil	1119	6	1.8	98	2	Q71VU1_MUNMU	Q71VU1 munmu
1047	6	1.8	96	1	CH10_BUCAP	CH10 buchiera ap	1120	6	1.8	98	2	Q71VU6_MUNKB	Q71VU6 munkb
1048	6	1.8	96	1	CH10_BUCAP	CH10 buchiera ap	1121	6	1.8	98	2	Q71VU6_MUNKB	Q71VU6 munkb
1049	6	1.8	96	1	CH10_BUCMP	CH10 buchiera ap	1122	6	1.8	98	2	Q85RW9_MUNMU	Q85RW9 munmu
1050	6	1.8	96	1	CH10_HAEIN	CH10 haemophilus	1123	6	1.8	98	2	Q8LWPA_TUPGB	Q8LWPA tupga
1051	6	1.8	96	1	CH10_PASMU	CH10 pasteurella	1124	6	1.8	98	2	Q94YCS_PIPAB	Q94YCS pipab
1052	6	1.8	96	1	CH10_PHOFR	CH10 photobacter	1125	6	1.8	98	2	Q9B1C5_MUNCR	Q9B1C5 muncr
1053	6	1.8	96	1	CH10_SHRON	CH10 shewanella	1126	6	1.8	98	2	Q9B9Y1_MUNMU	Q9B9Y1 munmu



1127	6	1.8	98	2	09G3R5_CHARTU	09G3R5_chalinojobu	1200	6	1.8	101	2	05C573_SCHUA	05C573_schistosoma
1128	6	1.8	98	2	09GA22_RUPGB	09GA22_tupaia glis	1201	6	1.8	101	2	08MKN8_DROME	08MKN8_drosophila
1129	6	1.8	98	2	0599C1_BALEN	0599C1_balaenopter	1202	6	1.8	101	2	09SK94_MACPA	09SK94_macaca fasc
1130	6	1.8	98	2	0598U3_3CETA	0598U3_eubalaena j	1203	6	1.8	101	2	06YNE6_MOUSE	06YNE6_mus muscull
1131	6	1.8	98	2	06PVM3_3CAUD	06PVM3_pseudomnas	1204	6	1.8	101	2	04RHX1_TETNG	04RHX1_tetraodon n
1132	6	1.8	98	2	07X811_ORYSA	07X811_oryza sativ	1205	6	1.8	101	2	04SGR2_TETNG	04SGR2_tetraodon n
1133	6	1.8	98	2	04LYR4_2BURK	04LYR4_burkholderi	1206	6	1.8	102	1	CH101_VIBNA	083V9_vibrio harv
1134	6	1.8	98	2	09QEW0_3CORO	09QEW0_porcine res	1207	6	1.8	102	2	0608Y6_METCA	0608Y6_methylcoc
1135	6	1.8	98	2	09QEW1_3CORO	09QEW1_porcine res	1208	6	1.8	102	2	09DFZ5_XENLA	09DFZ5_xenopus lae
1136	6	1.8	98	2	09QEW2_3CORO	09QEW2_porcine res	1209	6	1.8	102	2	04S175_TETNG	04S175_tetraodon n
1137	6	1.8	99	1	CCL2_HORSE	09133 equus caball	1210	6	1.8	102	2	091931_9HIV2	091931_human immu
1138	6	1.8	99	1	CCL2_HUMAN	P13500 homo sapien	1211	6	1.8	102	2	09YVG5_9HIV2	09YVG5_human immu
1139	6	1.8	99	1	CCL2_MACPA	P1274 macaca fasc	1212	6	1.8	103	2	05A411_CANAL	05A411_candida alb
1140	6	1.8	99	1	CCL2_MACMU	P12175 macaca mula	1213	6	1.8	103	2	081PRL_DROME	081PRL_drosophila
1141	6	1.8	99	1	CCL2_PIG	PA2831 sus scrofa	1214	6	1.8	103	2	09UIP6_CABSL	09UIP6_caenorhabdi
1142	6	1.8	99	1	CCL2_PONPY	05RA28 pongo pygma	1215	6	1.8	103	2	06H891_ORYSA	06H891_oryza sativ
1143	6	1.8	99	1	CCL7_HUMAN	P80098 homo sapien	1216	6	1.8	103	2	06BXT5_RICCY	06BXT5_rickettsia
1144	6	1.8	99	1	CCL8_BOVIN	009141 bos taurus	1217	6	1.8	103	2	08WMS9_BRLJA	08WMS9_bradrythzob
1145	6	1.8	99	1	CCL8_CANPA	068849 canis famli	1218	6	1.8	103	2	08XK86_CLOPE	08XK86_clostridium
1146	6	1.8	99	1	CCL8_HUMAN	P80075 homo sapien	1219	6	1.8	103	2	091930_9HIV2	091930_human immu
1147	6	1.8	99	1	CCL8_PIG	PA9873 sus scrofa	1220	6	1.8	104	1	CCL12_MOUSE	062401 mus muscull
1148	6	1.8	99	1	MCPA_BOVIN	P82931 bos taurus	1221	6	1.8	104	2	0874U5_SCYSE	0874U5_scylla sexr
1149	6	1.8	99	2	09C235_NEUCR	09C235_neutrosora	1222	6	1.8	104	2	04XWG0_PLACH	04XWG0_plasmodium
1150	6	1.8	99	2	0569U6_HUMAN	Q569J6 homo sapien	1223	6	1.8	104	2	0420Z8_ARATH	0420Z8_arabidopsis
1151	6	1.8	99	2	P92624_DIOAS	P92624_diodora asp	1224	6	1.8	104	2	06EUE0_ORYSA	06EUE0_oryza sativ
1152	6	1.8	99	2	0516F8_CANPA	0516F8_canis famli	1225	6	1.8	104	2	05WAE9_BACSK	05WAE9_bacillus cl
1153	6	1.8	99	2	05KSU7_CANPA	05KSU7_canis famli	1226	6	1.8	104	2	09FPM5_STRCO	09FPM5_streptococ
1154	6	1.8	99	2	06XVMS_MACNE	06XVMS_macaca neme	1227	6	1.8	104	2	074BS9_GEOSL	074BS9_geobacter s
1155	6	1.8	99	2	0865F4_MACNE	0865F4_macaca neme	1228	6	1.8	104	2	05SVB4_MOUSE	05SVB4_mus muscull
1156	6	1.8	99	2	08MKC8_HORSE	08MKC8_equus caball	1229	6	1.8	104	2	091929_9HIV2	091929_human immu
1157	6	1.8	99	2	08HYQ0_MACMU	08HYQ0_macaca mula	1230	6	1.8	104	2	091934_9HIV2	091934_human immu
1158	6	1.8	99	2	07IME7_MACMU	Q7IME7_macaca mula	1231	6	1.8	105	2	051IR1_MAGGR	051IR1_magnaporthe
1159	6	1.8	99	2	08GBV8_OSCAG	08GBV8_planttochri	1232	6	1.8	105	2	060384_HUMAN	060384_homo sapien
1160	6	1.8	99	2	08GBV9_3CYAN	08GBV9_planttochri	1233	6	1.8	105	2	070332_ANOGA	070332_anopheles g
1161	6	1.8	99	2	08GBW0_3CYAN	08GBW0_planttochri	1234	6	1.8	105	2	05DAB6_SCHUA	05DAB6_schistosoma
1162	6	1.8	99	2	08GBW1_3CYAN	08GBW1_planttochri	1235	6	1.8	105	2	05ZAI9_ORYSA	05ZAI9_oryza sativ
1163	6	1.8	99	2	08GBW2_3CYAN	08GBW2_planttochri	1236	6	1.8	105	2	04RA95_TETNG	04RA95_tetraodon n
1164	6	1.8	99	2	08GBW3_OSCAG	08GBW3_planttochri	1237	6	1.8	106	2	0847N9_ASTYP	0847N9_aeter yell
1165	6	1.8	99	2	08GBW4_OSCAG	08GBW4_planttochri	1238	6	1.8	106	2	0921Z5_RICCN	0921Z5_rickettsia
1166	6	1.8	99	2	08GBW5_OSCAG	08GBW5_planttochri	1239	6	1.8	106	2	091928_9HIV2	091928_human immu
1167	6	1.8	99	2	08GBZ0_3NOSO	Q8GBZ0_nostoc sp.	1240	6	1.8	106	2	091932_9HIV2	091932_human immu
1168	6	1.8	99	2	08GF14_3NOST	08GF14_anabaena sp	1241	6	1.8	107	2	06CMN4_KLUDL	06CMN4_kluyveromyc
1169	6	1.8	99	2	08GF15_3NOST	08GF15_anabaena sp	1242	6	1.8	107	2	04ZC10_9CAUD	04ZC10_bacterioph
1170	6	1.8	99	2	08GF16_3NOST	08GF16_anabaena sp	1243	6	1.8	107	2	0516S1_BORBU	0516S1_borrelia bu
1171	6	1.8	99	2	08GF17_3NOST	08GF17_anabaena le	1244	6	1.8	107	2	05NMG0_ZYMMO	05NMG0_zygomonas m
1172	6	1.8	99	2	08GF18_3NOST	08GF18_anabaena ci	1245	6	1.8	107	2	06GCM5_STARK	06GCM5_staphylococ
1173	6	1.8	99	2	08GFN4_ANAFL	Q8GFN4_anabaena fi	1246	6	1.8	107	2	08CAE6_MOUSE	08CAE6_mus muscull
1174	6	1.8	99	2	04TFE0_TETNG	Q4TFE0_tetraodon n	1247	6	1.8	107	2	091IT9_TUHV1	091IT9_tupaiid her
1175	6	1.8	99	2	06L7Q5_9DELA	Q6L7Q5_human t-lym	1248	6	1.8	107	2	04PRT2_MNV	04PRT2_west nile v
1176	6	1.8	99	2	06L7V4_9DELA	Q6L7V4_human t-lym	1249	6	1.8	107	2	04PRT3_MNV	04PRT3_west nile v
1177	6	1.8	99	2	08UI16_9HIV1	Q8UI16_human immu	1250	6	1.8	107	2	04PRT4_MNV	04PRT4_west nile v
1178	6	1.8	99	2	09IXS2_9HIV1	Q9IXS2_human immu	1251	6	1.8	107	2	04PRT5_MNV	04PRT5_west nile v
1179	6	1.8	99	2	098X59_9HIV1	Q98X59_human immu	1252	6	1.8	107	2	04PRT6_MNV	04PRT6_west nile v
1180	6	1.8	100	1	CCL11_HORSE	Q9CTG4_equus caball	1253	6	1.8	107	2	04RFB6_TETNG	04RFB6_tetraodon n
1181	6	1.8	100	1	NVOK_ECOLI	P33606 escherichia	1254	6	1.8	107	2	091910_9HIV2	091910_human immu
1182	6	1.8	100	1	YICE_BACSU	Q31627 bacillus su	1255	6	1.8	107	2	091920_9HIV2	091920_human immu
1183	6	1.8	100	2	Q9POF3_HUMAN	Q9POF3_homo sapien	1256	6	1.8	107	2	091927_9HIV2	091927_human immu
1184	6	1.8	100	2	Q4N4W1_THERA	Q4N4W1_thellieria p	1257	6	1.8	107	2	077WP8_9HIV2	077WP8_human immu
1185	6	1.8	100	2	Q8LIN51_ORYSA	Q8LIN51_oryza sativ	1258	6	1.8	107	2	077WP8_9HIV2	077WP8_human immu
1186	6	1.8	100	2	Q5EIK0_VIBFI	Q5EIK0_vibrio fisc	1259	6	1.8	107	2	09YIL5_9HIV2	09YIL5_human immu
1187	6	1.8	100	2	057M37_SALCH	Q57M37_salmonella	1260	6	1.8	107	2	09YVF6_9HIV2	09YVF6_human immu
1188	6	1.8	100	2	093IA4_STANU	Q93IA4_staphylococ	1261	6	1.8	107	2	09YVG7_9HIV2	09YVG7_human immu
1189	6	1.8	100	2	Q4UM11_RICPE	Q4UM11_rickettsia	1262	6	1.8	107	2	09YVH2_9HIV2	09YVH2_human immu
1190	6	1.8	100	2	Q7CQ53_SALTY	Q7CQ53_salmonella	1263	6	1.8	107	2	YCF54_FORPU	YCF54_forpura pu
1191	6	1.8	100	2	Q7N2U6_PHOHL	Q7N2U6_photobact	1264	6	1.8	108	1	07PC93_MAI2E	07PC93_maia
1192	6	1.8	100	2	Q8ZDL6_YERPE	Q8ZDL6_yersinia pe	1265	6	1.8	108	2	053NY6_ORYSA	053NY6_oryza sativ
1193	6	1.8	100	2	Q5PN65_SALPA	Q5PN65_salmonella	1266	6	1.8	108	2	044706_BORBU	044706_borrelia bu
1194	6	1.8	100	2	Q8XPA3_SALTI	Q8XPA3_salmonella	1267	6	1.8	108	2	045800_BACVU	045800_bacteroides
1195	6	1.8	100	2	Q669A9_YERPS	Q669A9_yersinia ps	1268	6	1.8	108	2	08KYR7_BACPR	08KYR7_bacteroides
1196	6	1.8	100	2	Q6D2S6_ERWCT	Q6D2S6_erwinia car	1269	6	1.8	108	2	Q4MOB4_9BUDK	Q4MOB4_burkholderi
1197	6	1.8	101	1	CCL2_CANPA	P52203 canis famli	1270	6	1.8	109	2	058093_PYRIO	058093_pyrococcus
1198	6	1.8	101	1	YGVA_YEAST	P53089 saccharomyc	1271	6	1.8	109	2	0727Q8_HUMAN	0727Q8_homo sapien
1199	6	1.8	101	2	Q4P3P8_USTWA	Q4P3P8_utililago ma	1272	6	1.8	109	2		



1273	6	1.8	109	2	Q4YU6_PLABE	Q4YU6_plasmidium	1346	6	1.8	118	1	VATG1_PANTR	O86Z6_pan_troglod
1274	6	1.8	109	2	Q6R58_SBACT	Q6R58_uncultured	1347	6	1.8	118	1	VATG2_HUMAN	O956T_homo sapien
1275	6	1.8	109	2	Q5YNZ6_NOCFA	Q5YNZ6_nocardia fa	1348	6	1.8	118	1	VATG2_MACMU	O5TM2_macha mula
1276	6	1.8	109	2	O88CE9_PSEPK	O88CE9_pseudomonas	1349	6	1.8	118	1	VATG2_MOUSE	O9T46_mus musculus
1277	6	1.8	109	2	Q5M419_STRT2	Q5M419_streptococc	1350	6	1.8	118	1	VATG2_PIG	O9T86_sus scrofa
1278	6	1.8	109	2	Q4S7R3_TETNG	Q4S7R3_tetradodon n	1351	6	1.8	118	2	Q4LIC2_9MAXI	Q4LIC2_lepeophthei
1279	6	1.8	110	2	Q5VAP1_HALMA	Q5VAP1_halaeconom	1352	6	1.8	118	2	Q7CX77_AGRYS	Q7CX77_agrobacteri
1280	6	1.8	110	2	Q7PE28_ANOCA	Q7PE28_anopheles g	1353	6	1.8	118	2	Q5LVJ1_SILPO	Q5LVJ1_silicibacte
1281	6	1.8	110	2	Q8T416_DROME	Q8T416_drosophila	1354	6	1.8	118	2	Q72A06_DESVH	Q72A06_desulfovibr
1282	6	1.8	110	2	Q5NBM6_ORYSA	Q5NBM6_oryza sativ	1355	6	1.8	118	2	Q8R2H0_RAT	O8R2H0_rattus norv
1283	6	1.8	110	2	Q571P2_AERPU	Q571P2_aeromonas p	1356	6	1.8	118	2	Q54A87_MOUSE	Q54A87_mus musculu
1284	6	1.8	110	2	Q4NFO5_9MICC	Q4NFO5_athrobacte	1357	6	1.8	118	2	Q9CRB3_MOUSE	Q9CRB3_mus muscu
1285	6	1.8	110	2	Q5RIE7_MOUSE	Q5RIE7_mus musculu	1358	6	1.8	118	2	Q5D9D6_SCHJA	Q5D9D6_schistosoma
1286	6	1.8	110	2	Q4Z454_TIRASC	Q4Z454_tirachemys s	1359	6	1.8	119	2	Q7RG12_PLAYO	Q7RG12_plasmidium
1287	6	1.8	111	1	RBFA_HELPJ	Q9ZM45_helicobacte	1360	6	1.8	119	2	Q4UZ29_XANCP	Q4UZ29_xanthomonas
1288	6	1.8	111	1	RBFA_HELPJ	Q5Y955_pyrococcus	1361	6	1.8	119	2	Q4P020_9DELT	Q4P020_aeromonas
1289	6	1.8	111	2	Q9UY95_PYPAB	Q9UY95_pyrococcus	1362	6	1.8	119	2	Q4P020_9DELT	Q4P020_aeromonas
1290	6	1.8	111	2	O8LHY8_ORYSA	O8LHY8_oryza sativ	1363	6	1.8	119	2	Q7W7B7_BORPA	Q7W7B7_bordetella
1291	6	1.8	111	2	O6LPTS_PHOPR	O6LPTS_photobacter	1364	6	1.8	119	2	O8PDQ7_XANCP	O8PDQ7_xanthomonas
1292	6	1.8	111	2	Q9HW55_PSEAR	Q9HW55_pseudomonas	1365	6	1.8	119	2	O8FQW8_XANCP	O8FQW8_xanthomonas
1293	6	1.8	111	2	O6N2H1_RHOPA	O6N2H1_rhodopseudo	1366	6	1.8	119	2	Q5XW58_MOUSE	Q5XW58_mus musculu
1294	6	1.8	111	2	O6FYF8_BAROV	O6FYF8_barthelme	1367	6	1.8	120	1	CCL2_CAVPO	O08782_cavia porce
1295	6	1.8	111	2	O8L1A7_RAT	O8L1A7_rattus norv	1368	6	1.8	120	1	Y5866_RHIME	Q92UG5_thizobium m
1296	6	1.8	112	2	O8ZTR9_PYPAR	O8ZTR9_pyrobaculum	1369	6	1.8	120	2	O5BSF2_SCHJA	O5BSF2_schistosoma
1297	6	1.8	112	2	Q03884_YEAST	Q03884_saccharomyc	1370	6	1.8	120	2	O86J35_DICDI	O86J35_dicystosteli
1298	6	1.8	112	2	Q7RQ76_PLAYO	Q7RQ76_plasmidium	1371	6	1.8	120	2	Q4QBS1_LEIMA	Q4QBS1_leishmania
1299	6	1.8	112	2	Q931B3_STAAU	Q931B3_staphylococ	1372	6	1.8	120	2	Q6LHC6_PHOPR	Q6LHC6_photobacter
1300	6	1.8	112	2	O8YOL8_RALSO	O8YOL8_ralstonia s	1373	6	1.8	120	2	O8C659_MOUSE	O8C659_mus musculu
1301	6	1.8	113	1	MIH_CALSI	P55321_callicnectes	1374	6	1.8	120	2	Q6IN12_XENLA	Q6IN12_xenopus lae
1302	6	1.8	113	2	Q7RGX8_PLAYO	Q7RGX8_plasmidium	1375	6	1.8	121	2	Q95TDD_DROME	Q95TDD_drosophila
1303	6	1.8	113	2	Q35015_MELUA	Q35015_meloidogyne	1376	6	1.8	121	2	O6Z1T7_ORYSA	O6Z1T7_oryza sativ
1304	6	1.8	113	2	O8ROR1_LACAC	O8ROR1_lactobacilli	1377	6	1.8	122	2	O8U1X6_PYPFU	O8U1X6_pyrococcus
1305	6	1.8	113	2	O57PA7_SALCH	O57PA7_salmonella	1378	6	1.8	122	2	Q8PS76_METWA	O8PS76_methanosarc
1306	6	1.8	113	2	Q4NM27_9MICC	Q4NM27_athrobacte	1379	6	1.8	122	2	Q8N8P7_HUMAN	Q8N8P7_homo sapien
1307	6	1.8	113	2	Q4ZX29_PSESY	Q4ZX29_pseudomonas	1380	6	1.8	122	2	Q9NV16_HUMAN	Q9NV16_homo sapien
1308	6	1.8	113	2	Q4K6U3_PSEFS	Q4K6U3_pseudomonas	1381	6	1.8	122	2	Q4VY08_HUMAN	Q4VY08_homo sapien
1309	6	1.8	113	2	O5PN89_SALPA	O5PN89_salmonella	1382	6	1.8	122	2	O6E2A0_ARATH	O6E2A0_arabidopsis
1310	6	1.8	113	2	O8UCV9_AGRIS	O8UCV9_agrobacteri	1383	6	1.8	122	2	O6K851_ORYSA	O6K851_oryza sativ
1311	6	1.8	113	2	O8ZPH6_SALTY	O8ZPH6_salmonella	1384	6	1.8	122	2	Q9AF23_9BACT	Q9AF23_uncultured
1312	6	1.8	113	2	Q7VXG6_BORPE	Q7VXG6_bordetella	1385	6	1.8	122	2	O5SHK5_THETR8	O5SHK5_thermus the
1313	6	1.8	113	2	Q7W8U8_BORPA	Q7W8U8_bordetella	1386	6	1.8	122	2	O89YH2_BACTN	O89YH2_bacteroides
1314	6	1.8	113	2	Q7WKS8_BORBR	Q7WKS8_bordetella	1387	6	1.8	122	2	O9H2U9_PSEBAR	O9H2U9_pseudomonas
1315	6	1.8	113	2	O886Z6_PSESM	O886Z6_bordetella	1388	6	1.8	122	2	O8CTD7_MOUSE	O8CTD7_mus musculu
1316	6	1.8	114	2	O8IWS4_HUMAN	O8IWS4_homo sapien	1389	6	1.8	123	1	Y5489_RHIME	O92V09_thizobium m
1317	6	1.8	114	2	O8U957_AGRIS	O8U957_agrobacteri	1390	6	1.8	123	2	Q64K37_9ACAR	Q64K37_caenorhabdit
1318	6	1.8	114	2	Q7USA6_RHOBA	Q7USA6_rhodopirelli	1391	6	1.8	123	2	O6OMN6_CABBR	O6OMN6_cryptosporax
1319	6	1.8	115	1	IR02_HCMVA	P16802_human cytooma	1392	6	1.8	123	2	Q7ONT2_GIALA	Q7ONT2_giardia lam
1320	6	1.8	115	2	O57VG1_9TRYP	O57VG1_rypanosoma	1393	6	1.8	123	2	O6U6O8_9MOLL	O6U6O8_cryptosporax
1321	6	1.8	115	2	Q4QI14_LEIMA	Q4QI14_leishmania	1394	6	1.8	123	2	O6Z440_ORYSA	O6Z440_oryza sativ
1322	6	1.8	115	2	O5DYS5_VIBFI	O5DYS5_vibrio fisc	1395	6	1.8	123	2	Q4HRB4_CAMOP	Q4HRB4_campylobact
1323	6	1.8	115	2	O8CMM1_STABP	O8CMM1_staphylococ	1396	6	1.8	123	2	Q9RT46_DEIRA	Q9RT46_delmococcus
1324	6	1.8	115	2	O8YI66_BRUME	O8YI66_brucella me	1397	6	1.8	123	2	Q90137_MARMO	Q90137_marmota mon
1325	6	1.8	115	2	Q4PRT7_MNV	Q4PRT7_mus musculu	1398	6	1.8	123	2	Q9DDX9_XENLA	Q9DDX9_xenopus lae
1326	6	1.8	115	2	Q4PRT8_MNV	Q4PRT8_mus musculu	1399	6	1.8	124	1	AP0C4_FABIT	P55057_oryctolagus
1327	6	1.8	115	2	Q4PRT9_MNV	Q4PRT9_mus musculu	1400	6	1.8	124	1	KABI_ODAPF	P56254_oryctolagus
1328	6	1.8	115	2	Q4PRU0_MNV	Q4PRU0_mus musculu	1401	6	1.8	124	2	Q6XHS7_DROYA	Q6XHS7_drosophila
1329	6	1.8	115	2	Q4PRU1_MNV	Q4PRU1_mus musculu	1402	6	1.8	124	2	Q69MW8_ORYSA	Q69MW8_oryza sativ
1330	6	1.8	115	2	Q4PRU2_MNV	Q4PRU2_mus musculu	1403	6	1.8	124	2	Q7MPD6_BORBR	Q7MPD6_bordetella
1331	6	1.8	115	2	Q4PRU3_MNV	Q4PRU3_mus musculu	1404	6	1.8	124	2	Q92B29_LISIN	Q92B29_listeria in
1332	6	1.8	115	2	Q4TUA9_MNV	Q4TUA9_mus musculu	1405	6	1.8	124	2	Q65085_9PRIC	Q65085_fecr-and-im
1333	6	1.8	115	2	Q7ZEU9_SHITV	Q7ZEU9_human immun	1406	6	1.8	124	2	Q4S4Y0_TETNG	Q4S4Y0_tetradodon n
1334	6	1.8	116	2	O6C7E9_YARLI	O6C7E9_yarilia li	1407	6	1.8	125	1	CCL2_RABIT	Q48470_cryptosporax
1335	6	1.8	116	2	Q4P2K6_USTMA	Q4P2K6_ustilago ma	1408	6	1.8	125	2	O5TL98_CLAPU	P28232_oryctolagus
1336	6	1.8	116	2	O6NVJ2_HUMAN	O6NVJ2_homo sapien	1409	6	1.8	125	2	O9DPZ6_XENLA	O9DPZ6_xenopus lae
1337	6	1.8	116	2	Q7VXO3_CAREL	Q7VXO3_cenorchabdi	1410	6	1.8	126	1	NU0A_BIOPAP	O8K9P7_bufo xeno
1338	6	1.8	116	2	O8Z3C0_CHLCV	O8Z3C0_chlamydomphi	1411	6	1.8	126	1	YIGF_BCOLI	P27842_escherichia
1339	6	1.8	116	2	O8XJV0_CLOPR	O8XJV0_clostridium	1412	6	1.8	126	1	YIGF_SALTY	P0AL8_salmonella
1340	6	1.8	117	2	O59ZS2_CANAL	O59ZS2_candida alb	1413	6	1.8	126	1	YIGF_SALTY	P0AL8_salmonella
1341	6	1.8	117	2	Q7QOQ5_ANOGA	Q7QOQ5_anopheles g	1414	6	1.8	126	2	P95861_SULSO	P95861_sulfolobus
1342	6	1.8	117	2	O7NKM9_PHOGL	O7NKM9_photobacter	1415	6	1.8	126	2	O9YEE3_AARPE	O9YEE3_aeropyrum p
1343	6	1.8	117	2	O8YUJ1_RALSO	O8YUJ1_ralstonia s	1416	6	1.8	126	2	Q7YIC7_ORYSA	Q7YIC7_oryza sativ
1344	6	1.8	117	2	O83063_TART	O83063_rattus norv	1417	6	1.8	127	2	O8J1W5_SHITL	O8J1W5_shigella fl
1345	6	1.8	118	1	VATG1_CANPA	Q5W709_canis famli	1418	6	1.8	127	2	O5QULW7_ORYSA	O5QULW7_oryza sativ



1419	6	1.8	127	2	08E1W3_SHEON	08e1w3 shewanella
1420	6	1.8	127	2	010457_VIVIRU	010457 venezuelan
1421	6	1.8	127	2	010460_VIVIRU	010460 venezuelan
1422	6	1.8	127	2	010461_VIVIRU	010461 venezuelan
1423	6	1.8	127	2	039813_EMCV	039813 encephalomy
1424	6	1.8	127	2	039DU1_XENULA	039du1 xenopus lae
1425	6	1.8	127	2	039DU1_XENULA	039du1 xenopus lae
1426	6	1.8	128	1	US384_GAHVG	US384 gallid herp
1427	6	1.8	128	1	W339_PASMU	W339 pseudomonas
1428	6	1.8	128	1	04J7E1_SULAC	04j7e1 sulfobolus
1429	6	1.8	128	2	05UX97_HALMA	05ux97 haloarcula
1430	6	1.8	128	2	0617P1_BOMKO	0617p1 bomdix mori
1431	6	1.8	128	2	09B030_VIVIRU	09b030 bacterioph
1432	6	1.8	128	2	094163_ORYSA	094163 oryza sativ
1433	6	1.8	128	2	07X3J9_PSEPU	07x3j9 pseudomonas
1434	6	1.8	128	2	07N0X8_PHOIL	07n0x8 photorhabd
1435	6	1.8	128	2	0928A1_LISTIN	0928a1 listeria in
1436	6	1.8	128	2	09RVX6_DEIRA	09rvx6 deinetococcus
1437	6	1.8	128	2	071WT6_LISMF	071wt6 listeria mo
1438	6	1.8	128	2	08Y4F2_LISMO	08y4f2 listeria mo
1439	6	1.8	128	2	08C2V3_MOUSE	08c2v3 mus musculu
1440	6	1.8	129	2	08TR81_MERTAC	08tr81 methanosaer
1441	6	1.8	129	2	086KR5_DICDI	086kr5 dictyostell
1442	6	1.8	129	2	0862M3_BOVIN	0862m3 bos taurus
1443	6	1.8	129	2	071J88_LACDL	071j88 lactobacill
1444	6	1.8	129	2	084GY0_PHOIL	084gy0 photorhabd
1445	6	1.8	129	2	06N0D2_RHOPA	06n0d2 rhodospirab
1446	6	1.8	129	2	08NNM5_CORGL	08nnm5 corynebacte
1447	6	1.8	129	2	070WH4_PLAFB	070wh4 platichtlys
1448	6	1.8	130	1	Y6524_BACAN	Y6524 bacillus an
1449	6	1.8	130	2	05BXR3_SCHJA	05bxr3 schistosoma
1450	6	1.8	131	2	05HFR3_SALCH	05hfr3 salmonella
1451	6	1.8	131	2	05LKT1_SILPO	05lkt1 silicibacte
1452	6	1.8	131	2	06ABN0_PROAC	06abn0 propionibac
1453	6	1.8	132	2	07Y7V2_92YGO	07y7v2 cunnanghame
1454	6	1.8	132	2	07Q0Q9_GIALA	07q0q9 giardia lam
1455	6	1.8	132	2	08TR82_DROME	08tr82 drosophila
1456	6	1.8	132	2	09W2M8_DROME	09w2m8 drosophila
1457	6	1.8	132	2	05H2N3_XANOR	05h2n3 xanthomonas
1458	6	1.8	132	2	09A895_CAUOR	09a895 caulobacter
1459	6	1.8	132	2	09RT34_DEIRA	09rt34 deinetococcus
1460	6	1.8	132	2	09KA40_BACHD	09ka40 bacillus ha
1461	6	1.8	132	2	039815_EMCV	039815 encephalomy
1462	6	1.8	133	2	055212_9ETRE	055212 streptococc
1463	6	1.8	133	2	07UVZ6_RHOBA	07uvz6 rhodospirill
1464	6	1.8	133	2	04TG08_TETNG	04tg08 tetradodon n
1465	6	1.8	133	2	064A03_9ARCH	064a03 uncultured
1466	6	1.8	134	2	064BE7_9ARCH	064be7 uncultured
1467	6	1.8	134	2	04WZU9_ASPFU	04wzu9 aspergillus
1468	6	1.8	134	2	061WU7_DROME	061wu7 drosophila
1469	6	1.8	134	2	04FV15_DROME	04fv15 psychrobact
1470	6	1.8	134	2	069567_MYCLE	069567 mycobacteri
1471	6	1.8	134	2	07V2U6_PROMP	07v2u6 psycholoco
1472	6	1.8	134	2	06X779_MNV	06x779 kunjin viru
1473	6	1.8	134	2	09DDX4_XENULA	09ddx4 xenopus lae
1474	6	1.8	134	2	04RA34_TETNG	04ra34 tetradodon n
1475	6	1.8	135	2	06Z7T9_HOMAN	06z7t9 homo sapien
1476	6	1.8	135	2	0541D6_DICDI	0541d6 dictyostell
1477	6	1.8	135	2	029049_PIG	029049 sus scrofa
1478	6	1.8	135	2	070LPO_PASMU	070lpo pasteurella
1479	6	1.8	135	2	095012_MYCTU	095012 mycobacteri
1480	6	1.8	135	2	07TTC5_MYCBO	07ttc5 mycobacteri
1481	6	1.8	135	2	09GBH3_MYCBL	09gbh3 mycobacteri
1482	6	1.8	135	2	091380_PSEAB	091380 pseudomonas
1483	6	1.8	135	2	08DVRS_STRMU	08dvrs streptococc
1484	6	1.8	136	1	YEDX_SALTY	YEDX salmonella
1485	6	1.8	136	1	YEDX_SALTY	YEDX salmonella
1486	6	1.8	136	1	YEDX_SALTY	YEDX salmonella
1487	6	1.8	136	1	06THUS_DROME	06thus drosophila
1488	6	1.8	136	1	045382_CABEL	045382 cenothabidi
1489	6	1.8	136	2	06MNAO_CYNVA	06mnao cynoccephalu
1490	6	1.8	136	2	06TUD4_ORYSA	06tud4 oryza sativ
1491	6	1.8	136	2	06YF6_ORYSA	06yfe6 oryza sativ

1492	6	1.8	136	2	057Q08_SALCH	057q08 salmonella
1493	6	1.8	136	2	04VY45_SALDU	04vy45 salmonella
1494	6	1.8	136	2	04KGB3_PSEPS	04kgb3 pseudomonas
1495	6	1.8	136	2	05PG45_SALPA	05pg45 salmonella
1496	6	1.8	136	2	07P116_CHRYO	07p116 chromobacte
1497	6	1.8	136	2	09COK5_MOUSE	09cok5 m mus muscu
1498	6	1.8	136	2	06X767_MNV	06x767 kunjin viru
1499	6	1.8	136	2	06X768_MNV	06x768 kunjin viru
1500	6	1.8	136	2	06X769_MNV	06x769 kunjin viru
ALIGNMENTS						
RESULT 1						
SLAF7 HUMAN						
ID	SLAF7 HUMAN	STANDARD;	PRT;	335 AA.		
AC	Q9N0Z5; Q8N6Y8; Q8ND32; Q9NV08; Q9NV23;					
DT	13-SEP-2005 (Rel. 48, Created)					
DT	13-SEP-2005 (Rel. 48, Last sequence update)					
DT	13-SEP-2005 (Rel. 48, Last annotation update)					
DE	SLAM family member 7 precursor (CD2-like receptor activating cytotoxic cell) (CRACC) (Protein 19A) (Membrane protein FOAP-12) (CD2 subunit 1) (Novel Ly9).					
DE	Name=SLAMF7; Synonyms=CS1; ORFNames=UHQ576/PRO138;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	NCBIOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND TISSUE SPECIFICITY.					
RX	MEDLINE=21151549; PubMed=11220635; DOI=10.1007/s002510000274;					
RA	Bales K.S., Mathew P.A.;					
RT	"Molecular cloning of CS1, a novel human natural killer cell receptor belonging to the CD2 subset of the immunoglobulin superfamily.";					
RL	Immunogenetics 52:302-307(2001).					
RN	[2]					
RP	NCBIOTIDE SEQUENCE [MRNA] (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.					
RX	PubMed=11698418;					
RA	Bouchon A., Cella M., Grierson H.L., Cohen J.I., Colonna M.;					
RT	"Activation of NK cell-mediated cytotoxicity by a SAP-independent receptor of the CD2 family.";					
RL	J. Immunol. 167:5517-5521(2001).					
RN	[3]					
RP	NCBIOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 3), FUNCTION, AND TISSUE SPECIFICITY.					
RX	MEDLINE=2161458; PubMed=11802771; DOI=10.1042/0264-6021.3610431;					
RA	Murphy J.J., Hobby P., Villarino-Varela J., Bishop B., Iordanidou P., Sutton B.J., Norton J.D.;					
RT	"A novel immunoglobulin superfamily receptor (19A) related to CD2 is expressed on activated lymphocytes and promotes homotypic B-cell adhesion.";					
RL	Biochem. J. 361:431-436(2002).					
RN	[4]					
RP	NCBIOTIDE SEQUENCE [MRNA] (ISOFORM 1).					
RC	TISSUE=Macrophage;					
RA	Fujii Y., Takayama K., Teuriltani K., Yajima Y., Amemiya T., Ukai Y., Naito K., Kawaguchi A.;					
RT	"Homo sapiens mRNA for FOAP-12 protein, complete cds.";					
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.					
RN	[5]					
RP	NCBIOTIDE SEQUENCE [LARGE SCALE MRNA]					
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;					
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brueh J., Bacon D., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M.R., Robbie R., Sanchez C., Schoenfeld J., Sehnagiri S., Simmons L., Singh J., Smith V., Stinson J., Vages A., Vanden R.L., Watanabe C., Wieand D., Woods K., Xie M.-H., Yamsura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,					



RA Wood W.I., Godowski P.J., Gray A.M.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RT Genome Res. 13:2265-2270(2003).  
RN [6]  
RP Nucleotide sequence [LARGE SCALE MRNA] (ISOFORM 2).  
RC TISSUE=Lymph node;  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP Nucleotide sequence [LARGE SCALE GENOMIC DNA].  
RG Human chromosome 1 international sequencing consortium;  
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP Nucleotide sequence [LARGE SCALE MRNA] (ISOFORM 3).  
RC TISSUE=Fetal lung, and Fetal spleen;  
RL MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullan S.J.,  
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fehy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schneringer A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [9]  
RP PROTEIN SEQUENCE OF 23-37.  
RX PubMed=15340161; DOI=10.1110/ps.04682504;  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites.";  
RL Protein Sci. 13:2819-2824(2004).  
RN [10]  
RP ALTERNATIVE SPLICING.  
RX PubMed=15368295; DOI=10.1002/eji.200424917;  
RA Lee J.K., Boles K.S., Mathew P.A.;  
RT "Molecular and functional characterization of a CSI (CRACC) splice  
RT variant expressed in human NK cells that does not contain  
RT immunoreceptor tyrosine-based switch motifs.";  
RL Eur. J. Immunol. 34:2791-2799(2004).  
RN [11]  
RP TISSUE SPECIFICITY, AND SAP-BINDING.  
RX MEDLINE=22226696; PubMed=12242590; DOI=10.1007/s00251-002-0483-3;  
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Plazuela P.,  
RA Bosch J., Terhorst C., Engel P.;  
RT "Mouse novel Iy9: a new member of the expanding CD150 (SLAM) family of  
RT leukocyte cell surface receptors.";  
RL Immunogenetics 54:394-402(2002).  
RN [12]  
RP FUNCTION: Isoform 1 mediates NK cell activation through a SAP-  
RN independent extracellular signal-regulated ERK-mediated pathway.  
RN May play a role in lymphocyte adhesion. Isoform 3 does not mediate  
RN any activation. SAP can bind the cytoplasmic tail of isoform 1  
RN when phosphorylated in the presence of Fyn (in vitro).  
RN [13]  
RP SUBCELLULAR LOCATION: Type I membrane protein.  
RN [14]  
RP ALTERNATIVE SPLICING: Named isoforms=3;  
RN Event=Alternative splicing; CDS1-L;  
RN Name=1; Synonyms=19A, CSI-L;  
RN IsoId=Q9NQ25-1; Sequence=Displayed;  
RN Name=2;  
RN IsoId=Q9NQ25-2; Sequence=VSP\_013781;

CC Note=No experimental confirmation available;  
CC Name=3; Synonyms=19A24, CSI-S;  
CC IsoId=Q9NQ25-3; Sequence=VSP\_013782;  
CC -1- TISSUE SPECIFICITY: Expressed in spleen, lymph node, peripheral  
CC blood leukocytes, bone marrow, small intestine, stomach, appendix,  
CC lung and trachea. Expression was detected in NK cells, activated  
CC B-cells, NK-cell line but not in promyelocytic, B-, or T-cell  
CC lines. The isoform 3 is expressed at much lower level than isoform  
CC 1.  
CC -1- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)  
CC domain.  
CC -1- CAUTION: Ref.3 (CAB76561) sequence differs from that shown due to  
CC frame-shifts.  
CC -----  
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; AF291815; AAK11549.1; -; mRNA.  
CC EMBL; AF390894; AAL26389.1; -; mRNA.  
CC EMBL; AJ271869; CAB76561.1; ALT FRAME; mRNA.  
CC EMBL; AJ276429; CAB81950.2; -; mRNA.  
CC EMBL; AB027233; BAB61022.1; -; mRNA.  
CC EMBL; AY358512; AAC88876.1; -; mRNA.  
CC EMBL; AL634424; CAD39085.1; -; mRNA.  
CC EMBL; AL121985; CAC005079.1; -; Genomic DNA.  
CC EMBL; AL121985; CAH73507.1; -; Genomic DNA.  
CC EMBL; AL121985; CAH73508.1; -; Genomic DNA.  
CC EMBL; BC027867; AAH27867.1; -; mRNA.  
CC EMBL; ENSG0000026751; Homo sapiens.  
CC HNC; HNC; 21394; SLAMF7.  
CC MIM; 606625; -;  
CC GO; GO:0016020; C:membrane; NAS.  
CC GO; GO:0007155; P:cell adhesion; NAS.  
CC GO; GO:0030101; P:natural killer cell activation; NAS.  
CC GO; GO:0042267; P:natural killer cell mediated cytotoxicity; NAS.  
CC DR InterPro; IPR007110; Ig-like.  
CC DR PROSITE; PS50835; IG\_LIKE; 1.  
CC KW Alternative splicing; Direct protein sequencing; Glycoprotein;  
CC Immunoglobulin domain; Receptor; Signal; Transmembrane.  
CC FT SIGNAL 1 22  
CC FT CHAIN 23 335 SLAM family member 7.  
CC FT TOPO\_DOM 23 226 Extracellular (Potential).  
CC FT TRANSMEM 227 247 Potential.  
CC FT TOPO\_DOM 248 335 Cytoplasmic (Potential).  
CC FT DOMAIN 131 206 Ig-like C2-type.  
CC FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 176 176 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).  
CC FT DISULFID 145 215 Potential.  
CC FT DISULFID 151 195 By similarity.  
CC FT DISULFID 151 195 Missing (in isoform 2).  
CC FT VARSPIC 19 125 /FtId=VSP\_013781.  
CC FT VARSPIC 258 296 YIEKKRVDICRETPNICPSGNTXDYDTIPIHNRITLK  
CC -> NNRKGRSKTGILHCGNTBDDGKSPILRAHARHTKALC  
CC L (in isoform 3).  
CC /FtId=VSP\_013782.  
CC M -> L (in Ref. 3).  
CC QUERY MATCH 335 AA; 37421 MW; D09ABBCPF7ABEBD4 CRC64;  
CC Best Local Similarity 100.0%; Score 335; DB 1; Length 335;  
CC Pred. No. 7; 5e-312; Indels 0; Gaps 0;  
CC Matches 335; Conservative 0; Mismatches 0;  
CC DB 1 MAGSPCTLTITLITIMOLTGSAAGPYKELVGSVGAATVPLPKSKVKQVDSIVWTPTPL 60  
CC 1 MAGSPCTLTITLITIMOLTGSAAGPYKELVGSVGAATVPLPKSKVKQVDSIVWTPTPL 60



QY 61 VTIOPEGGTTIVTONRRNRVDPDGGYSLKSLKIKKNDGSIYYGYSLSLQOPSTQEX 120  
 DB 61 VTIOPEGGTTIVTONRRNRVDPDGGYSLKSLKIKKNDGSIYYGYSLSLQOPSTQEX 120  
 QY 121 VLAHYEHLSKRTKMTGLOSNNGTCVTNLTTCMEHGEDVYVTKAKLQOANESHNGSL 180  
 DB 121 VLAHYEHLSKRTKMTGLOSNNGTCVTNLTTCMEHGEDVYVTKAKLQOANESHNGSL 180  
 QY 181 PISMRGSDMTFICVANRPVSRNPSPIILARKLCEGAADPDSSMTVLLCLVPLLTSL 240  
 DB 181 PISMRGSDMTFICVANRPVSRNPSPIILARKLCEGAADPDSSMTVLLCLVPLLTSL 240  
 QY 241 FVLGLFLWFLKREOEYIEBKRDVICTETPNICPHSGENTEXTDPTPTNRTILKEDPA 300  
 DB 241 FVLGLFLWFLKREOEYIEBKRDVICTETPNICPHSGENTEXTDPTPTNRTILKEDPA 300  
 QY 301 NTVYSTVAIPKRMENPHSLTMPDTPKFAVENYI 335  
 DB 301 NTVYSTVAIPKRMENPHSLTMPDTPKFAVENYI 335

RESULT 2  
 QYCY18 AERPE PRELIMINARY; PRT; 156 AA.  
 AC QYCY18;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Hypothetical protein APE1433;  
 GN OrderedLocusNames=APE1433;  
 OS Aeropyrum pernix.  
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcates;  
 OC Desulfurococcaceae; Aeropyrum.  
 CX NCBI\_TaxID=56636;  
 RN [1]  
 RP NCBILOTIDE SEQUENCE.  
 RC STRAIN=K1;  
 RX MEDLINE=99310339; PubMed=10382966;  
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankal A., Kosugi H.,  
 RA Hotoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,  
 RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,  
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 crenarchaeon, Aeropyrum pernix K1.";  
 RL DNA Rep. 6:83-101(1999).  
 DR EMBL; BA000002; BAA0430.1; -; Genomic\_DNA.  
 DR PIR; H72621; H72621.  
 KW Complete proteome; Hypothetical protein.  
 SO SEQUENCE 156 AA; 15954 MW; 73BBB5C99PBB453D CRC64;

Query Match 2.7%; Score 9; DB 2; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LTGSAAAGP 25  
 DB 105 LTGSAAAGP 113

RESULT 3  
 SLAF\_MOUSE STANDARD; PRT; 333 AA.  
 AC Q8BHK6; Q8BTL2; Q8CJ63; Q8CJ64; Q8CJ65; Q91XA0;  
 DT 13-SEP-2005 (Rel. 48, Created)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE SLAM family member 7 precursor (Leukocyte cell-surface antigen) (Novel  
 Ly9).  
 GN Name=Slamf7;  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP NCBILOTIDE SEQUENCE [MRNA] (ISOFORMS 2 AND 3).  
 RC STRAIN=BALB/c, and C57BL/6; TISSUE=Thymus;  
 RX MEDLINE=2228696; PubMed=1246590; DOI=10.1007/s00251-002-0483-3;  
 RA Toyar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,  
 RA Bosch J., Terhorst C., Engel P.;  
 RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of  
 leukocyte cell-surface receptors.";  
 RL Immunogenetics 54:394-402(2002).  
 RN [2]  
 RP NCBILOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).  
 RC STRAIN=C57BL/6J; TISSUE=Aorta, Testis, and Vain;  
 RX MEDLINE=22354683; PubMed=12468851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaio I., Osato N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojodori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schirni L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Choithia C., Corbani L.B., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.D., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedziarski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.O., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahnstedt C., Wang Y., Watande Y., Wells C.,  
 RA Wilming L.G., Wyshaw-Boris A., Yangisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume S., Sato K.,  
 RA Shiraki T., Waki K., Kawai T., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashino Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [3]  
 RP NCBILOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 4).  
 RC STRAIN=FVB/N; TISSUE=Salivary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feinogold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
 RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Steplaton M., Soares M.B., Bonaldo M.F., Casavani T.L., Scheetz T.B.,  
 RA Brownstein M.J., Udell T.B., Tothiyuki S., Cavancini P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Hyers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skaleja U., Smalins D.E.,  
 RA Scherf A., Schein J.B., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -I- FUNCTION: Mediates NK cell activation through a SAP-independent  
 extracellular signal-regulated ERK-mediated pathway. May play a  
 role in lymphocyte adhesion (By similarity). Isoform 1 does not  
 bind SAP (in vitro).  
 CC



CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1;  
 CC IsoId=Q8BHK6-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q8BHK6-2; Sequence=VSP\_013784;  
 CC Name=3;  
 CC IsoId=Q8BHK6-3; Sequence=VSP\_013783, VSP\_013784;  
 CC Name=4;  
 CC IsoId=Q8BHK6-4; Sequence=VSP\_013783;  
 CC Note=No experimental confirmation available;  
 CC -1- TISSUE SPECIFICITY: Expressed in spleen, lymph node, bone marrow  
 CC and testis. Lower levels detected in thymus. Expressed in NK cells  
 CC and B-cells.  
 CC -1- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)  
 CC domain.  
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to a  
 CC frameshift in position 255.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC -----  
 DR EMBL: AF467909; AAN63158.1; -; mRNA.  
 DR EMBL: AF467910; AAN63159.1; -; mRNA.  
 DR EMBL: AF467911; AAN63160.1; -; mRNA.  
 DR EMBL: AK030135; BAC26801.1; -; mRNA.  
 DR EMBL: AK030148; BAC26810.1; -; mRNA.  
 DR EMBL: AK040678; BAC30665.1; -; mRNA.  
 DR EMBL: AK089525; AAC40914.1; -; mRNA.  
 DR EMBL: BC011154; AAH11154.1; ALT\_FRAME; mRNA.  
 DR Ensemble: ENSMUSG00000038179; Mus musculus.  
 DR MGI: MGI:1922595; Slamf7.  
 DR GO: GO:0016021; C:Integral to membrane; TAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR PROSITE: PSS0835; IG\_LIKE; 1.  
 KW Alternative splicing; Glycoprotein; Immunoglobulin domain; Receptor;  
 KW signal; Transmembrane.  
 FT SIGNAL 1 22 By similarity.  
 FT CHAIN 23 333 SLAM family member 7.  
 FT TOPO\_DOM 23 224 Extracellular (Potential).  
 FT TRANSMEM 225 245 Potential.  
 FT TOPO\_DOM 246 333 Cytoplasmic (Potential).  
 FT DOMAIN 128 203 Ig-like C2-type.  
 FT CARBOHYD 42 42 N-linked (GLCNAc...) (Potential).  
 FT CARBOHYD 95 95 N-linked (GLCNAc...) (Potential).  
 FT CARBOHYD 139 139 N-linked (GLCNAc...) (Potential).  
 FT CARBOHYD 145 145 N-linked (GLCNAc...) (Potential).  
 FT CARBOHYD 156 156 N-linked (GLCNAc...) (Potential).  
 FT DISULFID 142 212 Potential.  
 FT DISULFID 148 192 By similarity.  
 FT VASAPPLIC 255 Missing (in isoform 3 and isoform 4).  
 FT VASAPPLIC 312 333 /FtId=VSP\_013783.  
 FT VASAPPLIC 312 333 KSPSLPAKPLVPSLSFENVY -> RSCPAHHHTCQPLS  
 FT VASAPPLIC 312 333 LDHRAQ (in isoform 2 and isoform 3).  
 FT VASAPPLIC 312 333 /FtId=VSP\_013784.  
 FT VASAPPLIC 312 333 V->A (in Ref. 1; AAN63158).  
 FT VASAPPLIC 312 333 T->M (in Ref. 1; AAN63158 and 2).  
 FT VASAPPLIC 312 333 G->R (in Ref. 1; AAN63159 and 3).  
 FT VASAPPLIC 312 333

Query Match 2.7%; Score 9; DB 1; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 138 QSNNGTGV 146  
 DB 135 QSNNGTGV 143

RESULT 4  
 ID Q5NS1\_CRYNE PRELIMINARY; PRT; 572 AA.  
 AC Q5NS1;  
 DT 13-SEP-2005 (Trembl:rel. 31, Created)  
 DT 13-SEP-2005 (Trembl:rel. 31, Last sequence update)  
 DT 13-SEP-2005 (Trembl:rel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=CNBH0180;  
 OS Cryptococcus neoformans var. neoformans B-3501A.  
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 CC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 CC NCBI\_TaxId=283643;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B-3501A;  
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,  
 RA Wicks B.L., Fu J., Davis R.W.;  
 RT "Cryptococcus neoformans serotype D sequencing."  
 CC Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL: AAFY0100041; EAL19324.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 KW SEQUENCE 572 AA; 63774 MW; A78BFC0BACCB812B CRC64;  
 SQ

Query Match 2.7%; Score 9; DB 2; Length 572;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 LVPLLLSL 240  
 DB 481 LVPLLLSL 489

RESULT 5  
 MAPB MOUSE STANDARD; PRT; 2464 AA.  
 AC P14873;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))  
 DE [Contains: MAP1 light chain LC1].  
 GN Name=Map1b; Synonyms=Mcap1b, Mtap5;  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 CC Muridae; Muridae; Murinae; Mus.  
 CC NCBI\_TaxId=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE AND DOMAIN.  
 RC STRAIN=Swiss Webster; Tissue=Brain;  
 RX MEDLINE=9009453; PubMed=2480963; DOI=10.1083/jcb.109.6.3367;  
 RA Noble M., Lewis S.A., Cowan N.J.;  
 RT "The microtubule binding domain of microtubule-associated protein  
 RT MAP1B contains a repeated sequence motif unrelated to that of MAP2 and  
 RT tau".  
 RT J. Cell Biol. 109:3367-3376(1989).  
 RL [2]  
 RP PHOSPHORYLATION SITES SER-828; SER-829; SER-1247; SER-1255; SER-1260;  
 RP SER-1307; SER-1317; TYR-1331; SER-1334; SER-1371; SER-1373; SER-1382;  
 RP SER-1384; SER-1391; SER-1395; SER-1616; SER-1621; SER-1768; SER-1775;  
 RP SER-1778; SER-1781; THR-1784; SER-1793; THR-1806; SER-1877; SER-1911;  
 RP SER-2030 AND SER-2094.  
 RX PubMed=15572359; DOI=10.1074/jbc.M411220200;  
 RA Collins M.O., Yu L., Coda M.P., Huel H., Campuzano I.,  
 RA Blackstock W.P., Choudhary J.S., Grant S.G.;  
 RT "Proteomic analysis of in vitro phosphorylated synaptic proteins."  
 RT J. Biol. Chem. 280:55972-55982(2005).  
 CC -1- FUNCTION: The function of brain MAPs is essentially unknown.  
 CC -1- PHOSPHORYLATION: MAP1B may play a role in the cytoskeletal changes



CC that accompany neurite extension. Possibly MAP1B binds to at least  
 CC two tubulin subunits in the polymer, and this bridging of subunits  
 CC might be involved in nucleating microtubule polymerization and in  
 CC stabilizing microtubules.  
 CC -1- SUBUNIT: 3 different light chains, LCL, LC2 and LC3, can associate  
 CC with MAP1A and MAP1B proteins.  
 CC -1- DOMAIN: Has a highly basic region with many copies of the sequence  
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is  
 CC responsible for the binding of MAP1B to microtubules.  
 CC -1- PPM: LCL is coexpressed with MAP1B. It is a polypeptide generated  
 CC from MAP1B by proteolytic processing. It is free to associate with  
 CC both MAP1A and MAP1B. It interacts with the amino-terminal region  
 CC of MAP1B.  
 CC -1- SIMILARITY: Belongs to the MAP1A/MAP1B family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; X51396; CA35761.1; -; mRNA.  
 CC PIR; S07549; QRMSP1.  
 CC DR Ensembl; ENSMUSG0000052727; Mus musculus.  
 CC DR MGI; MGI:1306778; Mcap1b.  
 CC DR GO; GO:0005875; C:microtubule associated complex; TAS.  
 CC DR GO; GO:0005519; F:cytoskeletal regulatory protein binding; TAS.  
 CC DR GO; GO:0016338; P:dendrite morphogenesis; IMP.  
 CC DR GO; GO:0001578; P:microtubule bundle formation; IMP.  
 CC DR GO; GO:0007017; P:microtubule-based process; TAS.  
 CC DR InterPro; IPR00102; MAP1B\_neuraxin.  
 CC Pfam; PF00414; MAP1B\_neuraxin; 10.  
 CC DR PROSITE; PS00230; MAP1B\_NEURAXIN; 7.  
 CC KM Microtubule; Phosphorylation; Repeat.  
 CC FT CHAIN ? 2464 Microtubule-associated protein 1B.  
 CC FT REPEAT 1 1890 MAP1B 1.  
 CC FT REPEAT 1891 1907 MAP1B 2.  
 CC FT REPEAT 1908 1924 MAP1B 3.  
 CC FT REPEAT 1925 1941 MAP1B 4.  
 CC FT REPEAT 1942 1958 MAP1B 5.  
 CC FT REPEAT 1959 1975 MAP1B 6.  
 CC FT REPEAT 1993 2009 MAP1B 7.  
 CC FT REPEAT 2010 2026 MAP1B 8.  
 CC FT REPEAT 2027 2043 MAP1B 9.  
 CC FT REPEAT 2044 2060 MAP1B 10.  
 CC FT COMPBIA5 589 787 Lys-rich (highly basic, contains many  
 CC KKEE and KKEI/V repeats).  
 CC FT MOD\_RES 828 828 Phosphoserine.  
 CC FT MOD\_RES 829 829 Phosphoserine.  
 CC FT MOD\_RES 1247 1247 Phosphoserine.  
 CC FT MOD\_RES 1255 1255 Phosphoserine.  
 CC FT MOD\_RES 1260 1260 Phosphoserine.  
 CC FT MOD\_RES 1307 1307 Phosphoserine.  
 CC FT MOD\_RES 1317 1317 Phosphoserine.  
 CC FT MOD\_RES 1331 1331 Phosphotyrosine.  
 CC FT MOD\_RES 1334 1334 Phosphoserine.  
 CC FT MOD\_RES 1371 1371 Phosphoserine.  
 CC FT MOD\_RES 1373 1373 Phosphoserine.  
 CC FT MOD\_RES 1382 1382 Phosphoserine.  
 CC FT MOD\_RES 1384 1384 Phosphoserine.  
 CC FT MOD\_RES 1391 1391 Phosphoserine.  
 CC FT MOD\_RES 1395 1395 Phosphoserine.  
 CC FT MOD\_RES 1616 1616 Phosphoserine.  
 CC FT MOD\_RES 1621 1621 Phosphoserine.  
 CC FT MOD\_RES 1768 1768 Phosphoserine.  
 CC FT MOD\_RES 1775 1775 Phosphoserine.  
 CC FT MOD\_RES 1778 1778 Phosphoserine.  
 CC FT MOD\_RES 1781 1781 Phosphoserine.  
 CC FT MOD\_RES 1784 1784 Phosphochreonine.  
 CC FT MOD\_RES 1793 1793 Phosphoserine.  
 CC FT MOD\_RES 1806 1806 Phosphochreonine.  
 CC FT MOD\_RES 1877 1877 Phosphoserine.

FT MOD\_RES 1911 1911 Phosphoserine.  
 FT MOD\_RES 2030 2030 Phosphoserine.  
 FT MOD\_RES 2094 2094 Phosphoserine.  
 SQ SEQUENCE 2464 AA; 270411 MW; FBD3DD9CFDDBDA87 CRC64;  
 Query Match 2.7%; Score 9; DB 1; Length 2464;  
 Best Local Similarity 100.0%; Pred. No.53;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 21 AASGPVKEL 29  
 Db 812 AASGPVKEL 820  
 RESULT 6  
 0884T6\_PSESM  
 ID 0884T6\_PSESM PRELIMINARY; PRT; 83 AA.  
 AC 0884T6;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Prevent-host-death family protein.  
 GN OrderedLocustNames=PSPT02000;  
 OS Pseudomonas syringae (pv. Tomato).  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 CC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=323;  
 RN [1]  
 RP NCLECTOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STEFAN=DC3000;  
 RX MEDLINE=2284015; PubMed=12928499; DOI=10.1073/pnas.1731982100;  
 RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,  
 RA Gwinn M.U., Dodson R.V., Deboy R.T., Durkin A.S., Kolonay J.F.,  
 RA Madupu R., Daugherty S.C., Brinkac L.M., Beaman M.J., Haft D.H.,  
 RA Nelson W.C., Daviden T.M., Zafar N., Zhou L., Liu J., Yuan Q.,  
 RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,  
 RA Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,  
 RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,  
 RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,  
 RA Bender C.L., White O., Fraser C.M., Collier A.;  
 RT "The complete genome sequence of the Arabidopsis and tomato pathogen  
 RT Pseudomonas syringae pv. tomato DC3000."  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).  
 DR EMBL; AEO16853; AAO55518.1; -; Genomic\_DNA.  
 DR TIGR; PSPTO2000; -;  
 DR InterPro; IPR006442; Phd.  
 DR TIGRFAMs; TIGR01552; phd\_fam; 1.  
 KM Complete proteome.  
 SQ SEQUENCE 83 AA; 8993 MW; ED9080CB44BCD3BE CRC64;  
 Query Match 2.4%; Score 8; DB 2; Length 83;  
 Best Local Similarity 100.0%; Pred. No.39;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 16 QLTGSAAS 23  
 Db 46 QLTGSAAS 53  
 RESULT 7  
 081VU0\_HUMAN  
 ID 081VU0\_HUMAN PRELIMINARY; PRT; 129 AA.  
 AC 081VU0;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE PAPLN protein.  
 GN Name=PAPLN;  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 CC Homo.  
 OX NCBI\_TaxID=9606;



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RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shennan C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Nak S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rata S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunatratte P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC042057; AAH42057.1; -, mRNA.
DR HSPB, P07996; IUSL.
DR InterPro: IPR000884; TSP1.
DR InterPro: IPR008085; TSP_1.
DR Pfam: PF00090; TSP_1; 1.
DR PRINTS: PR01705; TSP1REPEAT.
DR SMART: SM00209; TSP1.1.
DR PROSITE: PS50092; TSP1.1.
SQ SEQUENCE 129 AA; 14368 MW; D5114A494C12B3B CRC64;

Query Match 2.4%; Score 8; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 231 LLLVPLLL 238
Db 4 LLLVPLLL 11

RESULT 8
ID 054WZ7 D1CDI PRELIMINARY; PRT; 136 AA.
AC 054WZ7;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=DD80205707;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelid; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachbat J.A., Gloeckner G., Rajandream M.-A.,
RA Sungang R., Berriman M., Song J., Olsen R., Szafrenski K., Xu Q.,
RA Jungel B., Kummerfeld S., Madera M., Kontorov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., David P., Fey P.,
RA Plicher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Karhounou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Salto T., Buchrieser C.,

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RA Wardrop A., Falder M., Thangavelu M., Johnson D., Knights A.,
RA Loulseghe H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winkler T., Tanaka Y.,
RA Shinkley G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platter M., Kay R.A.,
RA Williams J., Dear P.H., Noegel A.A., Barrel B., Kupea A.,
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 0:0-0(2005).
CC -1 CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAF0100059; EAL67798.1; -, Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 136 AA; 15218 MW; C227B91721529F55 CRC64;

Query Match 2.4%; Score 8; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 NGSLIPIS 183
Db 77 NGSLIPIS 84

RESULT 9
ID 05YY9 NOCPA PRELIMINARY; PRT; 139 AA.
AC 05YY9;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderdlocusNames=nfa17560;
OS Nocardia farcinica.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardia.
OX NCBI_TaxID=37329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFW 10152; DOI=10.1073/pnas.0406410101;
RX PubMed=15466710;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Shiba T., Hattori M.;
RT "The complete genomic sequence of Nocardia farcinica IFW 10152."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL: AP006618; BAD56602.1; -, Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 139 AA; 14684 MW; E8A7E23F33C3BE7C CRC64;

Query Match 2.4%; Score 8; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 240 LFFVLGLFL 247
Db 48 LFFVLGLFL 55

RESULT 10
ID 06ERB1 ORYZA PRELIMINARY; PRT; 155 AA.
AC 06ERB1;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein P0448B1.30.
GN Name=P0448B1.30;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.

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OX NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC  
 clone: P0448B11."  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP005585; BAD28809.1; -; Genomic\_DNA.  
 DR Gramene; O6ERB1; -;  
 DR GO: GO:0000150; F:recombinase activity; IEA.  
 DR GO: GO:0006310; P:DNA recombination; IEA.  
 DR InterPro; IPR06118; Recombinase\_S.  
 DR PROSITE; PS00397; RECOMBINASE\_1; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 155 AA; 16880 MW; 34A8A2DAD9B82B87 CRC64;  
 Query Match 2.4%; Score 8; DB 2; Length 155;  
 Best Local Similarity 100.0%; Pred. No. 64;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 236 LLLSLFVL 243  
 DB 18 LLLSLFVL 25  
 RESULT 11  
 ID Q55866 SYN3 PRELIMINARY; PRT; 173 AA.  
 AC Q55866;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Yc36 protein.  
 GN Name=Yc36; OrderedLocustNames=s110584;  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 NC NCBI\_TaxID=1148;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=97061201; Pubmed=8905231;  
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hirosewa M., Sugiyama M., Sasamoto S., Kimura T.,  
 RA Hoshouchi T., Matsuno A., Muraki A., Nakazaki N., Naro K., Okumura S.,  
 RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions."  
 RL DNA Rep. 3:109-136(1996).  
 DR EMBL; BA000022; BA010625.1; -; Genomic\_DNA.  
 DR PIR; S76681; S76681.  
 DR InterPro; IPR009631; DUF1230.  
 DR Pfam; PF06799; DUF1230; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 173 AA; 19933 MW; 666079BBE094111 CRC64;  
 Query Match 2.4%; Score 8; DB 2; Length 173;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 236 LLLSLFVL 243  
 DB 85 LLLSLFVL 92  
 RESULT 12  
 ID Q7V2B6 PROMP PRELIMINARY; PRT; 202 AA.  
 AC Q7V2B6;  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Hypothetical protein.

GN OrderedLocustNames=PM00564;  
 OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).  
 OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococaceae;  
 OC Prochlorococcus.  
 OX NCBI\_TaxID=59919;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22825698; Pubmed=12917642; DOI=10.1038/nature01947;  
 RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chait P.,  
 RA Aylgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,  
 RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,  
 RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,  
 RA Webb E.A., Zinner B.R., Christol S.W.;  
 RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic  
 niche differentiation."  
 RL Nature 424:1042-1047(2003).  
 DR EMBL; BX572091; CAE19023.1; -; Genomic\_DNA.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 202 AA; 23132 MW; FF359586198F7P2E CRC64;  
 Query Match 2.4%; Score 8; DB 2; Length 202;  
 Best Local Similarity 100.0%; Pred. No. 78;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 92 LSKLKXND 99  
 DB 122 LSKLKXND 129  
 RESULT 13  
 ID Q9S488 PROS9 PRELIMINARY; PRT; 211 AA.  
 AC Q9S488;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Prochlorococcus sp. (strain PCC 9511).  
 OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococaceae;  
 OC Prochlorococcus.  
 NC NCBI\_TaxID=100363;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RP STRAIN=PCC 9511;  
 RX MEDLINE=21142517; Pubmed=11208789; DOI=10.1126/JB.183.3.915-920.2001;  
 RA Holtzendorff J., Partensky F., Jacquet S., Bryant F., Marie D.,  
 RA Gotszalk L., Mary I., Valot D., Hess W.R.,  
 RT "Diurnal expression of cell cycle-related genes in synchronized cultures  
 of Prochlorococcus sp. strain PCC 9511."  
 RL J. Bacteriol. 183:915-920(2001).  
 DR EMBL; AF158628; AAD45694.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 211 AA; 24129 MW; 6228068FF04673F2 CRC64;  
 Query Match 2.4%; Score 8; DB 2; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 81;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 92 LSKLKXND 99  
 DB 131 LSKLKXND 138  
 RESULT 14  
 ID Q5VID5 HALMA PRELIMINARY; PRT; 230 AA.  
 AC Q5VID5;  
 DT 01-FEB-2005 (TRENBLrel. 29, Created)  
 DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)  
 DE Proteasome subunit alpha.  
 GN Name=psma1; OrderedLocustNames=trnAC1772;  
 OS Haloarcula marismortui (Haloacterium marismortui).



OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
OC Halobacteriaceae; Halorcula.  
OX NCBI\_TaxID=2238;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 43049;  
RX PubMed=15520287; DOI=10.1101/gr.2700304;  
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,  
R Deutch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,  
R Date S.V., Marcotte E., Hood L., Ng W.V.;  
RT "Genome sequence of Halorcula marismortui: a halophilic archaeon from  
the Dead Sea."  
RL Genome Res. 14:2221-2234(2004).  
DR EMBL; AY596297; AAV46667.1; -; Genomic\_DNA.  
DR GO; GO:0005829; C:cytosol; IEA.  
DR GO; GO:0005839; C:proteasome core complex (sensu Eukaryota); IEA.  
DR GO; GO:0004298; F:chreonine endopeptidase activity; IEA.  
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.  
DR InterPro; IPR000243; Pept\_T1A\_subB.  
DR InterPro; IPR001353; Proteasome\_A\_B.  
DR Pfam; PF00227; Proteasome; 1.  
DR PRINTS; PR00141; PROTEASOME.  
KM Complete proteome; Proteasome.  
SQ SEQUENCE 230 AA; 24274 MW; A97828C417B98407 CRC64;

Query Match 2.4%; Score 8; DB 2; Length 230;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LVGSVGA 36  
|||  
Db 81 LVGSVGA 88

## RESULT 15

OSV4S6 HALMA PRELIMINARY; PRT; 240 AA.  
ID OSV4S6 HALMA PRELIMINARY;  
AC OSV4S6;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Proteasome subunit alpha.  
GN Name=psma3; OrderedLocNames=trnAC0442;  
OS Halorcula marismortui (Halobacterium marismortui).  
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
OC Halobacteriaceae; Halorcula.  
OX NCBI\_TaxID=2238;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 43049;  
RX PubMed=15520287; DOI=10.1101/gr.2700304;  
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,  
R Deutch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,  
R Date S.V., Marcotte E., Hood L., Ng W.V.;  
RT "Genome sequence of Halorcula marismortui: a halophilic archaeon from  
the Dead Sea."  
RL Genome Res. 14:2221-2234(2004).  
DR EMBL; AY596297; AAV45476.1; -; Genomic\_DNA.  
DR GO; GO:0005829; C:cytosol; IEA.  
DR GO; GO:0005839; C:proteasome core complex (sensu Eukaryota); IEA.  
DR GO; GO:0004298; F:chreonine endopeptidase activity; IEA.  
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.  
DR InterPro; IPR000243; Pept\_T1A\_subB.  
DR InterPro; IPR001353; Proteasome\_A\_B.  
DR Pfam; PF00227; Proteasome; 1.  
DR PRINTS; PR00141; PROTEASOME.  
KM Complete proteome; Proteasome.  
SQ SEQUENCE 240 AA; 25261 MW; 9274753670576304 CRC64;

Query Match 2.4%; Score 8; DB 2; Length 240;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LVGSVGA 36  
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Db 92 LVGSVGA 99

Search completed: December 16, 2005, 11:57:47  
Job time : 234 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 16, 2005, 11:49:55 ; Search time 47 Seconds  
(without alignments)  
589.284 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 335

Sequence: 1 MASPTCLTYILWQITGS.....PHSLTWPDPRLPAYENV1 335

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Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

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Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

Database :

Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/iaa/H.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PTUS.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RB.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backflist1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	335	100.0	335	2	US-09-991-181-253
2	335	100.0	335	2	US-09-990-444-253
3	335	100.0	335	2	US-09-997-333-253
4	335	100.0	335	2	US-09-992-598-253
5	97	29.0	97	2	US-09-513-999C-4472
6	8	2.4	289	2	US-09-466-778-8
7	8	2.4	360	2	US-09-907-794A-213
8	8	2.4	360	2	US-09-905-125A-213
9	8	2.4	360	2	US-09-902-775A-213
10	8	2.4	360	2	US-09-906-700-213
11	8	2.4	360	2	US-09-903-603A-213
12	8	2.4	360	2	US-09-904-920A-213
13	8	2.4	360	2	US-09-909-064-213
14	8	2.4	360	2	US-09-905-381A-213
15	8	2.4	360	2	US-09-906-618-213
16	8	2.4	360	2	US-09-906-646-213
17	8	2.4	360	2	US-09-904-462-213
18	8	2.4	360	2	US-09-902-736A-213
19	8	2.4	360	2	US-09-906-722A-213
20	8	2.4	410	2	US-09-252-991A-31174
21	8	2.4	1105	2	US-09-949-016-6148
22	8	2.4	1117	2	US-09-949-016-6148
23	7	2.1	63	2	US-09-646-681B-10
24	7	2.1	67	2	US-09-543-681A-4733
25	7	2.1	84	2	US-09-270-767-60733
26	7	2.1	85	2	US-09-248-796A-22136
27	7	2.1	97	2	US-09-886-319A-29

28	7	2.1	98	2	US-08-613--822-4	Sequence 4, Appl1
29	7	2.1	98	2	US-08-852-212-2	Sequence 2, Appl1
30	7	2.1	98	2	US-09-479-7295-4	Sequence 4, Appl1
31	7	2.1	98	2	US-09-261-201A-4	Sequence 4, Appl1
32	7	2.1	98	2	US-09-717-209-4	Sequence 4, Appl1
33	7	2.1	98	2	US-09-545-894-2	Sequence 2, Appl1
34	7	2.1	98	2	US-09-834-795A-25	Sequence 25, Appl1
35	7	2.1	98	2	US-10-164-621-4	Sequence 4, Appl1
36	7	2.1	98	2	US-10-125-451-4	Sequence 4, Appl1
37	7	2.1	137	2	US-09-270-767-33253	Sequence 33253, A
38	7	2.1	137	2	US-09-270-767-48470	Sequence 48470, A
39	7	2.1	156	2	US-09-270-767-45241	Sequence 45241, A
40	7	2.1	132	2	US-08-486-099-107	Sequence 107, App
41	7	2.1	132	2	US-08-360-107A-117	Sequence 117, App
42	7	2.1	132	2	US-08-484-223B-107	Sequence 107, App
43	7	2.1	132	2	US-08-919-597-107	Sequence 107, App
44	7	2.1	132	2	US-08-475-668A-107	Sequence 107, App
45	7	2.1	132	2	US-08-485-551A-107	Sequence 107, App
46	7	2.1	132	2	US-08-471-913A-107	Sequence 107, App
47	7	2.1	132	2	US-08-485-264A-107	Sequence 107, App
48	7	2.1	132	2	US-08-474-349A-107	Sequence 107, App
49	7	2.1	132	2	US-08-470-896-107	Sequence 107, App
50	7	2.1	132	2	US-08-485-546A-107	Sequence 107, App
51	7	2.1	132	2	US-08-487-266A-107	Sequence 107, App
52	7	2.1	132	2	US-08-484-741-107	Sequence 107, App
53	7	2.1	208	1	US-08-680-726A-72	Sequence 72, Appl1
54	7	2.1	208	1	US-09-092-409-72	Sequence 72, Appl1
55	7	2.1	229	2	US-09-078-691-4	Sequence 4, Appl1
56	7	2.1	244	2	US-09-328-352-4316	Sequence 4316, Ap
57	7	2.1	262	2	US-10-104-047-2006	Sequence 2006, Ap
58	7	2.1	264	2	US-09-069-023-7	Sequence 7, Appl1
59	7	2.1	266	2	US-09-107-433-2900	Sequence 2900, Ap
60	7	2.1	276	2	US-09-902-540-11303	Sequence 11303, A
61	7	2.1	276	2	US-09-583-110-2944	Sequence 2944, Ap
62	7	2.1	230	2	US-09-107-433-4262	Sequence 4262, Ap
63	7	2.1	300	2	US-09-099-041A-4	Sequence 4, Appl1
64	7	2.1	300	2	US-09-245-281-4	Sequence 4, Appl1
65	7	2.1	300	2	US-09-207-359B-4	Sequence 4, Appl1
66	7	2.1	300	2	US-09-340-620A-4	Sequence 4, Appl1
67	7	2.1	300	2	US-09-865-364-4	Sequence 4, Appl1
68	7	2.1	300	2	US-09-728-721-4	Sequence 4, Appl1
69	7	2.1	301	2	US-09-583-110-3523	Sequence 3523, Ap
70	7	2.1	303	2	US-09-632-947B-5	Sequence 5, Appl1
71	7	2.1	316	2	US-09-078-691-2	Sequence 2, Appl1
72	7	2.1	318	2	US-09-107-532A-6372	Sequence 6372, Ap
73	7	2.1	332	2	US-09-543-681A-6622	Sequence 6622, Ap
74	7	2.1	337	2	US-09-252-991A-32265	Sequence 32265, A
75	7	2.1	335	2	US-09-134-000C-4818	Sequence 4818, Ap
76	7	2.1	408	1	US-09-014-969-13	Sequence 13, Appl1
77	7	2.1	419	1	US-08-997-080-125	Sequence 125, App
78	7	2.1	419	1	US-08-997-362-125	Sequence 125, App
79	7	2.1	419	2	US-09-095-855-125	Sequence 125, App
80	7	2.1	419	2	US-09-324-542-125	Sequence 125, App
81	7	2.1	419	2	US-09-205-426-125	Sequence 125, App
82	7	2.1	437	2	US-09-134-000C-4837	Sequence 4837, Ap
83	7	2.1	433	2	US-10-152-886-11	Sequence 11, Appl1
84	7	2.1	439	2	US-09-282-305-6	Sequence 6, Appl1
85	7	2.1	439	2	US-09-883-720-6	Sequence 6, Appl1
86	7	2.1	438	2	US-09-724-797-44	Sequence 44, Appl1
87	7	2.1	467	2	US-09-489-039A-11144	Sequence 11144, A
88	7	2.1	472	2	US-09-107-532A-6117	Sequence 6117, Ap
89	7	2.1	478	2	US-09-069-023-4	Sequence 4, Appl1
90	7	2.1	478	2	US-09-302-540-10474	Sequence 10474, A
91	7	2.1	453	2	US-09-720-529A-2	Sequence 2, Appl1
92	7	2.1	532	2	US-09-605-703B-1378	Sequence 1378, A
93	7	2.1	530	2	US-09-069-023-3	Sequence 3, Appl1
94	7	2.1	531	2	US-09-069-023-1	Sequence 1, Appl1
95	7	2.1	539	2	US-09-800-170-16	Sequence 16, Appl1
96	7	2.1	540	2	US-09-019-842-1	Sequence 1, Appl1
97	7	2.1	540	2	US-09-099-041A-2	Sequence 2, Appl1
98	7	2.1	540	2	US-09-069-023-27	Sequence 27, Appl1
99	7	2.1	540	2	US-09-245-281-2	Sequence 2, Appl1
100	7	2.1	540	2	US-09-470-271-1	Sequence 1, Appl1



101	7	2.1	540	2	US-09-207-359B-2	Sequence 2, Appl1	174	6	1.8	28	4	PCT-US92-04531-6	Sequence 6, Appl1
102	7	2.1	540	2	US-09-340-620A-2	Sequence 2, Appl1	175	6	1.8	29	1	US-07-927-391-8	Sequence 8, Appl1
103	7	2.1	540	2	US-09-345-473B-28	Sequence 28, Appl1	176	6	1.8	30	2	US-08-619-198-7	Sequence 7, Appl1
104	7	2.1	540	2	US-09-865-364-2	Sequence 2, Appl1	177	6	1.8	33	2	US-07-927-391-9	Sequence 9, Appl1
105	7	2.1	540	2	US-09-748-537-1	Sequence 1, Appl1	178	6	1.8	33	2	US-08-789-333F-15	Sequence 15, Appl1
106	7	2.1	540	2	US-09-981-397A-14	Sequence 14, Appl1	179	6	1.8	33	2	US-09-169-015-25	Sequence 25, Appl1
107	7	2.1	540	2	US-09-862-027-28	Sequence 28, Appl1	180	6	1.8	33	2	US-09-133-944-15	Sequence 15, Appl1
108	7	2.1	540	2	US-09-728-721-2	Sequence 2, Appl1	181	6	1.8	33	2	US-09-208-827-16	Sequence 16, Appl1
109	7	2.1	540	2	US-09-771-161A-184	Sequence 184, App	182	6	1.8	33	2	US-08-787-738B-15	Sequence 15, Appl1
110	7	2.1	550	2	US-09-248-796A-20760	Sequence 20760, A	183	6	1.8	33	2	US-09-157-748-18	Sequence 18, Appl1
111	7	2.1	646	2	US-09-252-991A-18949	Sequence 18949, A	184	6	1.8	33	2	US-09-600-170-68	Sequence 68, Appl1
112	7	2.1	650	2	US-09-310-463-2	Sequence 2, Appl1	185	6	1.8	33	2	US-09-626-581B-28	Sequence 28, Appl1
113	7	2.1	650	2	US-08-842-248A-2	Sequence 2, Appl1	186	6	1.8	33	2	US-09-415-765B-28	Sequence 28, Appl1
114	7	2.1	650	2	US-09-949-002-590	Sequence 350, App	187	6	1.8	33	2	US-09-626-580C-28	Sequence 28, Appl1
115	7	2.1	650	2	US-10-104-047-3395	Sequence 3395, App	188	6	1.8	33	2	US-09-749-959-24	Sequence 24, Appl1
116	7	2.1	651	2	US-08-985-950-22	Sequence 22, Appl1	189	6	1.8	33	2	US-10-043-074-16	Sequence 16, Appl1
117	7	2.1	651	2	US-09-546-049-22	Sequence 22, Appl1	190	6	1.8	33	2	US-09-285-912A-78	Sequence 78, Appl1
118	7	2.1	652	2	US-09-310-463-4	Sequence 4, Appl1	191	6	1.8	33	2	US-09-578-030-19	Sequence 19, Appl1
119	7	2.1	652	2	US-08-842-248A-4	Sequence 4, Appl1	192	6	1.8	33	2	US-09-616-940-15	Sequence 15, Appl1
120	7	2.1	670	1	US-08-997-080-178	Sequence 178, App	193	6	1.8	33	2	US-09-419-381-62	Sequence 62, Appl1
121	7	2.1	670	1	US-08-997-362-178	Sequence 178, App	194	6	1.8	33	2	US-10-142-662-29	Sequence 29, Appl1
122	7	2.1	670	1	US-09-095-855-178	Sequence 178, App	195	6	1.8	33	2	US-09-308-992B-13	Sequence 13, Appl1
123	7	2.1	670	2	US-09-324-542-178	Sequence 178, App	196	6	1.8	33	2	US-09-308-992B-24	Sequence 24, Appl1
124	7	2.1	670	2	US-09-205-426-178	Sequence 178, App	197	6	1.8	33	2	US-09-308-992B-25	Sequence 25, Appl1
125	7	2.1	672	1	US-09-949-002-416	Sequence 416, App	198	6	1.8	33	2	US-10-096-550-15	Sequence 15, Appl1
126	7	2.1	722	1	US-08-997-080-174	Sequence 174, App	199	6	1.8	33	2	US-09-062-330-11	Sequence 11, Appl1
127	7	2.1	722	1	US-08-997-362-174	Sequence 174, App	200	6	1.8	33	2	US-10-226-877A-20	Sequence 20, Appl1
128	7	2.1	722	2	US-09-095-855-174	Sequence 174, App	201	6	1.8	33	2	US-10-177-725-144	Sequence 144, App
129	7	2.1	722	2	US-09-324-542-174	Sequence 174, App	202	6	1.8	36	2	US-09-308-992B-22	Sequence 22, Appl1
130	7	2.1	722	2	US-09-205-426-174	Sequence 174, App	203	6	1.8	40	2	US-08-776-971-113	Sequence 113, App
131	7	2.1	728	2	US-09-949-016-9813	Sequence 9813, App	204	6	1.8	40	2	US-09-576-290-113	Sequence 113, App
132	7	2.1	734	2	US-09-949-016-9115	Sequence 9115, App	205	6	1.8	40	2	US-09-716-147-113	Sequence 113, App
133	7	2.1	743	2	US-10-104-047-2340	Sequence 2340, App	206	6	1.8	43	1	US-07-998-003A-57	Sequence 57, Appl1
134	7	2.1	816	2	US-09-949-016-9116	Sequence 9116, App	207	6	1.8	43	1	US-08-453-274B-57	Sequence 57, Appl1
135	7	2.1	943	2	US-09-583-110-4794	Sequence 4794, App	208	6	1.8	43	1	US-08-453-695A-57	Sequence 57, Appl1
136	7	2.1	945	2	US-09-107-433-3340	Sequence 3340, App	209	6	1.8	43	1	US-08-268-161A-57	Sequence 57, Appl1
137	7	2.1	963	1	US-08-537-002A-3	Sequence 3, Appl1	210	6	1.8	43	1	US-08-453-702A-57	Sequence 57, Appl1
138	7	2.1	963	2	US-08-863-010-3	Sequence 3, Appl1	211	6	1.8	43	1	US-09-099-639-57	Sequence 57, Appl1
139	7	2.1	963	2	US-09-024-429-3	Sequence 3, Appl1	212	6	1.8	43	4	PCT-US93-1258B-57	Sequence 57, Appl1
140	7	2.1	964	2	US-09-543-681A-5035	Sequence 5035, App	213	6	1.8	43	4	PCT-US95-08071-57	Sequence 57, Appl1
141	7	2.1	972	2	US-09-489-039A-11867	Sequence 11867, A	214	6	1.8	46	2	US-09-471-276-1047	Sequence 1047, App
142	7	2.1	1019	1	US-08-271-364A-7	Sequence 7, Appl1	215	6	1.8	47	2	US-09-391-799-6	Sequence 6, Appl1
143	7	2.1	1019	1	US-08-222-715B-26	Sequence 26, Appl1	216	6	1.8	47	2	US-09-471-276-955	Sequence 955, App
144	7	2.1	1085	1	US-08-431-080-28	Sequence 28, Appl1	217	6	1.8	49	2	US-09-208-140-7	Sequence 7, Appl1
145	7	2.1	1085	1	US-08-938-534-28	Sequence 28, Appl1	218	6	1.8	49	2	US-09-208-140-31	Sequence 19, Appl1
146	7	2.1	1085	2	US-09-345-294-28	Sequence 28, Appl1	219	6	1.8	49	2	US-09-208-140-31	Sequence 31, Appl1
147	7	2.1	1161	2	US-09-252-991A-22872	Sequence 22872, A	220	6	1.8	49	2	US-09-208-140-32	Sequence 32, Appl1
148	7	2.1	1190	2	US-09-150-460B-6	Sequence 6, Appl1	221	6	1.8	56	2	US-09-621-976-5480	Sequence 5480, App
149	7	2.1	1291	2	US-09-150-460B-10	Sequence 10, Appl1	222	6	1.8	56	2	US-09-621-976-6983	Sequence 6983, App
150	7	2.1	1291	2	US-09-220-641-5	Sequence 5, Appl1	223	6	1.8	60	2	US-09-513-999C-5781	Sequence 5781, App
151	7	2.1	1566	2	US-09-581-472B-2	Sequence 2, Appl1	224	6	1.8	61	2	US-09-248-796A-25070	Sequence 25070, A
152	7	2.1	1581	2	US-09-110-517-2	Sequence 2, Appl1	225	6	1.8	62	2	US-09-621-976-4988	Sequence 4988, App
153	7	2.1	1607	2	US-09-902-540-16765	Sequence 16765, A	226	6	1.8	65	2	US-09-543-681A-5670	Sequence 5670, App
154	7	2.1	6239	2	US-09-214-286-4	Sequence 4, Appl1	227	6	1.8	65	2	US-09-513-999C-6592	Sequence 6592, App
155	6	1.8	8	2	US-09-248-588-66	Sequence 66, Appl1	228	6	1.8	67	2	US-09-621-976-6567	Sequence 6567, App
156	6	1.8	12	2	US-08-836-075A-130	Sequence 130, App	229	6	1.8	67	2	US-09-270-767-37915	Sequence 37915, App
157	6	1.8	18	2	US-09-470-830A-2	Sequence 2, Appl1	230	6	1.8	67	2	US-09-270-767-53132	Sequence 53132, A
158	6	1.8	19	2	US-08-848-580-8	Sequence 8, Appl1	231	6	1.8	67	2	US-09-248-796A-25766	Sequence 25766, A
159	6	1.8	19	2	US-08-488-123-8	Sequence 8, Appl1	232	6	1.8	67	2	US-09-513-999C-5199	Sequence 5199, App
160	6	1.8	19	2	US-09-470-830A-3	Sequence 3, Appl1	233	6	1.8	69	2	US-09-621-976-6740	Sequence 6740, App
161	6	1.8	19	2	US-09-470-830A-4	Sequence 4, Appl1	234	6	1.8	69	2	US-09-270-767-39496	Sequence 39496, A
162	6	1.8	19	4	PCT-US92-04537-4	Sequence 4, Appl1	235	6	1.8	69	2	US-09-270-767-58217	Sequence 58217, A
163	6	1.8	20	2	US-09-470-830A-43	Sequence 43, Appl1	236	6	1.8	71	2	US-09-270-767-62067	Sequence 62067, A
164	6	1.8	21	2	US-08-848-580-9	Sequence 9, Appl1	237	6	1.8	71	2	US-09-270-767-36918	Sequence 36918, A
165	6	1.8	21	2	US-08-488-123-9	Sequence 9, Appl1	238	6	1.8	72	2	US-09-270-767-52135	Sequence 52135, A
166	6	1.8	21	2	US-09-471-276-950	Sequence 950, App	239	6	1.8	72	2	US-09-543-681A-4655	Sequence 4655, App
167	6	1.8	21	4	PCT-US92-04537-5	Sequence 5, Appl1	240	6	1.8	74	2	US-08-905-223-294	Sequence 294, App
168	6	1.8	23	2	US-07-927-391-7	Sequence 7, Appl1	241	6	1.8	74	2	US-08-305-223-296	Sequence 296, App
169	6	1.8	25	2	US-09-690-454-200	Sequence 200, App	242	6	1.8	78	2	US-09-621-976-5293	Sequence 5293, App
170	6	1.8	28	2	US-08-848-580-10	Sequence 10, Appl1	243	6	1.8	79	2	US-09-270-767-58410	Sequence 58410, A
171	6	1.8	28	2	US-09-149-476-322	Sequence 322, App	244	6	1.8	80	2	US-09-328-352-5464	Sequence 5464, App
172	6	1.8	28	2	US-09-149-476-509	Sequence 509, App	245	6	1.8	80	2	US-09-328-352-5464	Sequence 5464, App
173	6	1.8	28	2	US-08-488-123-10	Sequence 10, Appl1	246	6	1.8	80	2	US-09-540-236-3087	Sequence 3087, App



247	6	1.8	81	2	US-09-248-796A-23117	Sequence 23117, A	320	6	1.8	99	1	US-08-347-492B-8	Sequence 8, Appl1
248	6	1.8	81	2	US-09-248-796A-27993	Sequence 27993, A	321	6	1.8	99	1	US-08-480-449-18	Sequence 18, Appl1
249	6	1.8	82	2	US-09-489-039A-13580	Sequence 13580, A	322	6	1.8	99	1	US-08-480-449-19	Sequence 19, Appl1
250	6	1.8	83	2	US-08-776-971-45	Sequence 45, Appl1	323	6	1.8	99	1	US-08-479-126B-5	Sequence 5, Appl1
251	6	1.8	83	2	US-08-776-971-124	Sequence 124, App	324	6	1.8	99	1	US-08-421-144A-5	Sequence 5, Appl1
252	6	1.8	83	2	US-08-776-971-137	Sequence 137, App	325	6	1.8	99	1	US-08-726-830A-5	Sequence 5, Appl1
253	6	1.8	83	2	US-09-576-290-45	Sequence 45, Appl1	326	6	1.8	99	1	US-08-660-542-18	Sequence 18, Appl1
254	6	1.8	83	2	US-09-576-290-124	Sequence 124, App	327	6	1.8	99	1	US-08-660-542-19	Sequence 19, Appl1
255	6	1.8	83	2	US-09-576-290-137	Sequence 137, App	328	6	1.8	99	1	US-08-798-143-8	Sequence 8, Appl1
256	6	1.8	83	2	US-09-716-147-45	Sequence 45, Appl1	329	6	1.8	99	2	US-07-927-391-24	Sequence 24, Appl1
257	6	1.8	83	2	US-09-716-147-124	Sequence 124, App	330	6	1.8	99	2	US-08-995-156A-5	Sequence 5, Appl1
258	6	1.8	83	2	US-09-716-147-137	Sequence 137, App	331	6	1.8	99	2	US-09-044-856A-5	Sequence 5, Appl1
259	6	1.8	83	2	US-10-012-819-250	Sequence 250, App	332	6	1.8	99	2	US-09-044-855A-5	Sequence 5, Appl1
260	6	1.8	84	2	US-09-248-796A-24714	Sequence 24714, A	333	6	1.8	99	2	US-08-613-822-18	Sequence 18, Appl1
261	6	1.8	84	2	US-09-248-796A-26339	Sequence 26339, A	334	6	1.8	99	2	US-08-928-183B-14	Sequence 14, Appl1
262	6	1.8	84	2	US-09-248-796A-27934	Sequence 27934, A	335	6	1.8	99	2	US-09-133-521-5	Sequence 5, Appl1
263	6	1.8	85	2	US-09-328-352-6104	Sequence 6104, A	336	6	1.8	99	2	US-08-679-492A-152	Sequence 152, App
264	6	1.8	85	2	US-10-178-213-230	Sequence 230, App	337	6	1.8	99	2	US-08-479-603-18	Sequence 18, Appl1
265	6	1.8	87	2	US-09-288-143-96	Sequence 96, Appl1	338	6	1.8	99	2	US-08-479-603-19	Sequence 19, Appl1
266	6	1.8	87	2	US-09-270-767-34042	Sequence 34042, A	339	6	1.8	99	2	US-09-419-281-5	Sequence 5, Appl1
267	6	1.8	87	2	US-09-270-767-49259	Sequence 49259, A	340	6	1.8	99	2	US-09-479-729B-18	Sequence 18, Appl1
268	6	1.8	89	2	US-09-543-681A-6121	Sequence 6121, Ap	341	6	1.8	99	2	US-09-366-887A-10	Sequence 10, Appl1
269	6	1.8	91	2	US-09-270-767-34720	Sequence 34720, A	342	6	1.8	99	2	US-08-939-107-18	Sequence 18, Appl1
270	6	1.8	91	2	US-09-270-767-49937	Sequence 49937, A	343	6	1.8	99	2	US-08-939-107-19	Sequence 19, Appl1
271	6	1.8	92	2	US-09-366-887A-14	Sequence 14, Appl1	344	6	1.8	99	2	US-09-886-319A-22	Sequence 22, Appl1
272	6	1.8	92	2	US-09-252-991A-28334	Sequence 28334, A	345	6	1.8	99	2	US-09-886-319A-30	Sequence 30, Appl1
273	6	1.8	92	2	US-09-621-976-5285	Sequence 5285, Ap	346	6	1.8	99	2	US-09-717-209-18	Sequence 18, Appl1
274	6	1.8	92	2	US-09-248-796A-22331	Sequence 22331, A	347	6	1.8	99	2	US-09-545-894-7	Sequence 7, Appl1
275	6	1.8	92	2	US-09-248-796A-26769	Sequence 26769, A	348	6	1.8	99	2	US-09-834-795A-27	Sequence 27, Appl1
276	6	1.8	92	2	US-09-517-204-14	Sequence 14, Appl1	349	6	1.8	99	2	US-09-834-795A-28	Sequence 28, Appl1
277	6	1.8	93	2	US-09-248-796A-27221	Sequence 27221, A	350	6	1.8	99	2	US-09-067-447B-18	Sequence 18, Appl1
278	6	1.8	94	1	US-08-150-203A-5	Sequence 5, Appl1	351	6	1.8	99	2	US-09-067-447B-19	Sequence 19, Appl1
279	6	1.8	94	1	US-08-454-730-5	Sequence 5, Appl1	352	6	1.8	99	2	US-09-517-204-10	Sequence 10, Appl1
280	6	1.8	94	2	US-08-949-788-5	Sequence 5, Appl1	353	6	1.8	99	2	US-09-513-599C-7700	Sequence 7700, Ap
281	6	1.8	94	2	US-09-621-976-6341	Sequence 6341, Ap	354	6	1.8	99	2	US-08-437-306-2	Sequence 2, Appl1
282	6	1.8	95	2	US-09-198-452A-1220	Sequence 1220, Ap	355	6	1.8	99	2	US-08-479-620-18	Sequence 18, Appl1
283	6	1.8	95	2	US-09-621-976-5712	Sequence 5712, Ap	356	6	1.8	99	2	US-08-479-620-19	Sequence 19, Appl1
284	6	1.8	96	2	US-09-366-887A-9	Sequence 9, Appl1	357	6	1.8	99	2	US-10-054-967-5	Sequence 5, Appl1
285	6	1.8	96	2	US-09-248-796A-18136	Sequence 18136, A	358	6	1.8	99	2	US-10-141-865-5	Sequence 5, Appl1
286	6	1.8	96	2	US-09-645-593-9	Sequence 9, Appl1	359	6	1.8	99	2	US-09-537-859D-1	Sequence 1, Appl1
287	6	1.8	96	2	US-09-517-204-9	Sequence 9, Appl1	360	6	1.8	99	2	US-09-537-859D-2	Sequence 2, Appl1
288	6	1.8	97	1	US-08-467-822-40	Sequence 40, Appl1	361	6	1.8	99	2	US-09-537-859D-1	Sequence 1, Appl1
289	6	1.8	97	2	US-09-472-971-4	Sequence 4, Appl1	362	6	1.8	99	2	US-10-125-451-18	Sequence 18, Appl1
290	6	1.8	97	2	US-08-433-697-40	Sequence 40, Appl1	363	6	1.8	99	4	PCT-US96-10087-5	Sequence 5, Appl1
291	6	1.8	97	2	US-08-466-248-40	Sequence 40, Appl1	364	6	1.8	99	6	5212073-2	Patent No. 5212073
292	6	1.8	97	2	US-09-886-319A-21	Sequence 21, Appl1	365	6	1.8	100	2	US-10-104-047-2869	Sequence 2869, Ap
293	6	1.8	97	2	US-09-545-894-13	Sequence 13, Appl1	366	6	1.8	103	2	US-08-894-173-77	Sequence 77, Appl1
294	6	1.8	97	2	US-09-545-894-16	Sequence 16, Appl1	367	6	1.8	103	2	US-09-398-193-77	Sequence 77, Appl1
295	6	1.8	98	2	US-08-776-971-1	Sequence 1, Appl1	368	6	1.8	103	2	US-09-084-303B-198	Sequence 198, App
296	6	1.8	98	2	US-08-776-971-44	Sequence 44, Appl1	369	6	1.8	103	2	US-09-248-796A-24695	Sequence 24695, A
297	6	1.8	98	2	US-08-776-971-115	Sequence 115, App	370	6	1.8	104	2	US-08-744-419-2	Sequence 2, Appl1
298	6	1.8	98	2	US-08-776-971-117	Sequence 117, App	371	6	1.8	104	2	US-09-543-681A-4881	Sequence 4881, Ap
299	6	1.8	98	2	US-08-776-971-122	Sequence 122, App	372	6	1.8	104	2	US-09-545-894-4	Sequence 4, Appl1
300	6	1.8	98	2	US-08-776-971-131	Sequence 131, App	373	6	1.8	105	2	US-09-489-039A-13803	Sequence 13803, A
301	6	1.8	98	2	US-08-776-971-136	Sequence 136, App	374	6	1.8	106	2	US-09-270-767-48695	Sequence 48695, A
302	6	1.8	98	2	US-09-248-796A-23678	Sequence 23678, A	375	6	1.8	107	2	US-09-489-039A-13627	Sequence 13627, A
303	6	1.8	98	2	US-09-248-796A-24583	Sequence 24583, A	376	6	1.8	107	2	US-09-830-230A-41	Sequence 41, Appl1
304	6	1.8	98	2	US-09-576-290-1	Sequence 1, Appl1	377	6	1.8	109	1	US-08-421-144A-7	Sequence 7, Appl1
305	6	1.8	98	2	US-09-576-290-44	Sequence 44, Appl1	378	6	1.8	109	1	US-07-927-391-16	Sequence 16, Appl1
306	6	1.8	98	2	US-09-576-290-115	Sequence 115, App	379	6	1.8	109	2	US-08-679-493A-153	Sequence 153, App
307	6	1.8	98	2	US-09-576-290-117	Sequence 117, App	380	6	1.8	109	2	US-09-886-319A-71	Sequence 71, Appl1
308	6	1.8	98	2	US-09-576-290-122	Sequence 122, App	381	6	1.8	110	2	US-09-366-887A-13	Sequence 13, Appl1
309	6	1.8	98	2	US-09-576-290-131	Sequence 131, App	382	6	1.8	110	2	US-09-540-236-2945	Sequence 2945, Ap
310	6	1.8	98	2	US-09-576-290-136	Sequence 136, App	383	6	1.8	110	2	US-09-517-204-13	Sequence 13, Appl1
311	6	1.8	98	2	US-09-716-147-1	Sequence 1, Appl1	384	6	1.8	112	2	US-09-489-039A-12524	Sequence 12524, A
312	6	1.8	98	2	US-09-716-147-44	Sequence 44, Appl1	385	6	1.8	114	2	US-08-894-173-97	Sequence 97, Appl1
313	6	1.8	98	2	US-09-716-147-115	Sequence 115, App	386	6	1.8	114	2	US-09-398-193-97	Sequence 97, Appl1
314	6	1.8	98	2	US-09-716-147-117	Sequence 117, App	387	6	1.8	114	2	US-09-134-000C-3879	Sequence 3879, App
315	6	1.8	98	2	US-09-716-147-122	Sequence 122, App	388	6	1.8	116	2	US-09-188-930-121	Sequence 121, App
316	6	1.8	98	2	US-09-716-147-131	Sequence 131, App	389	6	1.8	116	2	US-09-312-883C-121	Sequence 121, App
317	6	1.8	98	2	US-09-716-147-136	Sequence 136, App	390	6	1.8	117	2	US-09-489-039A-8566	Sequence 8566, Ap
318	6	1.8	99	1	US-08-127-499A-35	Sequence 35, Appl1	391	6	1.8	118	2	US-09-098-789-1	Sequence 1, Appl1
319	6	1.8	99	1	US-08-482-847-35	Sequence 35, Appl1	392	6	1.8	118	2	US-09-327-750F-34	Sequence 34, Appl1



393	6	1.8	122	1	US-09-109-266-8	Sequence 8, Appl1	466	6	1.8	159	2	US-09-489-039A-12575	Sequence 12575, A
394	6	1.8	122	2	US-09-424-840B-24	Sequence 24, Appl1	467	6	1.8	159	2	US-09-248-796A-18945	Sequence 18945, A
395	6	1.8	122	2	US-09-949-016-9711	Sequence 9711, Ap	468	6	1.8	160	2	US-09-270-767-42851	Sequence 42851, A
396	6	1.8	124	2	US-09-134-001C-2930	Sequence 2930, Ap	469	6	1.8	155	2	US-09-270-767-46481	Sequence 46481, A
397	6	1.8	125	1	US-08-473-981A-10	Sequence 10, Appl1	470	6	1.8	154	2	US-09-902-540-15344	Sequence 15344, A
398	6	1.8	125	1	US-08-474-087-10	Sequence 10, Appl1	471	6	1.8	166	2	US-08-916-576B-6	Sequence 6, Appl1
399	6	1.8	125	1	US-09-543-681A-4730	Sequence 4730, Ap	472	6	1.8	166	2	US-09-213-2930-18	Sequence 18, Appl1
400	6	1.8	127	2	US-09-513-999C-4184	Sequence 4184, Ap	473	6	1.8	166	2	US-10-078-337-6	Sequence 6, Appl1
401	6	1.8	127	2	US-09-513-999C-4185	Sequence 4185, Ap	474	6	1.8	168	1	US-08-193-977-9	Sequence 9, Appl1
402	6	1.8	128	2	US-09-461-325-165	Sequence 165, App	475	6	1.8	170	2	US-09-205-258-1011	Sequence 1011, Ap
403	6	1.8	128	2	US-10-012-542-165	Sequence 165, App	476	6	1.8	170	2	US-10-004-860-1011	Sequence 1011, Ap
404	6	1.8	128	2	US-10-115-123-165	Sequence 165, App	477	6	1.8	171	2	US-09-646-028-9	Sequence 9, Appl1
405	6	1.8	129	2	US-09-509-559B-13	Sequence 13, Appl1	478	6	1.8	172	2	US-09-252-991A-23876	Sequence 23876, A
406	6	1.8	130	2	US-09-248-796A-27313	Sequence 27313, A	479	6	1.8	172	2	US-09-198-452A-1195	Sequence 1195, Ap
407	6	1.8	130	2	US-09-605-703B-2870	Sequence 2870, Ap	480	6	1.8	174	1	US-08-768-564-13	Sequence 13, Appl1
408	6	1.8	131	2	US-09-248-796A-26343	Sequence 26343, A	481	6	1.8	174	2	US-09-005-299-13	Sequence 13, Appl1
409	6	1.8	131	2	US-09-640-211A-673	Sequence 673, App	482	6	1.8	174	2	US-09-515-331-13	Sequence 13, Appl1
410	6	1.8	132	2	US-09-513-999C-4373	Sequence 4373, Ap	483	6	1.8	174	2	US-09-640-211A-768	Sequence 768, App
411	6	1.8	133	2	US-09-252-991A-31726	Sequence 31726, A	484	6	1.8	175	2	US-09-270-767-32147	Sequence 32147, A
412	6	1.8	134	2	US-09-252-991A-18396	Sequence 18396, A	485	6	1.8	175	2	US-09-270-767-47384	Sequence 47384, A
413	6	1.8	134	2	US-09-759-143-910	Sequence 910, App	486	6	1.8	175	2	US-09-302-540-11358	Sequence 11358, A
414	6	1.8	134	2	US-10-012-896-910	Sequence 910, App	487	6	1.8	176	2	US-09-309-317-2	Sequence 2, Appl1
415	6	1.8	136	2	US-09-205-258-465	Sequence 465, App	488	6	1.8	176	2	US-09-949-016-6706	Sequence 6706, Ap
416	6	1.8	136	2	US-09-270-767-31763	Sequence 31763, A	489	6	1.8	176	2	US-09-902-540-11336	Sequence 11336, A
417	6	1.8	136	2	US-09-270-767-47000	Sequence 47000, A	490	6	1.8	177	2	US-09-252-991A-20614	Sequence 20614, A
418	6	1.8	136	2	US-10-004-860-465	Sequence 465, App	491	6	1.8	177	2	US-09-893-737-30	Sequence 30, Appl1
419	6	1.8	137	2	US-09-205-258-308	Sequence 308, App	492	6	1.8	179	2	US-09-438-185A-444	Sequence 444, App
420	6	1.8	137	2	US-10-004-860-308	Sequence 308, App	493	6	1.8	180	2	US-09-270-767-32273	Sequence 32273, A
421	6	1.8	137	2	US-10-104-047-3766	Sequence 3766, Ap	494	6	1.8	180	2	US-09-270-767-47490	Sequence 47490, A
422	6	1.8	140	2	US-09-543-681A-6488	Sequence 6488, Ap	495	6	1.8	182	2	US-09-107-532A-5701	Sequence 5701, Ap
423	6	1.8	141	2	US-09-248-796A-22756	Sequence 22756, A	496	6	1.8	183	2	US-08-858-207A-401	Sequence 401, App
424	6	1.8	141	2	US-09-902-540-13787	Sequence 13787, A	497	6	1.8	186	2	US-09-248-796A-21757	Sequence 21757, A
425	6	1.8	142	2	US-09-270-767-37079	Sequence 37079, A	498	6	1.8	186	2	US-09-949-016-9722	Sequence 9722, Ap
426	6	1.8	142	2	US-09-270-767-52296	Sequence 52296, A	499	6	1.8	187	2	US-09-583-110-5246	Sequence 5246, Ap
427	6	1.8	143	2	US-09-270-767-80539	Sequence 80539, A	500	6	1.8	187	2	US-09-949-016-11428	Sequence 11428, A
428	6	1.8	145	2	US-09-338-352-7720	Sequence 7720, Ap	501	6	1.8	188	2	US-09-270-767-43077	Sequence 43077, A
429	6	1.8	146	2	US-09-732-210-621	Sequence 621, App	502	6	1.8	188	2	US-09-902-540-13118	Sequence 13118, A
430	6	1.8	146	2	US-09-270-767-72099	Sequence 72099, A	503	6	1.8	190	2	US-09-605-703B-950	Sequence 950, App
431	6	1.8	146	2	US-09-270-767-47316	Sequence 47316, A	504	6	1.8	190	2	US-09-605-703B-952	Sequence 952, App
432	6	1.8	146	2	US-09-640-211A-680	Sequence 680, App	505	6	1.8	191	2	US-08-671-548C-30	Sequence 30, Appl1
433	6	1.8	147	2	US-09-355-160D-7	Sequence 7, Appl1	506	6	1.8	191	2	US-09-350-841A-1593	Sequence 1593, Ap
434	6	1.8	147	2	US-10-092-219-7	Sequence 7, Appl1	507	6	1.8	191	2	US-08-284-667A-30	Sequence 30, Appl1
435	6	1.8	148	2	US-09-270-767-35815	Sequence 35815, A	508	6	1.8	193	2	US-08-671-548C-20	Sequence 20, Appl1
436	6	1.8	148	2	US-09-270-767-51032	Sequence 51032, A	509	6	1.8	193	2	US-08-671-548C-36	Sequence 36, Appl1
437	6	1.8	149	2	US-08-836-075A-30	Sequence 30, Appl1	510	6	1.8	193	2	US-08-284-667A-20	Sequence 20, Appl1
438	6	1.8	149	2	US-08-635-886C-283	Sequence 283, App	511	6	1.8	193	2	US-08-284-667A-36	Sequence 36, Appl1
439	6	1.8	149	2	US-08-974-690C-283	Sequence 283, App	512	6	1.8	194	2	US-08-671-548C-26	Sequence 26, Appl1
440	6	1.8	149	2	US-09-270-767-37973	Sequence 37973, A	513	6	1.8	194	2	US-08-284-667A-26	Sequence 26, Appl1
441	6	1.8	149	2	US-09-270-767-54940	Sequence 54940, A	514	6	1.8	196	2	US-08-981-392-35	Sequence 35, Appl1
442	6	1.8	151	2	US-09-564-329A-15	Sequence 15, Appl1	515	6	1.8	196	2	US-09-328-352-5098	Sequence 5098, Ap
443	6	1.8	151	2	US-09-270-767-35961	Sequence 35961, A	516	6	1.8	196	2	US-09-908-322-35	Sequence 35, Appl1
444	6	1.8	151	2	US-09-270-767-51178	Sequence 51178, A	517	6	1.8	196	2	US-09-605-703B-1914	Sequence 1914, Ap
445	6	1.8	151	2	US-09-963-620-15	Sequence 15, Appl1	518	6	1.8	199	1	US-08-768-964-12	Sequence 12, Appl1
446	6	1.8	151	2	US-09-855-632-15	Sequence 15, Appl1	519	6	1.8	199	2	US-09-005-299-12	Sequence 12, Appl1
447	6	1.8	151	2	US-09-934-773-15	Sequence 15, Appl1	520	6	1.8	199	2	US-09-515-431-12	Sequence 12, Appl1
448	6	1.8	151	2	US-09-855-153-15	Sequence 15, Appl1	521	6	1.8	199	2	US-09-252-991A-30003	Sequence 30003, A
449	6	1.8	152	2	US-10-224-720-15	Sequence 15, Appl1	522	6	1.8	201	2	US-09-902-540-14022	Sequence 14022, A
450	6	1.8	152	2	US-09-270-767-33006	Sequence 33006, A	523	6	1.8	204	1	US-08-185-432-8	Sequence 8, Appl1
451	6	1.8	152	2	US-09-270-767-48223	Sequence 48223, A	524	6	1.8	205	2	US-09-134-000C-3393	Sequence 3393, Ap
452	6	1.8	153	2	US-09-270-767-44655	Sequence 44655, A	525	6	1.8	205	2	US-09-270-767-43874	Sequence 43874, A
453	6	1.8	153	2	US-09-605-703B-1634	Sequence 1634, Ap	526	6	1.8	206	2	US-09-562-737-51	Sequence 51, Appl1
454	6	1.8	154	2	US-09-583-110-4155	Sequence 4155, Ap	527	6	1.8	206	2	US-09-562-737-55	Sequence 55, Appl1
455	6	1.8	155	2	US-09-107-532A-6942	Sequence 6942, Ap	528	6	1.8	206	2	US-09-562-737-56	Sequence 56, Appl1
456	6	1.8	156	2	US-09-646-028-4	Sequence 4, Appl1	529	6	1.8	206	2	US-09-562-737-57	Sequence 57, Appl1
457	6	1.8	156	2	US-09-148-545-136	Sequence 136, App	530	6	1.8	206	2	US-09-538-092-795	Sequence 795, App
458	6	1.8	156	2	US-09-949-016-9452	Sequence 9452, App	531	6	1.8	206	2	US-09-489-847-285	Sequence 285, App
459	6	1.8	156	2	US-09-621-011-136	Sequence 136, App	532	6	1.8	207	2	US-09-270-767-32689	Sequence 32689, A
460	6	1.8	157	2	US-08-872-855-6	Sequence 6, Appl1	533	6	1.8	207	2	US-09-270-767-47906	Sequence 47906, A
461	6	1.8	157	2	US-08-981-392-68	Sequence 68, Appl1	534	6	1.8	208	2	US-08-657-749D-21	Sequence 21, Appl1
462	6	1.8	157	2	US-09-252-991A-22516	Sequence 22516, A	535	6	1.8	208	2	US-08-235-836C-32	Sequence 32, Appl1
463	6	1.8	157	2	US-09-908-322-68	Sequence 68, Appl1	536	6	1.8	209	2	US-09-697-367-10	Sequence 10, Appl1
464	6	1.8	157	2	US-09-310-685-20	Sequence 20, Appl1	537	6	1.8	210	2	US-09-134-001C-4790	Sequence 4790, Ap
465	6	1.8	158	2	US-09-252-991A-26205	Sequence 26205, A	538	6	1.8	210	2		



539	6	1.8	210	2	US-09-918-909A-10	Sequence 10, Appl	612	6	1.8	251	2	US-09-248-796A-18124	Sequence 18124, A
540	6	1.8	211	2	US-09-252-991A-25965	Sequence 25965, A	613	6	1.8	252	2	US-09-949-016-10380	Sequence 10380, A
541	6	1.8	212	1	US-08-158-353-4	Sequence 4, Appl1	614	6	1.8	253	2	US-09-352-991A-17553	Sequence 17553, A
542	6	1.8	212	1	US-08-763-121-1	Sequence 1, Appl1	615	6	1.8	253	2	US-09-310-463-36	Sequence 36, Appl
543	6	1.8	212	1	US-08-878-957-54	Sequence 34, Appl	616	6	1.8	253	2	US-09-370-767-42144	Sequence 42144, A
544	6	1.8	212	2	US-09-196-293-11	Sequence 11, Appl	617	6	1.8	254	2	US-09-240-915-7	Sequence 7, Appl1
545	6	1.8	212	2	US-08-209-603E-11	Sequence 11, Appl	618	6	1.8	254	2	US-09-591-435-7	Sequence 7, Appl1
546	6	1.8	212	2	US-08-235-836C-34	Sequence 34, Appl	619	6	1.8	254	2	US-10-098-600B-7	Sequence 7, Appl1
547	6	1.8	212	2	US-09-216-066-1	Sequence 1, Appl1	620	6	1.8	256	2	US-09-543-681A-482	Sequence 482, Ap
548	6	1.8	212	2	US-09-711-546-11	Sequence 11, Appl	621	6	1.8	257	1	US-07-781-355-2	Sequence 2, Appl1
549	6	1.8	212	2	US-09-270-767-56499	Sequence 36499, A	622	6	1.8	257	1	US-08-287-959-4	Sequence 4, Appl1
550	6	1.8	212	2	US-09-270-767-38211	Sequence 51716, A	623	6	1.8	258	2	US-09-252-991A-25067	Sequence 25067, A
551	6	1.8	212	2	US-09-270-767-51716	Sequence 53428, A	624	6	1.8	258	2	US-09-352-991A-29435	Sequence 29435, A
552	6	1.8	212	2	US-09-270-767-53428	Sequence 7, Appl1	625	6	1.8	260	2	US-09-352-991A-22230	Sequence 23230, A
553	6	1.8	212	2	US-09-974-992B-7	Sequence 11, Appl	626	6	1.8	261	2	US-09-502-540-10632	Sequence 10632, A
554	6	1.8	212	2	US-10-289-795-11	Sequence 3, Appl1	627	6	1.8	263	1	US-08-768-964-2	Sequence 2, Appl1
555	6	1.8	213	1	US-08-763-121-3	Sequence 3, Appl1	628	6	1.8	263	2	US-09-005-299-2	Sequence 2, Appl1
556	6	1.8	213	2	US-09-216-066-3	Sequence 13705, A	629	6	1.8	263	2	US-09-515-431-2	Sequence 2, Appl1
557	6	1.8	213	2	US-09-902-540-13705	Sequence 9, Appl1	630	6	1.8	263	2	US-09-198-452A-1063	Sequence 1063, Ap
558	6	1.8	214	2	US-09-187-789-9	Sequence 9, Appl1	631	6	1.8	263	2	US-09-438-185A-785	Sequence 785, Ap
559	6	1.8	214	2	US-09-989-903-9	Sequence 7, Appl1	632	6	1.8	263	2	US-10-104-047-3558	Sequence 3558, Ap
560	6	1.8	215	2	US-09-583-110-5435	Sequence 3435, Ap	633	6	1.8	265	2	US-09-310-463-34	Sequence 34, Appl
561	6	1.8	216	2	US-09-489-039A-7265	Sequence 7265, Ap	634	6	1.8	266	1	US-07-857-224B-40	Sequence 40, Appl
562	6	1.8	217	2	US-09-630-454-196	Sequence 186, App	635	6	1.8	266	2	US-09-147-550-11	Sequence 11, Appl
563	6	1.8	217	2	US-09-252-991A-30641	Sequence 30641, A	636	6	1.8	266	2	US-09-557-917-11	Sequence 11, Appl
564	6	1.8	218	1	US-08-463-115-92	Sequence 92, Appl	637	6	1.8	267	2	US-09-543-681A-5904	Sequence 5904, Ap
565	6	1.8	218	1	US-08-465-388-92	Sequence 92, Appl	638	6	1.8	267	2	US-09-134-000C-5723	Sequence 5723, Ap
566	6	1.8	219	2	US-09-270-767-41489	Sequence 41489, A	639	6	1.8	269	2	US-09-270-767-44310	Sequence 44310, A
567	6	1.8	219	2	US-09-248-796A-21540	Sequence 21540, A	640	6	1.8	272	1	US-08-690-095-1	Sequence 1, Appl1
568	6	1.8	221	2	US-09-583-110-3552	Sequence 3352, Ap	641	6	1.8	272	2	US-09-510-367C-19	Sequence 19, Appl
569	6	1.8	221	2	US-09-107-433-3993	Sequence 3993, Ap	642	6	1.8	274	2	US-09-525-991A-27466	Sequence 27466, A
570	6	1.8	222	2	US-09-589-733C-11	Sequence 11, Appl	643	6	1.8	274	2	US-09-915-524-19	Sequence 19, Appl
571	6	1.8	222	2	US-10-104-047-3510	Sequence 3510, Ap	644	6	1.8	274	2	US-09-934-634-19	Sequence 19, Appl
572	6	1.8	223	1	US-08-394-189B-22	Sequence 22, Appl	645	6	1.8	274	2	US-09-917-278-19	Sequence 19, Appl
573	6	1.8	223	2	US-09-465-901-12	Sequence 12, Appl	646	6	1.8	274	6	5489533-2	Patent No. 5489533
574	6	1.8	223	2	US-09-888-243-22	Sequence 22, Appl	647	6	1.8	274	6	5512660-2	Patent No. 5512660
575	6	1.8	226	2	US-09-869-388-10	Sequence 10, Appl	648	6	1.8	275	2	US-09-248-796A-18804	Sequence 18804, A
576	6	1.8	227	2	US-09-593-887-16	Sequence 16, Appl	649	6	1.8	276	2	US-09-270-767-44216	Sequence 44216, A
577	6	1.8	227	2	US-09-869-388-6	Sequence 6, Appl1	650	6	1.8	278	2	US-09-570-367C-2	Sequence 2, Appl1
578	6	1.8	229	2	US-09-764-803B-4	Sequence 4, Appl1	651	6	1.8	278	2	US-09-570-367C-21	Sequence 21, Appl
579	6	1.8	230	2	US-09-187-789-7	Sequence 7, Appl1	652	6	1.8	278	2	US-09-915-524-2	Sequence 2, Appl1
580	6	1.8	230	2	US-09-989-903-7	Sequence 7, Appl1	653	6	1.8	278	2	US-09-915-524-2	Sequence 2, Appl1
581	6	1.8	231	2	US-09-252-991A-25675	Sequence 25675, A	654	6	1.8	278	2	US-09-915-524-21	Sequence 21, Appl1
582	6	1.8	232	1	US-08-425-763-2	Sequence 2, Appl1	655	6	1.8	278	2	US-09-934-634-21	Sequence 21, Appl1
583	6	1.8	232	1	US-07-934-373C-32	Sequence 32, Appl	656	6	1.8	278	2	US-09-917-278-2	Sequence 2, Appl1
584	6	1.8	232	2	US-08-437-642B-32	Sequence 32, Appl	657	6	1.8	278	2	US-09-917-278-21	Sequence 21, Appl
585	6	1.8	232	2	US-08-811-757-2	Sequence 2, Appl1	658	6	1.8	278	2	US-09-917-278-21	Sequence 21, Appl
586	6	1.8	232	2	US-09-249-230-2	Sequence 2, Appl1	659	6	1.8	282	2	US-09-247-890-16	Sequence 16, Appl
587	6	1.8	232	4	PCT-US93-07832-32	Sequence 32, Appl1	660	6	1.8	282	2	US-09-724-969-16	Sequence 16, Appl
588	6	1.8	233	2	US-09-107-433-8676	Sequence 2676, Ap	661	6	1.8	282	2	US-09-724-852-16	Sequence 16, Appl
589	6	1.8	234	2	US-09-270-767-56898	Sequence 56898, A	662	6	1.8	282	2	US-09-134-000C-4468	Sequence 4468, Ap
590	6	1.8	237	2	US-09-107-522A-6553	Sequence 6553, Ap	663	6	1.8	283	2	US-09-904-615-106	Sequence 106, App
591	6	1.8	237	2	US-09-710-279-162	Sequence 162, App	664	6	1.8	283	2	US-10-054-988-106	Sequence 106, App
592	6	1.8	238	1	US-08-768-964-7	Sequence 7, Appl1	665	6	1.8	285	2	US-09-583-110-4775	Sequence 4775, Ap
593	6	1.8	238	2	US-09-005-299-7	Sequence 7, Appl1	666	6	1.8	287	2	US-09-310-463-32	Sequence 32, Appl1
594	6	1.8	238	2	US-09-515-431-7	Sequence 7, Appl1	667	6	1.8	287	2	US-09-252-991A-30447	Sequence 30447, A
595	6	1.8	238	2	US-09-149-476-485	Sequence 485, App	668	6	1.8	287	2	US-09-489-039A-14187	Sequence 14187, A
596	6	1.8	238	2	US-09-949-016-11628	Sequence 11628, A	669	6	1.8	287	2	US-09-949-016-7477	Sequence 7477, Ap
597	6	1.8	241	2	US-09-489-039A-7888	Sequence 7888, Ap	670	6	1.8	288	2	US-09-489-039A-12218	Sequence 12218, A
598	6	1.8	242	2	US-09-187-789-5	Sequence 5, Appl1	671	6	1.8	292	2	US-09-107-433-3232	Sequence 3232, Ap
599	6	1.8	242	2	US-09-252-991A-24652	Sequence 24652, A	672	6	1.8	293	2	US-09-252-991A-26267	Sequence 26267, A
600	6	1.8	242	2	US-09-764-803B-25	Sequence 25, Appl	673	6	1.8	294	2	US-09-270-767-56859	Sequence 56859, A
601	6	1.8	242	2	US-09-764-803B-26	Sequence 26, Appl	674	6	1.8	295	2	US-09-902-540-13497	Sequence 13497, A
602	6	1.8	242	2	US-09-764-803B-26	Sequence 26, Appl	675	6	1.8	297	2	US-09-632-847B-4	Sequence 4, Appl1
603	6	1.8	242	2	US-09-989-903-5	Sequence 5, Appl1	676	6	1.8	298	2	US-09-232-160-17	Sequence 17, Appl
604	6	1.8	242	2	US-09-851-873-105	Sequence 105, App	677	6	1.8	298	2	US-09-252-991A-23700	Sequence 23700, A
605	6	1.8	244	2	US-09-724-823-82	Sequence 82, Appl	678	6	1.8	298	2	US-09-800-729-87	Sequence 87, Appl
606	6	1.8	245	2	US-09-413-614-6	Sequence 6, Appl1	679	6	1.8	298	2	US-09-800-729-121	Sequence 121, App
607	6	1.8	245	2	US-08-425-630-30	Sequence 20, Appl	680	6	1.8	298	2	US-09-582-934-2	Sequence 2, Appl1
608	6	1.8	246	2	US-09-198-452A-22	Sequence 22, Appl	681	6	1.8	298	2	US-09-248-796A-27392	Sequence 27392, A
609	6	1.8	246	2	US-09-438-185A-13	Sequence 13, Appl	682	6	1.8	298	2	US-10-000-489-22	Sequence 22, Appl
610	6	1.8	248	2	US-09-482-273-126	Sequence 126, App	683	6	1.8	298	2	US-09-832-129-50	Sequence 50, Appl
611	6	1.8	251	2	US-09-602-787A-434	Sequence 434, App	684	6	1.8	298	2	US-10-104-047-2809	Sequence 2809, App



685	6	1.8	299	2	US-09-310-463-30	Sequence 30, Appl	758	6	1.8	332	1	US-08-442-281-7	Sequence 7, Appl1
686	6	1.8	300	2	US-09-343-681A-6670	Sequence 6670, Ap	759	6	1.8	332	1	US-08-939-727-7	Sequence 7, Appl1
687	6	1.8	300	2	US-09-107-532A-4953	Sequence 4953, Ap	760	6	1.8	333	2	US-09-198-452E-652	Sequence 652, App
688	6	1.8	301	2	US-09-582-934-1	Sequence 1, Appl1	761	6	1.8	334	2	US-09-252-991A-18120	Sequence 18120, A
689	6	1.8	302	2	US-09-874-923-122	Sequence 122, App	762	6	1.8	334	2	US-09-252-991A-22395	Sequence 22395, A
690	6	1.8	303	1	US-08-185-432-5	Sequence 5, Appl1	763	6	1.8	335	1	US-07-947-130-3	Sequence 3, Appl1
691	6	1.8	304	2	US-09-632-947B-7	Sequence 7, Appl1	764	6	1.8	335	1	US-08-421-822-3	Sequence 3, Appl1
692	6	1.8	304	2	US-09-489-039A-11906	Sequence 11906, A	765	6	1.8	335	1	US-08-421-823-3	Sequence 3, Appl1
693	6	1.8	305	2	US-09-540-236-5603	Sequence 3603, Ap	766	6	1.8	335	2	US-09-543-681A-7733	Sequence 7733, Ap
694	6	1.8	306	2	US-09-902-540-15500	Sequence 15500, A	767	6	1.8	335	2	US-09-438-185A-615	Sequence 615, App
695	6	1.8	307	2	US-09-949-016-9817	Sequence 9817, Ap	768	6	1.8	337	1	US-09-013-634-4	Sequence 7, Appl1
696	6	1.8	307	2	US-09-949-016-9818	Sequence 9818, Ap	769	6	1.8	339	2	US-10-169-048-40	Sequence 40, Appl
697	6	1.8	307	2	US-09-303-518D-404	Sequence 404, App	770	6	1.8	340	2	US-09-543-681A-5967	Sequence 5967, Ap
698	6	1.8	307	2	US-09-303-518D-406	Sequence 406, App	771	6	1.8	342	2	US-09-071-035-104	Sequence 104, App
699	6	1.8	307	2	US-09-303-518D-408	Sequence 408, App	772	6	1.8	342	2	US-10-206-576-104	Sequence 104, Appl
700	6	1.8	308	2	US-09-252-991A-20337	Sequence 20337, A	773	6	1.8	344	2	US-09-110-116-4	Sequence 4, Appl1
701	6	1.8	308	2	US-09-710-279-1072	Sequence 1072, Ap	774	6	1.8	344	2	US-10-121-575B-20	Sequence 20, Appl
702	6	1.8	308	2	US-09-710-279-7706	Sequence 2706, Ap	775	6	1.8	345	2	US-09-252-991A-16669	Sequence 16669, A
703	6	1.8	308	2	US-10-014-269-31	Sequence 31, Appl	776	6	1.8	346	2	US-09-724-924-6	Sequence 6, Appl1
704	6	1.8	308	2	US-10-002-974-31	Sequence 31, Appl	777	6	1.8	346	2	US-10-093-317-6	Sequence 6, Appl1
705	6	1.8	309	1	US-08-729-202-1	Sequence 1, Appl1	778	6	1.8	346	4	PCT-US96-10602-2	Sequence 2, Appl1
706	6	1.8	309	1	US-08-896-371-1	Sequence 1, Appl1	779	6	1.8	347	2	US-08-857-076-100	Sequence 100, App
707	6	1.8	309	2	US-08-996-338-22	Sequence 22, Appl	780	6	1.8	348	2	US-09-270-767-46628	Sequence 46628, A
708	6	1.8	309	2	US-09-556-972-22	Sequence 22, Appl	781	6	1.8	349	1	US-08-118-270-7	Sequence 7, Appl1
709	6	1.8	309	2	US-09-902-540-13383	Sequence 13383, A	782	6	1.8	349	4	PCT-US93-08528-7	Sequence 7, Appl1
710	6	1.8	310	2	US-09-252-991A-16914	Sequence 16914, A	783	6	1.8	350	2	US-09-161-241-9	Sequence 9, Appl1
711	6	1.8	310	2	US-09-270-767-52725	Sequence 32725, A	784	6	1.8	350	2	US-09-907-794A-236	Sequence 236, App
712	6	1.8	311	2	US-09-222-939-8	Sequence 8, Appl1	785	6	1.8	350	2	US-09-905-125A-236	Sequence 236, App
713	6	1.8	311	2	US-09-252-991A-28068	Sequence 28068, A	786	6	1.8	350	2	US-09-902-775A-236	Sequence 236, App
714	6	1.8	311	2	US-09-543-681A-4963	Sequence 4963, Ap	787	6	1.8	350	2	US-09-906-700-236	Sequence 236, App
715	6	1.8	311	2	US-10-023-528-8	Sequence 8, Appl1	788	6	1.8	350	2	US-09-903-603A-236	Sequence 236, App
716	6	1.8	311	2	US-10-423-330-8	Sequence 8, Appl1	789	6	1.8	350	2	US-09-904-920A-236	Sequence 236, App
717	6	1.8	312	1	US-08-808-931-22	Sequence 22, Appl	790	6	1.8	350	2	US-09-909-064-236	Sequence 236, App
718	6	1.8	312	1	US-08-808-933-22	Sequence 22, Appl	791	6	1.8	350	2	US-09-905-381A-236	Sequence 236, App
719	6	1.8	312	2	US-09-050-603A-22	Sequence 22, Appl	792	6	1.8	350	2	US-09-906-618-236	Sequence 236, App
720	6	1.8	312	2	US-09-102-420B-22	Sequence 22, Appl	793	6	1.8	350	2	US-09-906-646-236	Sequence 236, App
721	6	1.8	312	2	US-09-487-688-22	Sequence 22, Appl	794	6	1.8	350	2	US-09-904-462-236	Sequence 236, App
722	6	1.8	312	2	US-09-107-532A-6219	Sequence 6219, Ap	795	6	1.8	350	2	US-09-902-736A-236	Sequence 236, App
723	6	1.8	312	2	US-09-730-525-22	Sequence 22, Appl	796	6	1.8	350	2	US-09-906-722A-236	Sequence 236, App
724	6	1.8	313	2	US-09-347-803-25	Sequence 25, Appl	797	6	1.8	352	1	US-08-933-750C-46	Sequence 46, Appl1
725	6	1.8	313	2	US-09-252-991A-22411	Sequence 22411, A	798	6	1.8	352	2	US-09-234-613-46	Sequence 46, Appl1
726	6	1.8	313	2	US-09-252-991A-24305	Sequence 24305, A	799	6	1.8	353	2	US-09-252-991A-25209	Sequence 25209, A
727	6	1.8	313	2	US-09-248-796A-20918	Sequence 20918, A	800	6	1.8	353	2	US-09-543-681A-7190	Sequence 7190, Ap
728	6	1.8	314	2	US-09-107-532A-4919	Sequence 4919, Ap	801	6	1.8	353	2	US-09-949-016-7210	Sequence 7210, Ap
729	6	1.8	315	1	US-07-757-390-8	Sequence 8, Appl1	802	6	1.8	354	1	US-08-394-189B-20	Sequence 20, Appl
730	6	1.8	315	1	US-08-442-282-8	Sequence 8, Appl1	803	6	1.8	354	2	US-09-888-243-20	Sequence 20, Appl
731	6	1.8	315	1	US-08-442-281-8	Sequence 8, Appl1	804	6	1.8	356	2	US-09-198-452A-526	Sequence 526, App
732	6	1.8	315	1	US-08-939-727-8	Sequence 8, Appl1	805	6	1.8	358	2	US-09-934-901-8	Sequence 8, Appl1
733	6	1.8	315	2	US-09-252-991A-25763	Sequence 25763, A	806	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
734	6	1.8	315	2	US-09-311-021-56	Sequence 26, Appl	807	6	1.8	358	2	US-09-710-279-18	Sequence 18, Appl
735	6	1.8	316	2	US-09-252-991A-18829	Sequence 18829, A	808	6	1.8	358	2	US-10-321-210-8	Sequence 8, Appl1
736	6	1.8	317	2	US-09-252-991A-22489	Sequence 22489, A	809	6	1.8	358	2	US-10-320-874-8	Sequence 8, Appl1
737	6	1.8	318	2	US-09-134-001C-3852	Sequence 3852, Ap	810	6	1.8	358	2	US-10-320-924-8	Sequence 8, Appl1
738	6	1.8	318	2	US-09-902-540-11076	Sequence 11076, A	811	6	1.8	358	2	US-10-701-300-18	Sequence 18, Appl
739	6	1.8	319	2	US-09-134-000C-5242	Sequence 5242, Ap	812	6	1.8	360	2	US-09-602-787A-364	Sequence 364, App
740	6	1.8	319	2	US-09-438-185A-989	Sequence 989, App	813	6	1.8	360	2	US-09-270-767-46743	Sequence 46743, A
741	6	1.8	320	2	US-09-248-796A-20977	Sequence 20977, A	814	6	1.8	361	2	US-09-668-097B-36	Sequence 36, Appl
742	6	1.8	321	2	US-09-107-433-6282	Sequence 4282, Ap	815	6	1.8	362	2	US-09-134-001C-5403	Sequence 5403, Ap
743	6	1.8	324	2	US-09-252-991A-24664	Sequence 24664, A	816	6	1.8	363	2	US-09-252-991A-18016	Sequence 18016, A
744	6	1.8	325	2	US-09-248-796A-25600	Sequence 25600, A	817	6	1.8	363	2	US-09-252-991A-25052	Sequence 25052, A
745	6	1.8	328	2	US-09-270-767-58409	Sequence 38409, A	818	6	1.8	364	2	US-09-205-258-1008	Sequence 1008, Ap
746	6	1.8	328	2	US-09-270-767-53626	Sequence 53626, A	819	6	1.8	364	2	US-09-417-4850-49	Sequence 49, Appl
747	6	1.8	328	2	US-09-477-962-124	Sequence 124, App	820	6	1.8	364	2	US-10-004-860-1008	Sequence 1008, Ap
748	6	1.8	329	1	US-08-225-477B-3	Sequence 3, Appl1	821	6	1.8	365	2	US-09-949-016-8601	Sequence 8601, Ap
749	6	1.8	329	1	US-08-562-535C-4	Sequence 4, Appl1	822	6	1.8	365	2	US-09-348-796A-16945	Sequence 16945, A
750	6	1.8	329	1	US-08-742-605D-4	Sequence 4, Appl1	823	6	1.8	368	2	US-09-248-796A-16492	Sequence 16492, A
751	6	1.8	329	2	US-09-259-294-6	Sequence 4, Appl1	824	6	1.8	368	2	US-09-949-016-8544	Sequence 8544, Ap
752	6	1.8	329	2	US-09-489-039A-10276	Sequence 10276, A	825	6	1.8	368	2	US-09-605-703B-1708	Sequence 1708, Ap
753	6	1.8	329	4	PCT-US95-04353-3	Sequence 3, Appl1	826	6	1.8	369	2	US-09-902-540-11382	Sequence 11382, A
754	6	1.8	329	4	PCT-US95-04353-3	Sequence 3, Appl1	827	6	1.8	370	2	US-09-724-224-2	Sequence 2, Appl1
755	6	1.8	331	1	US-08-356-180-3	Sequence 3, Appl1	828	6	1.8	370	2	US-10-093-317-2	Sequence 2, Appl1
756	6	1.8	332	1	US-07-757-390-7	Sequence 7, Appl1	829	6	1.8	371	1	US-08-225-477B-8	Sequence 8, Appl1
757	6	1.8	332	1	US-08-442-282-7	Sequence 7, Appl1	830	6	1.8	371	2	US-09-148-545-259	Sequence 259, App



831	6	1.8	371	2	US-09-621-011-259	Sequence 259, App	904	6	1.8	414	2	US-09-248-796A-19046	Sequence 19046, A
832	6	1.8	371	4	PCT-US95-04353-8	Sequence 8, Appl1	905	6	1.8	414	2	US-09-908-9928-10	Sequence 10, Appl1
833	6	1.8	372	2	US-09-071-035-102	Sequence 102, App	906	6	1.8	415	1	US-07-757-390-5	Sequence 5, Appl1
834	6	1.8	372	2	US-09-252-991A-28586	Sequence 28586, A	907	6	1.8	415	1	US-08-442-282-5	Sequence 5, Appl1
835	6	1.8	372	2	US-09-252-991A-30132	Sequence 30132, A	908	6	1.8	415	1	US-08-442-281-5	Sequence 5, Appl1
836	6	1.8	372	2	US-09-270-767-45792	Sequence 45792, A	909	6	1.8	415	1	US-08-939-727-5	Sequence 5, Appl1
837	6	1.8	372	2	US-10-206-576-102	Sequence 102, App	910	6	1.8	415	2	US-09-886-319A-23	Sequence 23, Appl1
838	6	1.8	375	2	US-09-949-016-7856	Sequence 7856, Ap	911	6	1.8	417	2	US-09-489-039A-12272	Sequence 12272, A
839	6	1.8	375	2	US-09-949-016-7857	Sequence 7857, Ap	912	6	1.8	419	2	US-08-974-691-3	Sequence 3, Appl1
840	6	1.8	375	2	US-09-949-016-7858	Sequence 7858, Ap	913	6	1.8	419	2	US-09-705-448-10	Sequence 10, Appl1
841	6	1.8	375	2	US-09-902-540-12456	Sequence 12456, A	914	6	1.8	421	2	US-09-543-681A-7791	Sequence 7791, Ap
842	6	1.8	376	2	US-09-270-767-44545	Sequence 44545, A	915	6	1.8	423	1	US-08-290-731C-10	Sequence 10, Appl1
843	6	1.8	377	2	US-08-888-077A-27	Sequence 27, Appl	916	6	1.8	423	1	US-08-290-731C-11	Sequence 11, Appl1
844	6	1.8	377	2	US-09-665-479A-16	Sequence 16, Appl	917	6	1.8	423	2	US-08-855-910-13	Sequence 13, Appl
845	6	1.8	377	2	US-09-710-279-2926	Sequence 2926, Ap	918	6	1.8	424	2	US-09-328-352-4199	Sequence 4199, Ap
846	6	1.8	378	4	PCT-US95-04353-9	Sequence 9, Appl1	919	6	1.8	426	2	US-09-252-991A-20025	Sequence 20025, A
847	6	1.8	378	4	PCT-US95-04353-9	Sequence 9, Appl1	920	6	1.8	426	2	US-10-332-795-14	Sequence 14, Appl1
848	6	1.8	379	2	US-09-489-039A-11991	Sequence 11991, A	921	6	1.8	427	2	US-09-134-000C-5142	Sequence 5142, Ap
849	6	1.8	379	2	US-09-724-797-54	Sequence 54, Appl	922	6	1.8	430	2	US-08-956-171B-5244	Sequence 5244, Ap
850	6	1.8	380	2	US-09-710-279-1402	Sequence 1402, Ap	923	6	1.8	430	2	US-08-781-986A-5244	Sequence 5244, Ap
851	6	1.8	380	2	US-09-902-540-16242	Sequence 16242, A	924	6	1.8	430	2	US-09-248-796A-14556	Sequence 14556, A
852	6	1.8	382	2	US-09-029-333-2	Sequence 2, Appl1	925	6	1.8	433	2	US-09-252-991A-20728	Sequence 20728, A
853	6	1.8	382	2	US-09-270-767-42344	Sequence 42344, A	926	6	1.8	433	2	US-09-302-540-15313	Sequence 15313, A
854	6	1.8	383	2	US-09-248-796A-19589	Sequence 19589, A	927	6	1.8	436	2	US-09-252-991A-22081	Sequence 22081, A
855	6	1.8	384	2	US-08-946-026-27	Sequence 27, Appl	928	6	1.8	437	2	US-09-248-796A-20561	Sequence 20561, A
856	6	1.8	386	2	US-09-724-623-70	Sequence 70, Appl	929	6	1.8	437	2	US-09-252-991A-32048	Sequence 32048, A
857	6	1.8	386	2	US-10-154-515A-2	Sequence 2, Appl1	930	6	1.8	438	2	US-09-583-110-4975	Sequence 4975, Ap
858	6	1.8	386	2	US-10-122-706-2	Sequence 2, Appl1	931	6	1.8	440	1	US-08-808-931-24	Sequence 24, Appl1
859	6	1.8	387	1	US-08-123-161A-10	Sequence 10, Appl	932	6	1.8	440	2	US-08-808-323-24	Sequence 24, Appl1
860	6	1.8	387	1	US-08-123-161A-12	Sequence 12, Appl	933	6	1.8	440	2	US-09-050-603A-24	Sequence 24, Appl1
861	6	1.8	387	1	US-08-483-278-10	Sequence 10, Appl	934	6	1.8	440	2	US-09-102-420B-24	Sequence 24, Appl
862	6	1.8	387	1	US-08-483-278-12	Sequence 12, Appl	935	6	1.8	440	2	US-09-497-698-24	Sequence 24, Appl
863	6	1.8	387	2	US-09-134-001C-3625	Sequence 3607, A	936	6	1.8	440	2	US-09-730-525-24	Sequence 24, Appl
864	6	1.8	389	2	US-09-248-796A-17305	Sequence 17305, A	937	6	1.8	442	2	US-09-252-991A-30607	Sequence 30607, A
865	6	1.8	390	1	US-07-817-920-6	Sequence 6, Appl1	938	6	1.8	443	2	US-09-107-433-5150	Sequence 5150, Ap
866	6	1.8	390	1	US-08-117-006-6	Sequence 6, Appl1	939	6	1.8	446	2	US-09-370-767-57633	Sequence 57633, A
867	6	1.8	390	1	US-08-216-594-6	Sequence 6, Appl1	940	6	1.8	446	2	US-09-502-540-12677	Sequence 12677, A
868	6	1.8	390	1	US-08-461-812-4	Sequence 4, Appl1	941	6	1.8	446	2	US-09-489-039A-12786	Sequence 12786, A
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870	6	1.8	390	2	US-08-281-526B-15	Sequence 15, Appl	943	6	1.8	452	2	US-09-328-352-5528	Sequence 5528, Ap
871	6	1.8	390	2	US-09-450-790A-15	Sequence 15, Appl	944	6	1.8	453	2	US-09-270-767-44967	Sequence 44967, A
872	6	1.8	390	2	US-09-332-837-15	Sequence 15, Appl	945	6	1.8	454	1	US-07-934-373C-22	Sequence 22, Appl
873	6	1.8	390	2	US-09-371-705-4	Sequence 4, Appl1	946	6	1.8	454	2	US-08-437-642B-22	Sequence 22, Appl1
874	6	1.8	390	2	US-09-826-509-427	Sequence 427, App	947	6	1.8	454	2	US-08-929-329-8	Sequence 8, Appl1
875	6	1.8	390	4	PCT-US93-00149-6	Sequence 6, Appl1	948	6	1.8	454	2	US-08-146-206C-22	Sequence 22, Appl1
876	6	1.8	392	2	US-09-949-016-9728	Sequence 9728, Ap	949	6	1.8	454	2	US-09-705-686-22	Sequence 22, Appl1
877	6	1.8	394	2	US-09-270-767-43783	Sequence 43783, A	950	6	1.8	454	2	US-09-705-392A-22	Sequence 22, Appl
878	6	1.8	395	2	US-09-328-352-6660	Sequence 6660, Ap	951	6	1.8	454	2	US-09-902-540-12301	Sequence 12501, A
879	6	1.8	395	2	US-09-543-681A-6203	Sequence 6, Appl1	952	6	1.8	454	4	PCT-US93-07832-22	Sequence 22, Appl
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883	6	1.8	398	1	US-08-542-358-6	Sequence 6, Appl1	956	6	1.8	459	1	US-08-870-518-4	Sequence 4, Appl1
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885	6	1.8	398	1	US-08-939-727-6	Sequence 6, Appl1	958	6	1.8	459	2	US-09-606-304-4	Sequence 4, Appl1
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891	6	1.8	406	2	US-09-134-001C-3544	Sequence 3544, Ap	964	6	1.8	461	2	US-09-949-016-8839	Sequence 8839, Ap
892	6	1.8	409	2	US-09-258-754-449	Sequence 449, App	965	6	1.8	461	2	US-10-104-047-3865	Sequence 3865, Ap
893	6	1.8	409	2	US-09-676-475A-449	Sequence 449, App	966	6	1.8	462	1	US-08-865-597A-2	Sequence 2, Appl1
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902	6	1.8	414	2	US-09-543-681A-4320	Sequence 4320, Ap	975	6	1.8	466	2	US-09-009-656-14	Sequence 14, Appl
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995	6	1.8	479	2	US-09-489-039A-10571	Sequence 10571, A	1068	6	1.8	509	2	US-10-018-386-5	Sequence 5, Appli
996	6	1.8	479	2	US-09-540-236-2292	Sequence 2292, Ap	1069	6	1.8	509	2	US-10-215-224-2	Sequence 2, Appli
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1005	6	1.8	481	2	US-09-102-420B-6	Sequence 6, Appli	1078	6	1.8	511	2	US-09-759-143-909	Sequence 909, Appli
1006	6	1.8	481	2	US-09-015-683-6	Sequence 6, Appli	1079	6	1.8	511	2	US-10-012-896-909	Sequence 909, App
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1016	6	1.8	487	2	US-09-724-224-8	Sequence 8, Appli	1089	6	1.8	515	2	US-09-949-016-6445	Sequence 6445, Ap
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1129	6	1.8	537	2	US-09-102-420B-2	Sequence 2, Appl1	1202	6	1.8	590	2	US-09-895-752-54	Sequence 54, Appl
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1131	6	1.8	537	2	US-09-196-268-2	Sequence 2, Appl1	1204	6	1.8	590	2	US-09-800-797-54	Sequence 54, Appl
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1134	6	1.8	537	2	US-09-497-698-2	Sequence 2, Appl1	1207	6	1.8	597	2	US-09-302-540-11095	Sequence 2632, Ap
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1138	6	1.8	539	1	US-08-808-333-16	Sequence 16, Appl	1211	6	1.8	611	2	US-09-662-254B-19	Sequence 19, Appl
1139	6	1.8	539	2	US-09-050-603A-16	Sequence 16, Appl	1212	6	1.8	613	1	US-08-915-207-2	Sequence 2, Appl1
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1141	6	1.8	539	2	US-09-497-698-16	Sequence 16, Appl	1214	6	1.8	613	2	US-09-238-555-2	Sequence 2, Appl1
1142	6	1.8	539	2	US-09-730-525-16	Sequence 16, Appl	1215	6	1.8	613	2	US-09-238-555-4	Sequence 4, Appl1
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1145	6	1.8	541	2	US-09-110-618-2	Sequence 2, Appl1	1218	6	1.8	616	1	US-08-268-161A-115	Sequence 115, App
1146	6	1.8	541	2	US-09-173-151A-28	Sequence 28, Appl1	1219	6	1.8	616	1	US-08-453-702A-115	Sequence 115, App
1147	6	1.8	541	2	US-09-578-178-2	Sequence 2, Appl1	1220	6	1.8	616	4	US-09-099-639-115	Sequence 115, App
1148	6	1.8	541	2	US-09-577-806-2	Sequence 2, Appl1	1221	6	1.8	616	4	PCT-US95-08071-115	Sequence 115, App
1149	6	1.8	541	2	US-09-621-502-4	Sequence 4, Appl1	1222	6	1.8	617	2	US-08-679-493A-77	Sequence 77, Appl
1150	6	1.8	541	2	US-09-949-002-360	Sequence 360, App	1223	6	1.8	618	2	US-09-603-208A-32	Sequence 32, Appl
1151	6	1.8	543	1	US-08-808-931-12	Sequence 12, Appl	1224	6	1.8	618	2	US-09-603-208A-34	Sequence 34, Appl
1152	6	1.8	543	2	US-08-808-333-12	Sequence 12, Appl	1225	6	1.8	619	2	US-09-949-016-6308	Sequence 6308, Ap
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1165	6	1.8	548	2	US-08-687-590-31	Sequence 31, Appl	1238	6	1.8	641	2	US-10-267-311-51	Sequence 51, Appl
1166	6	1.8	548	2	US-09-508-418A-2	Sequence 2, Appl1	1239	6	1.8	648	2	US-08-800-291B-8	Sequence 8, Appl1
1167	6	1.8	552	2	US-09-949-016-9572	Sequence 9572, Ap	1240	6	1.8	648	2	US-09-487-358B-422	Sequence 422, App
1168	6	1.8	552	2	US-09-955-732A-15	Sequence 15, Appl	1241	6	1.8	648	2	US-09-595-684B-35	Sequence 35, Appl
1169	6	1.8	552	2	US-09-775-925-4	Sequence 2, Appl1	1242	6	1.8	649	2	US-09-489-039A-10538	Sequence 1, Appl1
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1178	6	1.8	560	2	US-09-102-420B-18	Sequence 18, Appl	1251	6	1.8	661	2	US-09-487-358B-422	Sequence 35, Appl
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Sequence 11, Appl1

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US-08-056-200-94

Sequence 94, Appl1

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US-08-800-644-94

Sequence 94, Appl1

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US-09-538-092-1280

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Sequence 6756, Ap

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US-08-514-975B-2

Sequence 2, Appl1

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US-09-368-076-29

Sequence 29, Appl1

RESULT 1

US-09-991-181-253

Sequence 253, Application US/09991181

Patent No. 6913919

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gunney, Austin L.

APPLICANT: Kijavini, Ivar J.

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APPLICANT: Tumas, Daniel

APPLICANT: Matanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C53

CURRENT APPLICATION NUMBER: US/09/991,181

CURRENT FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

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PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

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PRIOR FILING DATE: 1998-04-28

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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

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Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Patent No. 6953836  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Kljavin, Ivar J.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin



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FILE REFERENCE: P2730P1C27  
CURRENT FILING DATE: 2001-11-15  
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QY 61 VTIOBGGTIIVTQNRNRERVDPPDGYSLKLSKLKNDGSIYVGIYSSSLQDPSTQEX 120  
DB 61 VTIOBGGTIIVTQNRNRERVDPPDGYSLKLSKLKNDGSIYVGIYSSSLQDPSTQEX 120  
QY 121 VLAHYEHLSKRPVTMGLQSNKGTCTNLTCCMEHGEEDVITYWKALGOANESHNGSIL 180  
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QY 181 PISRWGSDMTFICVANPVSRYNPSPIILARKLCEGAADPDSSMTLLCLLVPILLSL 240  
DB 181 PISRWGSDMTFICVANPVSRYNPSPIILARKLCEGAADPDSSMTLLCLLVPILLSL 240  
QY 241 FVLGLFLWFLKREOEYIEBKKEVDLCRETPNICPHSGENTYDTPHTNRITLIKEDPA 300  
DB 241 FVLGLFLWFLKREOEYIEBKKEVDLCRETPNICPHSGENTYDTPHTNRITLIKEDPA 300  
QY 301 NTVYSTVEIPKKNPHSLTMPDTPRLPAYENVY 335  
DB 301 NTVYSTVEIPKKNPHSLTMPDTPRLPAYENVY 335

RESULT 4  
US-09-992-598-253  
; Sequence 253, Application US/09992538  
; Patent No. 6956108  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Batron, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerbstein, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.

;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas P.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tamas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C20  
;; CURRENT APPLICATION NUMBER: US/09/992,598  
;; CURRENT FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
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;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066770  
;; PRIOR FILING DATE: 1997-11-24  
;; PRIOR APPLICATION NUMBER: 60/075945  
;; PRIOR FILING DATE: 1998-02-25  
;; PRIOR APPLICATION NUMBER: 60/078910  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/083322  
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;; PRIOR FILING DATE: 1998-05-07  
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;; PRIOR FILING DATE: 1998-05-28  
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;; PRIOR FILING DATE: 1998-06-02  
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;; PRIOR FILING DATE: 1998-06-09  
;; PRIOR APPLICATION NUMBER: 60/088734



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PRIOR FILING DATE: 1998-06-22  
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PRIOR FILING DATE: 1998-06-23  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24

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PRIOR FILING DATE: 1998-06-26  
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PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 3.6e-314;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MAGSPCTCTTIIYITMOLITGSAASGPVKEIVGSGAVTFPLKSKVKQVDSITVMTFNTPL 60  
61 VTIOPEGGTTIIVTONRRRERVDPPDGGYSLKSLTKKNDSGIYYVGIYSSSLQOPSTQEX 120  
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61 VTIOPEGGTTIIVTONRRRERVDPPDGGYSLKSLTKKNDSGIYYVGIYSSSLQOPSTQEX 120  
121 VLAHYEHLSPKXYTMGLQSNKNGTCVTNLTCCMEHGEDVITYWKALQOANESHNGSIL 180  
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121 VLAHYEHLSPKXYTMGLQSNKNGTCVTNLTCCMEHGEDVITYWKALQOANESHNGSIL 180  
181 PISWRGSDMTFCVARNPYSRFPSSPILARKLCEGAADPDSSMTLLCLLVPILLSL 240  
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181 PISWRGSDMTFCVARNPYSRFPSSPILARKLCEGAADPDSSMTLLCLLVPILLSL 240  
241 FVLGLFLMPLKREKQSEYIEKKKVDICRETPTNICPSGENTEXDTIPIHRTTIKEDPA 300  
|||||  
241 FVLGLFLMPLKREKQSEYIEKKKVDICRETPTNICPSGENTEXDTIPIHRTTIKEDPA 300  
301 NTVYSTEIIPKQENPHSLTMDPTPRLFAVENYI 335  
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301 NTVYSTEIIPKQENPHSLTMDPTPRLFAVENYI 335

RESULT 5  
US-09-513-999C-4472  
; Sequence 4472, Application US/0951399C



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; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4472
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -22...-1
; OTHER INFORMATION: score 5.9
; OTHER INFORMATION: seq LYLIMOLTGSA/SG
US-09-513-999C-4472
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Qy      61 VTIOPEGTIIIVTONRNRERVPFDGGYSLKSLK 97
Db      61 VTIOPEGTIIIVTONRNRERVPFDGGYSLKSLK 97
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RESULT 6
US-09-466-778-8
; Sequence 8, Application US/09466778
; Patent No. 6872546
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg et al.
; TITLE OF INVENTION: No. 6872546e1 Hyaluronan-Binding Proteins and Encoding Genes
; FILE REFERENCE: PF487
; CURRENT APPLICATION NUMBER: US/09/466,778
; CURRENT FILING DATE: 1999-12-20
; EARLIER APPLICATION NUMBER: 60/113,871
; EARLIER FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-466-778-8
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Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      231 LLAVPLLL 238
Db      4 LLAVPLLL 11
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RESULT 7
US-09-907-794A-213
; Sequence 213, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
```

```
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsens, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jenite P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 213
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-213

Query Match          2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 231 LLLVPLLL 238  
 Db 4 LLLVPLLL 11

RESULT 8  
 US-09-905-125A-213  
 ; Sequence 213, Application US/09905125A  
 ; Patent No. 6664376  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genentech, Inc.  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Deenoyers, Luc  
 ; APPLICANT: Baton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, A.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth, J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Mather, Jennie P.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William, I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: 10466-14  
 ; CURRENT APPLICATION NUMBER: US/09/905,125A  
 ; CURRENT FILING DATE: 2001-07-12  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: 2000-02-22  
 ; PRIOR APPLICATION NUMBER: US 60/143,048  
 ; PRIOR FILING DATE: 1999-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/145,698  
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 ; PRIOR APPLICATION NUMBER: US 60/146,222  
 ; PRIOR FILING DATE: 1999-07-28  
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 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089  
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 ; PRIOR FILING DATE: 1999-11-30  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565  
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 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911  
 ; PRIOR FILING DATE: 1999-12-20  
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 ; PRIOR FILING DATE: 1999-12-20

;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
 ;; PRIOR FILING DATE: 2000-01-05  
 ;; NUMBER OF SEQ ID NOS: 423  
 ;; SEQ ID NO 213  
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 ;; TYPE: PRT  
 ;; ORGANISM: Homo sapiens  
 US-09-905-125A-213

Query Match 2.4%; Score 8; DB 2; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 231 LLLVPLLL 238  
 Db 4 LLLVPLLL 11

RESULT 9  
 US-09-902-775A-213  
 ; Sequence 213, Application US/09902775A  
 ; Patent No. 6686451  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genentech, Inc.  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Deenoyers, Luc  
 ; APPLICANT: Baton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, A.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth, J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Mather, Jennie P.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William, I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: 10466-14  
 ; CURRENT APPLICATION NUMBER: US/09/902,775A  
 ; CURRENT FILING DATE: 2001-07-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: 2000-02-22  
 ; PRIOR APPLICATION NUMBER: US 60/143,048  
 ; PRIOR FILING DATE: 1999-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/145,698  
 ; PRIOR FILING DATE: 1999-07-26  
 ; PRIOR APPLICATION NUMBER: US 60/146,222  
 ; PRIOR FILING DATE: 1999-07-28  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594  
 ; PRIOR FILING DATE: 1999-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944  
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 ; PRIOR APPLICATION NUMBER: PCT/US99/23089  
 ; PRIOR FILING DATE: 1999-10-05  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214  
 ; PRIOR FILING DATE: 1999-11-29



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;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
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;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 213
;; LENGTH: 360
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-902-775A-213

Query Match      2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      231 LLLVPLLL 238
Db      4 LLLVPLLL 11

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US-09-906-700-213
; Sequence 213, Application US/09906700
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Macher, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906, 700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143, 048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145, 698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146, 222
; PRIOR FILING DATE: 1999-07-28
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;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 213
;; LENGTH: 360
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-906-700-213
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Query Match 2.4%; Score 8; DB 2; Length 360;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      4 LLLVPLLL 11
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US-09-903-603A-213
; Sequence 213, Application US/09903603A
; Patent No. 6'6795
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Macher, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903.603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
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; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-903-603A-213

Query Match      2.4% Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      4  LLLVPLLL 11

RESULT 12
US-09-904-920A-213
; Sequence 213, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

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; APPLICANT: Gurney, Auecin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904.920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
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; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/28564
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 213
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-904-920A-213

Query Match      2.4% Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      231  LLLVPLLL 238
Db      4  LLLVPLLL 11

RESULT 13
US-09-909-064-213
; Sequence 213, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
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APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Balon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OR INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/909,064  
CURRENT FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
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PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 213  
LENGTH: 360  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-909-064-213

Query Match 2.4%; Score 8; DB 2; Length 360;  
Best Local Similarity 100.0%; Pred. NO. 24;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 LLLVPLL 238  
Db 4 LLLVPLL 11

RESULT 14  
US-09-905-381A-213  
Sequence 213, Application US/09905381A  
Patent No. 6818746  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Balon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OR INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/905,381A  
CURRENT FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
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PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219



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; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
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; ORGANISM: Homo sapiens
US-09-905-381A-213

Query Match      2.4%; Score 8; DB 2; Length 360;
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Db      4 LLLVPLLL 11

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; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: US/09/906,618
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
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; PRIOR FILING DATE: 1999-12-20
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; PRIOR FILING DATE: 2000-01-05
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; SEQ ID NO 213
; LENGTH: 360
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; ORGANISM: Homo sapiens
US-09-906-618-213

Query Match      2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      231 LLLVPLLL 238
Db      4 LLLVPLLL 11
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Gapop 60.0 , Gapext 60.0

Searched: 51470 seqs, 6736768 residues

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

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Published Applications AA-New:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	7	2.1	104	6 US-10-689-742-206	Sequence 206, Appl
4	7	2.1	539	7 US-11-069-642-16	Sequence 16, Appl
5	7	2.1	540	6 US-10-770-726-80	Sequence 80, Appl
6	6	1.8	33	7 US-11-069-642-146	Sequence 146, Appl
7	6	1.8	33	7 US-11-198-847-3	Sequence 3, Appl1
8	6	1.8	33	7 US-11-198-847-237	Sequence 237, Appl
9	6	1.8	51	6 US-10-467-657-2114	Sequence 2114, Appl
10	6	1.8	83	7 US-11-198-847-2	Sequence 2, Appl1
11	6	1.8	86	7 US-11-123-896-230	Sequence 230, Appl
12	6	1.8	101	7 US-11-053-076-157	Sequence 157, Appl
13	6	1.8	140	6 US-10-467-657-2486	Sequence 2486, Appl
14	6	1.8	168	7 US-11-108-172-631	Sequence 631, Appl
15	6	1.8	169	6 US-10-467-657-1526	Sequence 1526, Appl
16	6	1.8	176	6 US-10-467-657-1526	Sequence 1526, Appl
17	6	1.8	209	7 US-11-196-475-12	Sequence 12, Appl
18	6	1.8	212	7 US-11-196-475-14	Sequence 14, Appl
19	6	1.8	222	6 US-10-821-234-4117	Sequence 4117, Appl
20	6	1.8	232	7 US-11-173-564-2	Sequence 2, Appl1
21	6	1.8	237	6 US-10-793-626-162	Sequence 162, Appl
22	6	1.8	252	7 US-11-054-515-1994	Sequence 1994, Appl
23	6	1.8	256	6 US-11-137-465-34	Sequence 34, Appl
24	6	1.8	265	6 US-10-689-742-188	Sequence 188, Appl
25	6	1.8	280	6 US-10-467-657-4208	Sequence 4208, Appl
26	6	1.8	286	7 US-11-194-246-320	Sequence 320, Appl

27	6	1.8	288	6 US-10-821-234-1062	Sequence 1062, Appl
28	6	1.8	307	6 US-10-467-657-6016	Sequence 6016, Appl
29	6	1.8	308	6 US-10-793-626-1072	Sequence 1072, Appl
30	6	1.8	308	6 US-10-793-626-2706	Sequence 2706, Appl
31	6	1.8	317	6 US-10-485-517-196	Sequence 196, Appl
32	6	1.8	339	6 US-10-467-657-4318	Sequence 4318, Appl
33	6	1.8	350	7 US-11-102-240-8	Sequence 8, Appl1
34	6	1.8	355	6 US-10-503-051-2	Sequence 2, Appl1
35	6	1.8	358	6 US-10-485-517-227	Sequence 227, Appl
36	6	1.8	358	6 US-10-793-626-18	Sequence 18, Appl1
37	6	1.8	360	7 US-11-082-389-90	Sequence 90, Appl1
38	6	1.8	360	7 US-11-082-389-92	Sequence 92, Appl1
39	6	1.8	364	6 US-10-995-561-783	Sequence 783, Appl
40	6	1.8	371	6 US-10-821-234-1010	Sequence 1010, Appl
41	6	1.8	377	6 US-10-793-626-2926	Sequence 2926, Appl
42	6	1.8	380	6 US-10-793-626-1402	Sequence 1402, Appl
43	6	1.8	403	6 US-10-793-626-1522	Sequence 1522, Appl
44	6	1.8	443	7 US-11-196-475-166	Sequence 166, Appl
45	6	1.8	446	7 US-11-143-980-39	Sequence 39, Appl1
46	6	1.8	447	6 US-10-467-657-364	Sequence 364, Appl
47	6	1.8	468	6 US-10-957-569-28	Sequence 28, Appl1
48	6	1.8	468	6 US-10-995-561-907	Sequence 907, Appl
49	6	1.8	468	7 US-11-076-187-2	Sequence 2, Appl1
50	6	1.8	468	7 US-11-055-822-68	Sequence 68, Appl1
51	6	1.8	480	7 US-11-074-176-2	Sequence 2, Appl1
52	6	1.8	484	7 US-11-078-735-43	Sequence 43, Appl1
53	6	1.8	497	6 US-10-821-234-1358	Sequence 1358, Appl
54	6	1.8	525	6 US-10-467-657-5462	Sequence 5462, Appl
55	6	1.8	543	7 US-11-113-324-6	Sequence 6, Appl1
56	6	1.8	557	6 US-10-821-234-1593	Sequence 1593, Appl
57	6	1.8	553	7 US-11-113-424-18	Sequence 18, Appl1
58	6	1.8	567	6 US-10-503-051-5	Sequence 5, Appl1
59	6	1.8	635	6 US-10-467-657-2076	Sequence 2076, Appl
60	6	1.8	635	6 US-10-467-657-6374	Sequence 6374, Appl
61	6	1.8	671	7 US-11-029-003-6	Sequence 6, Appl1
62	6	1.8	684	6 US-10-714-781A-55	Sequence 55, Appl1
63	6	1.8	684	6 US-10-714-781A-57	Sequence 57, Appl1
64	6	1.8	684	6 US-10-714-781A-61	Sequence 61, Appl1
65	6	1.8	686	6 US-10-714-781A-59	Sequence 59, Appl1
66	6	1.8	723	7 US-11-078-735-17	Sequence 17, Appl1
67	6	1.8	733	6 US-10-821-234-1147	Sequence 1147, Appl
68	6	1.8	745	7 US-11-135-855-37	Sequence 37, Appl1
69	6	1.8	794	6 US-10-793-626-1050	Sequence 1050, Appl
70	6	1.8	816	7 US-11-143-980-67	Sequence 67, Appl1
71	6	1.8	827	6 US-10-821-234-1685	Sequence 1685, Appl
72	6	1.8	830	6 US-10-995-561-1899	Sequence 899, Appl
73	6	1.8	843	6 US-10-645-441-7	Sequence 7, Appl1
74	6	1.8	843	6 US-10-645-441-8	Sequence 8, Appl1
75	6	1.8	843	6 US-11-137-465-35	Sequence 35, Appl1
76	6	1.8	897	7 US-11-137-465-35	Sequence 35, Appl1
77	6	1.8	961	7 US-11-137-465-58	Sequence 58, Appl1
78	6	1.8	965	7 US-11-113-424-2	Sequence 2, Appl1
79	6	1.8	965	7 US-11-147-047-51	Sequence 51, Appl1
80	6	1.8	993	7 US-11-137-465-36	Sequence 36, Appl1
81	6	1.8	1041	6 US-10-995-561-780	Sequence 780, Appl
82	6	1.8	1041	6 US-10-995-561-782	Sequence 782, Appl
83	6	1.8	1097	6 US-10-995-561-781	Sequence 781, Appl
84	6	1.8	1468	6 US-10-467-657-1088	Sequence 1088, Appl
85	6	1.8	1767	6 US-10-995-561-911	Sequence 911, Appl
86	6	1.8	1767	6 US-10-995-561-914	Sequence 912, Appl
87	6	1.8	1806	6 US-10-995-561-912	Sequence 910, Appl
88	6	1.8	1806	6 US-10-995-561-915	Sequence 915, Appl
89	6	1.8	1818	6 US-10-995-561-910	Sequence 913, Appl
90	6	1.8	1818	6 US-10-995-561-913	Sequence 913, Appl
91	6	1.8	1818	6 US-10-714-781A-67	Sequence 67, Appl1
92	6	1.8	5732	6 US-11-143-980-47	Sequence 47, Appl1
93	6	1.8	7102	7 US-11-143-980-48	Sequence 48, Appl1
94	6	1.8	7968	7 US-11-119-098-15	Sequence 15, Appl1
95	6	1.8	8	7 US-11-045-024-1583	Sequence 1583, Appl
96	6	1.8	8	7 US-11-045-024-5290	Sequence 5290, Appl
97	6	1.8	8	7 US-11-045-024-1575	Sequence 1575, Appl
98	6	1.8	8	7 US-11-045-024-1685	Sequence 1685, Appl
99	6	1.8	8	7 US-11-045-024-1685	Sequence 1685, Appl
100	6	1.8	8	7 US-11-045-024-1685	Sequence 1685, Appl
101	6	1.8	8	7 US-11-045-024-1685	Sequence 1685, Appl
102	6	1.8	8	7 US-11-045-024-1685	Sequence 1685, Appl



103	5	1.5	9	7	US-11-045-024-4424	Sequence 4424, Ap	176	5	1.5	59	6	US-10-667-295-170	Sequence 170, App
104	5	1.5	9	7	US-11-045-024-5817	Sequence 5817, Ap	177	5	1.5	59	6	US-10-467-657-1236	Sequence 1236, Ap
105	5	1.5	9	7	US-11-045-024-12723	Sequence 12723, A	178	5	1.5	59	6	US-10-467-657-5178	Sequence 5178, Ap
106	5	1.5	9	7	US-11-045-024-13889	Sequence 13889, A	179	5	1.5	59	7	US-11-068-717-14	Sequence 14, Appl
107	5	1.5	9	7	US-11-045-024-13805	Sequence 13905, A	180	5	1.5	64	7	US-11-000-463-262	Sequence 262, App
108	5	1.5	10	6	US-10-491-096-6	Sequence 6, Appl1	181	5	1.5	64	7	US-11-000-463-734	Sequence 734, App
109	5	1.5	10	6	US-10-491-096-69	Sequence 69, Appl1	182	5	1.5	66	6	US-10-467-657-2614	Sequence 2614, App
110	5	1.5	10	6	US-10-491-096-101	Sequence 101, App	183	5	1.5	66	6	US-10-995-561-801	Sequence 801, App
111	5	1.5	10	6	US-10-491-096-166	Sequence 166, App	184	5	1.5	66	7	US-11-000-463-419	Sequence 419, App
112	5	1.5	10	7	US-11-045-024-2018	Sequence 2018, App	185	5	1.5	66	7	US-11-000-463-891	Sequence 891, App
113	5	1.5	10	7	US-11-045-024-2020	Sequence 2020, App	186	5	1.5	66	7	US-11-068-717-13	Sequence 13, Appl1
114	5	1.5	10	7	US-11-045-024-4573	Sequence 4573, Ap	187	5	1.5	69	6	US-10-467-657-7568	Sequence 7568, Ap
115	5	1.5	10	7	US-11-045-024-7583	Sequence 7583, Ap	188	5	1.5	70	6	US-10-467-657-4268	Sequence 4268, Ap
116	5	1.5	10	7	US-11-045-024-7660	Sequence 7660, Ap	189	5	1.5	70	7	US-11-000-463-235	Sequence 235, App
117	5	1.5	11	7	US-11-045-024-2249	Sequence 2249, App	190	5	1.5	70	7	US-11-000-463-737	Sequence 737, App
118	5	1.5	11	7	US-11-045-024-2251	Sequence 2251, Ap	191	5	1.5	73	7	US-11-102-240-140	Sequence 148, App
119	5	1.5	11	7	US-11-045-024-3360	Sequence 3360, App	192	5	1.5	74	7	US-11-000-463-420	Sequence 420, App
120	5	1.5	11	7	US-11-045-024-4726	Sequence 4726, Ap	193	5	1.5	74	7	US-11-000-463-892	Sequence 892, App
121	5	1.5	11	7	US-11-045-024-4727	Sequence 4727, Ap	194	5	1.5	74	7	US-11-123-896-380	Sequence 380, App
122	5	1.5	11	7	US-11-045-024-4729	Sequence 4729, Ap	195	5	1.5	76	6	US-10-467-657-8532	Sequence 8532, Ap
123	5	1.5	11	7	US-11-045-024-6621	Sequence 6621, Ap	196	5	1.5	76	7	US-11-123-896-263	Sequence 263, App
124	5	1.5	11	7	US-11-045-024-9736	Sequence 9736, Ap	197	5	1.5	76	7	US-11-123-896-404	Sequence 404, App
125	5	1.5	11	7	US-11-045-024-11724	Sequence 11724, A	198	5	1.5	77	7	US-11-102-240-56	Sequence 56, Appl1
126	5	1.5	11	7	US-11-045-024-12701	Sequence 12701, A	199	5	1.5	77	7	US-11-123-896-371	Sequence 371, App
127	5	1.5	12	6	US-10-467-657-1386	Sequence 1386, Ap	200	5	1.5	78	7	US-11-102-240-66	Sequence 66, Appl1
128	5	1.5	12	6	US-10-467-657-7526	Sequence 7526, Ap	201	5	1.5	79	6	US-10-467-657-1146	Sequence 1146, Ap
129	5	1.5	14	7	US-11-054-515-2768	Sequence 2768, Ap	202	5	1.5	79	6	US-10-467-657-5402	Sequence 5402, Ap
130	5	1.5	14	7	US-11-054-515-2815	Sequence 2815, Ap	204	5	1.5	82	7	US-11-123-896-287	Sequence 287, App
131	5	1.5	15	7	US-11-106-932-134	Sequence 134, App	205	5	1.5	85	6	US-10-485-517-205	Sequence 205, App
132	5	1.5	15	7	US-11-045-024-13233	Sequence 13233, A	206	5	1.5	85	6	US-10-485-517-237	Sequence 237, App
133	5	1.5	15	7	US-11-045-024-13243	Sequence 13243, A	207	5	1.5	86	7	US-11-123-896-227	Sequence 227, App
134	5	1.5	15	7	US-11-045-024-13267	Sequence 13267, A	208	5	1.5	86	7	US-11-123-896-233	Sequence 233, App
135	5	1.5	19	6	US-10-503-575-330	Sequence 330, App	210	5	1.5	87	7	US-11-184-574-8	Sequence 8, Appl1
136	5	1.5	19	6	US-10-503-575-332	Sequence 332, App	219	5	1.5	89	6	US-10-467-657-2164	Sequence 2164, Ap
137	5	1.5	19	6	US-10-503-575-333	Sequence 333, App	211	5	1.5	95	6	US-10-467-657-4134	Sequence 4134, Ap
138	5	1.5	19	6	US-10-503-575-334	Sequence 334, App	212	5	1.5	96	6	US-10-467-657-8706	Sequence 8706, Ap
139	5	1.5	19	6	US-10-503-575-340	Sequence 340, App	213	5	1.5	97	7	US-11-144-248-36	Sequence 36, Appl1
140	5	1.5	20	6	US-10-509-170-6	Sequence 6, Appl1	215	5	1.5	97	7	US-11-144-248-44	Sequence 44, Appl1
141	5	1.5	20	6	US-11-094-142-24	Sequence 24, Appl1	216	5	1.5	97	7	US-11-053-076-126	Sequence 126, App
142	5	1.5	21	6	US-10-986-501-260	Sequence 260, App	217	5	1.5	97	7	US-11-054-669-40	Sequence 40, Appl1
143	5	1.5	22	7	US-11-108-185-43	Sequence 43, Appl1	218	5	1.5	97	7	US-11-054-669-42	Sequence 42, Appl1
144	5	1.5	22	7	US-11-108-185-44	Sequence 44, Appl1	219	5	1.5	97	7	US-11-054-669-49	Sequence 49, Appl1
145	5	1.5	22	7	US-11-108-185-45	Sequence 45, Appl1	220	5	1.5	97	7	US-11-054-669-51	Sequence 51, Appl1
146	5	1.5	22	7	US-11-108-185-48	Sequence 48, Appl1	221	5	1.5	97	7	US-11-054-669-52	Sequence 52, Appl1
147	5	1.5	25	7	US-11-058-735-58	Sequence 58, Appl1	222	5	1.5	97	7	US-11-054-669-53	Sequence 53, Appl1
148	5	1.5	27	7	US-11-098-674-9	Sequence 9, Appl1	223	5	1.5	97	7	US-11-084-554-53	Sequence 54, Appl1
149	5	1.5	30	6	US-10-467-657-1044	Sequence 1044, Ap	224	5	1.5	98	7	US-11-084-554-54	Sequence 54, Appl1
150	5	1.5	30	7	US-11-106-932-18	Sequence 18, Appl1	225	5	1.5	98	6	US-10-816-768-43	Sequence 43, Appl1
151	5	1.5	30	7	US-11-106-932-43	Sequence 43, Appl1	226	5	1.5	98	6	US-10-816-768-44	Sequence 44, Appl1
152	5	1.5	30	7	US-11-106-932-44	Sequence 44, Appl1	227	5	1.5	98	7	US-11-144-248-34	Sequence 34, Appl1
153	5	1.5	34	6	US-10-816-768-32	Sequence 32, Appl1	228	5	1.5	98	7	US-11-012-353-74	Sequence 74, Appl1
154	5	1.5	34	6	US-10-816-768-33	Sequence 33, Appl1	229	5	1.5	98	7	US-11-054-669-34	Sequence 34, Appl1
155	5	1.5	34	6	US-10-990-877-1	Sequence 1, Appl1	230	5	1.5	98	7	US-11-054-669-35	Sequence 35, Appl1
156	5	1.5	36	6	US-10-467-657-7060	Sequence 7060, Ap	231	5	1.5	98	7	US-11-054-669-44	Sequence 44, Appl1
157	5	1.5	37	6	US-10-821-234-1693	Sequence 1693, App	232	5	1.5	98	7	US-11-084-554-49	Sequence 49, Appl1
158	5	1.5	37	7	US-11-069-642-147	Sequence 147, App	233	5	1.5	98	7	US-11-084-554-51	Sequence 51, Appl1
159	5	1.5	37	7	US-11-006-031-18	Sequence 18, Appl1	234	5	1.5	99	7	US-11-054-669-36	Sequence 36, Appl1
160	5	1.5	38	6	US-10-816-768-20	Sequence 20, Appl1	235	5	1.5	99	7	US-11-054-669-37	Sequence 37, Appl1
161	5	1.5	39	6	US-10-485-517-259	Sequence 259, App	240	5	1.5	99	7	US-11-054-669-38	Sequence 38, Appl1
162	5	1.5	39	6	US-10-467-657-4216	Sequence 4216, Ap	241	5	1.5	99	7	US-11-054-669-39	Sequence 39, Appl1
163	5	1.5	42	6	US-10-532-480-33	Sequence 33, Appl1	242	5	1.5	99	7	US-11-054-669-41	Sequence 41, Appl1
164	5	1.5	43	6	US-10-982-545-10	Sequence 10, Appl1	243	5	1.5	99	7	US-11-054-669-43	Sequence 43, Appl1
165	5	1.5	43	6	US-10-957-887B-91	Sequence 91, Appl1	244	5	1.5	99	7	US-11-084-554-50	Sequence 50, Appl1
166	5	1.5	45	6	US-10-467-657-6976	Sequence 6976, Ap	245	5	1.5	99	7	US-11-084-554-52	Sequence 52, Appl1
167	5	1.5	47	6	US-10-467-657-6650	Sequence 6650, Ap	246	5	1.5	99	7	US-11-084-554-55	Sequence 55, Appl1
168	5	1.5	48	6	US-10-467-657-4322	Sequence 4322, Ap	247	5	1.5	99	7	US-11-186-284-87	Sequence 87, Appl1
169	5	1.5	51	6	US-10-467-657-4506	Sequence 4506, Ap	248	5	1.5	100	6	US-10-793-626-2158	Sequence 2158, Ap
170	5	1.5	51	6	US-10-467-657-7160	Sequence 7160, Ap	249	5	1.5	100	6	US-10-793-626-2550	Sequence 2550, Ap
171	5	1.5	51	7	US-11-069-642-145	Sequence 145, App	250	5	1.5	100	6	US-11-084-554-46	Sequence 46, Appl1
172	5	1.5	53	6	US-10-467-657-2666	Sequence 2666, App	251	5	1.5	104	6	US-10-793-626-92	Sequence 92, Appl1
173	5	1.5	53	6	US-10-467-657-3714	Sequence 3714, Ap	252	5	1.5	104	6	US-10-793-626-2232	Sequence 2232, Ap
174	5	1.5	53	6	US-10-467-657-4942	Sequence 4942, Ap	253	5	1.5	104	6	US-10-793-626-2380	Sequence 2380, Ap
175	5	1.5	58	6	US-10-467-657-3828	Sequence 3828, Ap	254	5	1.5	105	6	US-10-816-768-61	Sequence 61, Appl1



250	5	1.5	107	6	US-10-467-657-1054	Sequence 1054, Ap	323	5	1.5	152	7	US-11-174-398-9	Sequence 9, Appl1
251	5	1.5	107	7	US-11-000-463-500	Sequence 300, App	324	5	1.5	153	6	US-10-467-657-3392	Sequence 3392, Ap
252	5	1.5	107	7	US-11-124-215-12	Sequence 12, Appl	325	5	1.5	163	6	US-10-467-657-2674	Sequence 2674, Ap
253	5	1.5	108	6	US-10-793-626-592	Sequence 592, App	326	5	1.5	165	6	US-10-467-657-6012	Sequence 6012, Ap
254	5	1.5	108	6	US-10-999-866-6	Sequence 6, Appl1	327	5	1.5	165	6	US-10-821-234-1293	Sequence 22, Appl
255	5	1.5	108	6	US-10-925-366A-146	Sequence 146, App	328	5	1.5	165	7	US-11-082-389-68	Sequence 68, Appl
256	5	1.5	108	6	US-10-925-366A-166	Sequence 166, App	329	5	1.5	166	6	US-10-821-234-1293	Sequence 1293, Ap
257	5	1.5	108	6	US-10-925-366A-204	Sequence 204, App	330	5	1.5	166	6	US-10-821-234-1293	Sequence 20, Appl
258	5	1.5	108	7	US-11-061-821-6	Sequence 6, Appl1	331	5	1.5	168	6	US-10-793-626-724	Sequence 724, App
259	5	1.5	108	7	US-11-053-076-210	Sequence 210, App	332	5	1.5	170	6	US-10-467-657-104	Sequence 104, App
260	5	1.5	112	6	US-10-967-457-76	Sequence 76, Appl	333	5	1.5	170	6	US-10-467-657-8078	Sequence 8078, Ap
261	5	1.5	112	6	US-10-392-224A-44	Sequence 44, Appl	334	5	1.5	172	6	US-10-667-295-2	Sequence 2838, Ap
262	5	1.5	113	7	US-11-144-248-70	Sequence 20, Appl	335	5	1.5	174	6	US-10-667-295-2	Sequence 2, Appl1
263	5	1.5	113	7	US-11-073-605-8	Sequence 8, Appl1	336	5	1.5	175	6	US-10-793-626-1336	Sequence 1336, Ap
264	5	1.5	114	6	US-10-793-626-2298	Sequence 2298, App	337	5	1.5	176	7	US-11-055-822-1084	Sequence 1084, Ap
265	5	1.5	114	6	US-10-995-561-836	Sequence 836, App	338	5	1.5	177	7	US-11-068-717-8	Sequence 8, Appl1
266	5	1.5	114	7	US-11-186-284-47	Sequence 47, Appl	339	5	1.5	177	7	US-10-522-883-17	Sequence 17, Appl
267	5	1.5	115	7	US-11-189-817-2	Sequence 2, Appl1	340	5	1.5	179	6	US-10-522-883-21	Sequence 21, Appl
268	5	1.5	116	6	US-10-793-626-1680	Sequence 1680, App	341	5	1.5	179	6	US-10-821-234-1265	Sequence 1265, Ap
269	5	1.5	116	7	US-11-054-669-112	Sequence 112, App	342	5	1.5	179	6	US-10-467-657-6542	Sequence 6542, Ap
270	5	1.5	116	7	US-11-125-837-35	Sequence 35, Appl	343	5	1.5	179	6	US-10-467-657-7772	Sequence 7772, Ap
271	5	1.5	117	7	US-11-012-353-72	Sequence 72, Appl	344	5	1.5	180	6	US-10-821-234-1552	Sequence 1552, Ap
272	5	1.5	117	7	US-11-012-353-75	Sequence 75, Appl	345	5	1.5	180	6	US-10-467-657-2	Sequence 2, Appl1
273	5	1.5	117	7	US-11-012-353-79	Sequence 79, Appl	346	5	1.5	180	6	US-10-467-657-3732	Sequence 3732, Ap
274	5	1.5	117	7	US-11-012-353-83	Sequence 83, Appl	347	5	1.5	180	6	US-10-665-455-8	Sequence 8, Appl1
275	5	1.5	117	7	US-11-012-353-162	Sequence 162, App	348	5	1.5	180	6	US-10-665-455-9	Sequence 9, Appl1
276	5	1.5	117	7	US-11-075-184A-2	Sequence 2, Appl1	349	5	1.5	180	6	US-10-665-455-10	Sequence 10, Appl1
277	5	1.5	120	6	US-10-507-662-23	Sequence 23, Appl	350	5	1.5	180	6	US-10-665-455-11	Sequence 11, Appl
278	5	1.5	120	6	US-10-507-662-24	Sequence 24, Appl	351	5	1.5	180	6	US-10-665-455-12	Sequence 12, Appl
279	5	1.5	120	6	US-11-102-201-1	Sequence 1, Appl1	352	5	1.5	180	6	US-10-665-455-13	Sequence 13, Appl
280	5	1.5	121	6	US-10-485-517-363	Sequence 363, App	353	5	1.5	180	7	US-11-157-049-12	Sequence 12, Appl
281	5	1.5	126	6	US-10-793-626-2766	Sequence 2766, App	354	5	1.5	181	6	US-10-467-657-8206	Sequence 8206, Ap
282	5	1.5	129	6	US-10-967-527A-11	Sequence 11, Appl	355	5	1.5	182	6	US-10-485-517-269	Sequence 269, App
283	5	1.5	130	7	US-11-194-246-145	Sequence 45, App	356	5	1.5	182	6	US-10-793-626-620	Sequence 620, App
284	5	1.5	131	6	US-10-689-742-192	Sequence 192, App	357	5	1.5	184	6	US-10-742-634-9	Sequence 9, Appl1
285	5	1.5	131	7	US-11-084-591-3	Sequence 3, Appl1	358	5	1.5	184	6	US-10-967-527A-8	Sequence 8, Appl1
286	5	1.5	133	6	US-10-667-295-221	Sequence 221, App	359	5	1.5	185	7	US-11-147-047-41	Sequence 41, Appl1
287	5	1.5	133	6	US-10-793-626-1106	Sequence 1106, App	360	5	1.5	186	7	US-11-044-899-24	Sequence 24, Appl
288	5	1.5	133	6	US-11-128-420-13	Sequence 13, Appl	361	5	1.5	186	7	US-11-044-899-25	Sequence 25, Appl
289	5	1.5	135	6	US-10-821-234-1018	Sequence 1018, App	362	5	1.5	187	6	US-10-980-388-39	Sequence 39, Appl
290	5	1.5	135	7	US-11-012-353-77	Sequence 77, Appl	363	5	1.5	187	6	US-10-980-388-98	Sequence 98, Appl
291	5	1.5	135	7	US-11-012-353-81	Sequence 81, Appl	365	5	1.5	188	6	US-10-821-234-1316	Sequence 1316, App
292	5	1.5	135	7	US-11-012-353-85	Sequence 85, Appl	366	5	1.5	188	6	US-10-467-657-3332	Sequence 3332, App
293	5	1.5	138	6	US-10-789-273-4	Sequence 4, Appl1	367	5	1.5	189	6	US-10-793-626-2976	Sequence 2976, App
294	5	1.5	138	6	US-10-667-295-176	Sequence 176, App	368	5	1.5	189	6	US-10-793-626-3000	Sequence 3000, App
295	5	1.5	138	7	US-11-008-727-2	Sequence 2, Appl1	370	5	1.5	193	6	US-10-793-626-1240	Sequence 1240, App
296	5	1.5	138	7	US-11-055-822-1074	Sequence 1074, App	371	5	1.5	193	6	US-10-967-527A-28	Sequence 28, Appl
297	5	1.5	139	7	US-11-125-837-24	Sequence 24, Appl1	372	5	1.5	193	7	US-11-144-889A-4	Sequence 4, Appl1
298	5	1.5	140	7	US-11-083-800-7	Sequence 7, Appl1	373	5	1.5	194	6	US-10-995-561-784	Sequence 784, App
299	5	1.5	140	7	US-11-084-591-4	Sequence 4, Appl1	374	5	1.5	194	7	US-11-108-172-1126	Sequence 1126, App
300	5	1.5	140	7	US-11-193-512-23	Sequence 23, Appl	375	5	1.5	196	6	US-10-793-626-2014	Sequence 2014, App
301	5	1.5	141	7	US-11-044-899-32	Sequence 32, Appl	376	5	1.5	197	6	US-10-467-657-4944	Sequence 4944, App
302	5	1.5	141	7	US-11-000-463-435	Sequence 435, App	377	5	1.5	201	7	US-11-069-642-25	Sequence 25, Appl
303	5	1.5	142	6	US-10-467-657-5116	Sequence 5116, App	378	5	1.5	201	1	US-09-940-308-5	Sequence 5, Appl1
304	5	1.5	146	6	US-10-721-763-17	Sequence 17, Appl	379	5	1.5	202	6	US-11-055-822-1166	Sequence 166, App
305	5	1.5	146	6	US-10-721-763-21	Sequence 21, Appl	380	5	1.5	202	6	US-10-980-388-109	Sequence 109, App
306	5	1.5	147	7	US-11-128-420-14	Sequence 14, Appl	381	5	1.5	203	7	US-11-074-176-366	Sequence 366, App
307	5	1.5	150	6	US-10-793-626-3228	Sequence 3228, App	383	5	1.5	204	7	US-11-128-440-7	Sequence 7, Appl1
308	5	1.5	151	6	US-10-821-234-1378	Sequence 3278, App	384	5	1.5	205	7	US-11-082-389-374	Sequence 374, Appl
309	5	1.5	151	6	US-10-528-031-9	Sequence 9, Appl1	385	5	1.5	205	7	US-11-082-389-378	Sequence 378, App
310	5	1.5	152	6	US-10-793-626-1122	Sequence 1122, App	386	5	1.5	207	6	US-10-793-626-3290	Sequence 3290, App
311	5	1.5	153	6	US-10-793-626-1838	Sequence 1838, App	387	5	1.5	208	6	US-10-793-626-124	Sequence 124, App
312	5	1.5	153	6	US-10-467-657-4546	Sequence 4546, App	388	5	1.5	208	6	US-10-467-657-6686	Sequence 6686, App
313	5	1.5	154	6	US-10-721-763-25	Sequence 25, Appl	389	5	1.5	209	6	US-10-793-626-688	Sequence 688, App
314	5	1.5	154	6	US-10-821-234-1366	Sequence 1366, App	390	5	1.5	209	6	US-10-793-626-2236	Sequence 2236, App
315	5	1.5	155	6	US-10-793-626-2704	Sequence 2704, App	391	5	1.5	209	6	US-10-467-657-4090	Sequence 4090, App
316	5	1.5	155	7	US-11-069-642-97	Sequence 97, Appl	392	5	1.5	211	6	US-10-858-730-102	Sequence 102, App
317	5	1.5	155	7	US-11-097-632-8	Sequence 8, Appl1	393	5	1.5	211	7	US-11-098-662-16	Sequence 16, Appl
318	5	1.5	157	6	US-10-793-626-1168	Sequence 1168, App	394	5	1.5	211	7	US-11-165-141-21	Sequence 21, Appl
319	5	1.5	158	7	US-11-097-622-10	Sequence 10, Appl	395	5	1.5	212	6	US-10-467-657-5486	Sequence 5486, App
320	5	1.5	161	6	US-10-467-962B-67	Sequence 67, Appl	396	5	1.5	212	6	US-10-467-657-7404	Sequence 7404, App
321	5	1.5	161	6	US-10-510-386-80	Sequence 80, Appl	397	5	1.5	213	6	US-10-467-657-8566	Sequence 8566, App
322	5	1.5	162	6	US-10-516-768-21	Sequence 21, Appl	398	5	1.5	214	6	US-10-467-657-7796	Sequence 7796, App



399	5	1.5	216	6	US-10-821-234-1483	Sequence 1483, Ap	472	5	1.5	246	7	US-11-054-515-2075	Sequence 2075, Ap
400	5	1.5	216	6	US-10-878-556A-191	Sequence 191, App	473	5	1.5	247	7	US-11-054-515-1651	Sequence 1651, Ap
401	5	1.5	219	6	US-10-467-657-446	Sequence 446, App	474	5	1.5	247	7	US-11-113-424-76	Sequence 76, Appl
402	5	1.5	220	7	US-11-174-150-32	Sequence 32, Appl	475	5	1.5	248	6	US-10-793-626-2982	Sequence 2982, Ap
403	5	1.5	221	6	US-10-485-517-142	Sequence 142, App	476	5	1.5	248	7	US-11-054-515-1198	Sequence 1198, Ap
404	5	1.5	221	6	US-10-793-626-2778	Sequence 2778, App	477	5	1.5	248	7	US-11-054-515-1660	Sequence 1660, Ap
405	5	1.5	223	6	US-10-467-657-2382	Sequence 2382, App	478	5	1.5	249	6	US-10-467-657-1938	Sequence 1938, Ap
406	5	1.5	223	6	US-10-793-626-3266	Sequence 3266, App	479	5	1.5	249	7	US-11-054-515-946	Sequence 946, App
407	5	1.5	224	6	US-10-884-730-5	Sequence 5, Appli	480	5	1.5	249	7	US-11-054-515-957	Sequence 957, App
408	5	1.5	225	6	US-10-884-730-5	Sequence 26, Appl	481	5	1.5	249	7	US-11-054-515-1138	Sequence 1138, Ap
409	5	1.5	225	6	US-10-467-657-26	Sequence 26, Appl	482	5	1.5	249	7	US-11-054-515-1442	Sequence 1442, Ap
410	5	1.5	226	6	US-10-793-626-1734	Sequence 1734, Ap	483	5	1.5	249	7	US-11-054-515-1618	Sequence 1618, Ap
411	5	1.5	227	6	US-10-821-234-1301	Sequence 1301, Ap	484	5	1.5	249	7	US-11-054-515-1629	Sequence 1629, Ap
412	5	1.5	228	6	US-10-467-657-1242	Sequence 1242, Ap	485	5	1.5	249	7	US-11-054-515-1730	Sequence 1730, Ap
413	5	1.5	228	6	US-10-467-657-5176	Sequence 5176, Ap	486	5	1.5	249	7	US-11-054-515-12065	Sequence 2065, App
414	5	1.5	230	6	US-10-884-730-370	Sequence 370, App	487	5	1.5	250	6	US-10-821-234-987	Sequence 987, App
415	5	1.5	230	6	US-10-884-730-371	Sequence 371, App	489	5	1.5	250	7	US-11-054-515-993	Sequence 993, App
416	5	1.5	230	6	US-10-884-730-372	Sequence 372, App	490	5	1.5	250	7	US-11-054-515-993	Sequence 993, App
417	5	1.5	230	6	US-10-884-730-373	Sequence 373, App	491	5	1.5	250	7	US-11-054-515-1413	Sequence 1413, Ap
418	5	1.5	230	6	US-10-884-730-374	Sequence 374, App	492	5	1.5	250	7	US-11-054-515-1548	Sequence 1548, Ap
419	5	1.5	230	6	US-10-884-730-375	Sequence 375, App	493	5	1.5	250	7	US-11-054-515-110	Sequence 110, App
420	5	1.5	230	6	US-10-884-730-376	Sequence 376, App	494	5	1.5	251	6	US-10-467-657-2306	Sequence 2306, Ap
421	5	1.5	230	6	US-10-884-730-377	Sequence 377, App	495	5	1.5	251	7	US-11-054-515-990	Sequence 990, App
422	5	1.5	231	6	US-10-688-742-132	Sequence 132, App	496	5	1.5	251	7	US-11-054-515-1152	Sequence 1152, Ap
423	5	1.5	231	6	US-11-000-463-745	Sequence 745, App	497	5	1.5	251	7	US-11-054-515-1316	Sequence 1316, Ap
424	5	1.5	232	6	US-10-467-657-3352	Sequence 3352, Ap	498	5	1.5	251	7	US-11-054-515-1510	Sequence 1510, Ap
425	5	1.5	232	6	US-11-100-183-38	Sequence 38, Appl	499	5	1.5	252	7	US-11-054-515-1223	Sequence 1223, Ap
426	5	1.5	232	6	US-11-170-653-64	Sequence 64, Appl	500	5	1.5	252	7	US-11-054-515-1329	Sequence 1329, Ap
427	5	1.5	233	6	US-10-793-626-1380	Sequence 1380, Ap	501	5	1.5	252	7	US-11-055-822-22	Sequence 22, Appl
428	5	1.5	233	6	US-11-074-176-272	Sequence 272, App	502	5	1.5	253	6	US-10-485-517-373	Sequence 373, App
429	5	1.5	236	6	US-10-467-657-3480	Sequence 3480, Ap	503	5	1.5	253	7	US-11-054-515-954	Sequence 954, App
430	5	1.5	236	6	US-10-878-556A-33	Sequence 33, Appl	504	5	1.5	253	7	US-11-054-515-1333	Sequence 1333, App
431	5	1.5	236	7	US-11-000-463-378	Sequence 378, App	505	5	1.5	253	7	US-11-054-515-1545	Sequence 1545, Ap
432	5	1.5	237	6	US-10-510-386-34	Sequence 34, Appl	506	5	1.5	253	7	US-11-054-515-1602	Sequence 1602, Ap
433	5	1.5	237	6	US-10-884-730-2	Sequence 2, Appli	507	5	1.5	253	7	US-11-054-515-1619	Sequence 1619, Ap
434	5	1.5	237	6	US-10-884-730-10	Sequence 10, Appl	508	5	1.5	254	6	US-10-467-657-1534	Sequence 1534, Ap
435	5	1.5	237	6	US-10-884-730-12	Sequence 12, Appl	509	5	1.5	254	7	US-11-054-515-1659	Sequence 1659, Ap
436	5	1.5	237	6	US-10-884-730-175	Sequence 175, App	510	5	1.5	255	7	US-11-054-515-1642	Sequence 1642, Ap
437	5	1.5	237	6	US-10-884-730-36	Sequence 36, Appl	511	5	1.5	255	7	US-11-185-111-36	Sequence 36, Appl
438	5	1.5	237	6	US-10-884-730-41	Sequence 41, Appl	512	5	1.5	256	7	US-11-054-515-1150	Sequence 1150, Ap
439	5	1.5	237	6	US-10-884-730-113	Sequence 113, App	513	5	1.5	256	7	US-11-054-515-1607	Sequence 1607, Ap
440	5	1.5	237	6	US-10-884-730-120	Sequence 120, App	514	5	1.5	256	7	US-11-083-800-6	Sequence 6, Appli
441	5	1.5	237	6	US-10-884-730-175	Sequence 175, App	515	5	1.5	257	6	US-10-821-234-1484	Sequence 1484, Ap
442	5	1.5	237	6	US-10-884-730-177	Sequence 177, App	516	5	1.5	257	6	US-10-467-657-2358	Sequence 2358, Ap
443	5	1.5	237	6	US-10-884-730-273	Sequence 273, App	517	5	1.5	257	7	US-11-054-515-1327	Sequence 1327, Ap
444	5	1.5	237	6	US-10-884-730-307	Sequence 307, App	518	5	1.5	257	7	US-11-135-855-42	Sequence 42, Appl
445	5	1.5	237	6	US-10-884-730-317	Sequence 317, App	519	5	1.5	258	6	US-10-995-561-583	Sequence 583, App
446	5	1.5	237	6	US-10-884-730-318	Sequence 318, App	520	5	1.5	258	6	US-11-055-822-390	Sequence 390, App
447	5	1.5	237	6	US-10-884-730-329	Sequence 329, App	521	5	1.5	259	6	US-10-995-561-883	Sequence 883, App
448	5	1.5	237	6	US-10-884-730-336	Sequence 336, App	522	5	1.5	259	7	US-11-075-185-74	Sequence 74, Appl
449	5	1.5	237	6	US-10-884-730-355	Sequence 355, App	523	5	1.5	260	6	US-10-467-657-4848	Sequence 4848, Ap
450	5	1.5	237	6	US-10-884-730-356	Sequence 356, App	524	5	1.5	261	6	US-10-467-657-3926	Sequence 3926, App
451	5	1.5	237	6	US-10-884-730-357	Sequence 357, App	525	5	1.5	262	6	US-10-884-730-289	Sequence 289, App
452	5	1.5	237	6	US-10-884-730-358	Sequence 358, App	526	5	1.5	262	6	US-10-793-626-516	Sequence 516, App
453	5	1.5	237	6	US-10-884-730-359	Sequence 359, App	527	5	1.5	263	6	US-10-793-626-876	Sequence 876, App
454	5	1.5	237	6	US-10-884-730-360	Sequence 360, App	528	5	1.5	263	6	US-10-512-184-29	Sequence 29, Appl
455	5	1.5	237	6	US-10-884-730-361	Sequence 361, App	529	5	1.5	263	6	US-10-467-657-6102	Sequence 6102, App
456	5	1.5	237	6	US-10-884-730-362	Sequence 362, App	530	5	1.5	263	7	US-11-040-638-2	Sequence 2, Appli
457	5	1.5	237	6	US-10-073-301A-9	Sequence 9, Appli	531	5	1.5	263	7	US-11-042-889-2	Sequence 2, Appli
458	5	1.5	238	6	US-10-467-657-4954	Sequence 4954, Ap	532	5	1.5	264	6	US-10-884-730-35	Sequence 35, Appl
459	5	1.5	240	6	US-10-467-657-7890	Sequence 7890, Ap	533	5	1.5	264	7	US-11-188-743-24	Sequence 24, Appl
460	5	1.5	240	6	US-10-508-263-98	Sequence 98, Appl	534	5	1.5	265	7	US-11-188-743-25	Sequence 25, Appl
461	5	1.5	243	6	US-10-793-626-3066	Sequence 3066, Ap	535	5	1.5	265	7	US-11-082-389-190	Sequence 190, App
462	5	1.5	243	7	US-11-147-047-40	Sequence 40, Appl	536	5	1.5	266	6	US-10-884-730-1	Sequence 1, Appli
463	5	1.5	244	6	US-10-821-234-1264	Sequence 1264, Ap	537	5	1.5	266	6	US-10-884-730-4	Sequence 4, Appli
464	5	1.5	244	7	US-11-054-515-1210	Sequence 1210, Ap	538	5	1.5	266	6	US-10-884-730-33	Sequence 33, Appl
465	5	1.5	244	7	US-11-054-515-1214	Sequence 1214, Ap	539	5	1.5	266	6	US-10-884-730-38	Sequence 38, Appl
466	5	1.5	244	7	US-11-054-515-1371	Sequence 1371, Ap	540	5	1.5	266	6	US-10-884-730-47	Sequence 47, Appl
467	5	1.5	244	7	US-11-054-515-1372	Sequence 1372, Ap	541	5	1.5	266	6	US-10-884-730-79	Sequence 79, Appl
468	5	1.5	244	7	US-11-054-515-1507	Sequence 1507, Ap	542	5	1.5	266	6	US-10-884-730-85	Sequence 85, Appl
469	5	1.5	246	7	US-11-054-515-1300	Sequence 1300, Ap	543	5	1.5	266	6	US-10-884-730-114	Sequence 114, App
470	5	1.5	246	7	US-11-054-515-1655	Sequence 1655, Ap	544	5	1.5	266	6	US-10-884-730-116	Sequence 116, App
471	5	1.5	246	7	US-11-054-515-1702	Sequence 1702, Ap	545	5	1.5	266	6	US-10-884-730-121	Sequence 121, App



546	5	1.5	266	6	US-10-884-730-165	Sequence 165, App	621	5	1.5	305	6	US-10-995-561-582	Sequence 582, App
547	5	1.5	266	6	US-10-884-730-166	Sequence 166, App	622	5	1.5	307	6	US-10-467-657-2792	Sequence 2792, App
548	5	1.5	266	6	US-10-884-730-167	Sequence 270, App	623	5	1.5	307	6	US-10-467-657-6738	Sequence 6738, App
549	5	1.5	266	6	US-10-884-730-285	Sequence 285, App	624	5	1.5	307	7	US-11-000-463-244	Sequence 244, App
550	5	1.5	266	6	US-10-884-730-287	Sequence 287, App	625	5	1.5	308	6	US-10-467-657-4192	Sequence 4192, App
551	5	1.5	266	6	US-10-884-730-295	Sequence 295, App	626	5	1.5	308	6	US-10-995-561-814	Sequence 814, App
552	5	1.5	266	6	US-10-884-730-296	Sequence 296, App	627	5	1.5	308	7	US-11-074-176-254	Sequence 254, App
553	5	1.5	266	6	US-10-884-730-306	Sequence 306, App	628	5	1.5	308	7	US-11-092-140-37	Sequence 37, App
554	5	1.5	266	6	US-10-884-730-326	Sequence 326, App	629	5	1.5	309	6	US-10-467-657-666	Sequence 666, App
555	5	1.5	266	6	US-10-884-730-328	Sequence 328, App	630	5	1.5	310	6	US-10-467-657-1590	Sequence 1590, App
556	5	1.5	266	6	US-10-884-730-330	Sequence 330, App	631	5	1.5	311	6	US-10-980-388-111	Sequence 111, App
557	5	1.5	266	6	US-10-884-730-334	Sequence 334, App	632	5	1.5	311	6	US-10-980-388-113	Sequence 113, App
558	5	1.5	266	6	US-10-884-730-345	Sequence 345, App	633	5	1.5	311	6	US-10-467-657-2334	Sequence 2334, App
559	5	1.5	266	6	US-11-000-463-381	Sequence 381, App	634	5	1.5	312	6	US-10-995-561-700	Sequence 700, App
560	5	1.5	266	7	US-11-000-463-381	Sequence 853, App	635	5	1.5	312	6	US-11-129-143-94	Sequence 94, App
561	5	1.5	267	7	US-11-194-246-290	Sequence 290, App	636	5	1.5	314	6	US-10-485-517-230	Sequence 230, App
562	5	1.5	269	6	US-10-972-587-16	Sequence 16, App	637	5	1.5	314	7	US-11-055-822-410	Sequence 410, App
563	5	1.5	271	7	US-11-091-100-17	Sequence 17, App	638	5	1.5	314	7	US-11-143-980-56	Sequence 56, App
564	5	1.5	271	7	US-11-112-882-74	Sequence 74, App	639	5	1.5	316	6	US-10-467-657-4040	Sequence 4040, App
565	5	1.5	272	6	US-10-986-501-120	Sequence 120, App	640	5	1.5	317	6	US-10-674-767-2	Sequence 2, App
566	5	1.5	272	6	US-10-467-657-40	Sequence 40, App	641	5	1.5	317	6	US-10-995-561-798	Sequence 798, App
567	5	1.5	273	6	US-10-467-657-6782	Sequence 6782, App	642	5	1.5	317	7	US-11-129-143-67	Sequence 67, App
568	5	1.5	273	6	US-10-467-657-7462	Sequence 7462, App	643	5	1.5	318	6	US-10-821-234-1590	Sequence 1590, App
569	5	1.5	273	7	US-11-196-475-7	Sequence 7, App	644	5	1.5	318	7	US-11-186-284-69	Sequence 69, App
570	5	1.5	273	7	US-11-196-475-13	Sequence 13, App	645	5	1.5	318	7	US-11-194-246-294	Sequence 294, App
571	5	1.5	273	7	US-11-196-475-92	Sequence 92, App	646	5	1.5	319	6	US-10-793-626-1844	Sequence 1844, App
572	5	1.5	273	7	US-11-196-475-95	Sequence 95, App	647	5	1.5	320	6	US-10-793-626-2988	Sequence 2988, App
573	5	1.5	273	7	US-11-196-475-98	Sequence 98, App	648	5	1.5	320	6	US-10-858-730-111	Sequence 111, App
574	5	1.5	273	7	US-11-196-475-101	Sequence 101, App	649	5	1.5	320	7	US-11-074-176-216	Sequence 216, App
575	5	1.5	273	7	US-11-196-475-104	Sequence 104, App	650	5	1.5	320	7	US-11-000-463-354	Sequence 354, App
576	5	1.5	273	7	US-11-196-475-144	Sequence 144, App	651	5	1.5	321	6	US-10-793-626-2816	Sequence 2816, App
577	5	1.5	273	7	US-11-196-475-186	Sequence 186, App	652	5	1.5	321	7	US-11-102-240-10	Sequence 10, App
578	5	1.5	274	6	US-10-495-597-7	Sequence 7, App	653	5	1.5	322	7	US-11-074-176-36	Sequence 36, App
579	5	1.5	274	7	US-11-196-475-9	Sequence 9, App	654	5	1.5	323	6	US-10-467-657-7180	Sequence 7180, App
580	5	1.5	274	7	US-11-196-475-86	Sequence 86, App	655	5	1.5	324	7	US-11-092-140-34	Sequence 34, App
581	5	1.5	274	7	US-11-196-475-138	Sequence 138, App	656	5	1.5	325	1	US-09-940-308-8	Sequence 8, App
582	5	1.5	276	6	US-10-467-657-8460	Sequence 8460, App	657	5	1.5	325	6	US-10-821-234-1261	Sequence 1261, App
583	5	1.5	276	6	US-11-186-284-95	Sequence 95, App	658	5	1.5	326	6	US-10-467-657-7224	Sequence 7224, App
584	5	1.5	277	6	US-10-793-626-314	Sequence 314, App	659	5	1.5	326	6	US-10-821-234-1671	Sequence 1671, App
585	5	1.5	277	6	US-10-793-626-2178	Sequence 2178, App	660	5	1.5	328	6	US-10-995-561-884	Sequence 884, App
586	5	1.5	277	6	US-11-102-240-28	Sequence 28, App	661	5	1.5	328	6	US-10-995-561-884	Sequence 1460, App
587	5	1.5	279	7	US-11-074-176-100	Sequence 100, App	662	5	1.5	329	6	US-10-793-626-1460	Sequence 36, App
588	5	1.5	281	7	US-11-082-389-58	Sequence 58, App	663	5	1.5	331	7	US-11-102-240-36	Sequence 36, App
589	5	1.5	282	6	US-10-353-783-56	Sequence 56, App	664	5	1.5	332	7	US-11-113-424-55	Sequence 55, App
591	5	1.5	286	6	US-10-858-730-199	Sequence 199, App	665	5	1.5	333	6	US-10-793-626-2890	Sequence 2890, App
592	5	1.5	286	6	US-11-082-389-196	Sequence 196, App	666	5	1.5	334	7	US-11-055-822-980	Sequence 980, App
593	5	1.5	287	6	US-10-793-626-1146	Sequence 1146, App	667	5	1.5	334	7	US-11-055-822-1072	Sequence 80, App
594	5	1.5	287	7	US-11-174-150-30	Sequence 30, App	668	5	1.5	334	7	US-11-113-424-80	Sequence 86, App
595	5	1.5	289	7	US-11-060-008-12	Sequence 12, App	669	5	1.5	335	6	US-10-995-561-866	Sequence 86, App
597	5	1.5	290	7	US-11-113-424-77	Sequence 77, App	670	5	1.5	335	7	US-11-182-946-7	Sequence 7, App
598	5	1.5	292	6	US-10-858-730-127	Sequence 127, App	671	5	1.5	336	6	US-10-793-626-1858	Sequence 1858, App
599	5	1.5	292	6	US-10-467-657-2590	Sequence 2590, App	672	5	1.5	336	6	US-10-980-388-120	Sequence 120, App
600	5	1.5	292	7	US-11-129-143-95	Sequence 95, App	673	5	1.5	336	7	US-11-113-424-83	Sequence 83, App
601	5	1.5	294	6	US-10-467-657-934	Sequence 934, App	674	5	1.5	337	6	US-10-467-657-9628-97	Sequence 97, App
602	5	1.5	294	6	US-10-467-657-2876	Sequence 2876, App	675	5	1.5	337	6	US-10-793-626-444	Sequence 444, App
603	5	1.5	295	6	US-10-995-561-581	Sequence 581, App	676	5	1.5	337	7	US-10-875-716-2	Sequence 2, App
604	5	1.5	295	7	US-11-091-100-2	Sequence 2, App	677	5	1.5	337	7	US-11-102-240-74	Sequence 74, App
605	5	1.5	295	7	US-11-055-822-62	Sequence 62, App	678	5	1.5	338	6	US-10-467-657-3178	Sequence 3178, App
606	5	1.5	296	6	US-10-793-626-866	Sequence 866, App	679	5	1.5	338	6	US-10-467-657-8208	Sequence 8208, App
607	5	1.5	296	6	US-10-965-972-8	Sequence 8, App	680	5	1.5	338	7	US-10-467-657-8384	Sequence 8384, App
608	5	1.5	296	6	US-11-196-475-22	Sequence 22, App	681	5	1.5	338	7	US-11-000-463-445	Sequence 445, App
609	5	1.5	297	6	US-10-858-730-115	Sequence 115, App	682	5	1.5	339	6	US-10-467-657-8034	Sequence 8034, App
610	5	1.5	297	6	US-10-858-730-116	Sequence 116, App	683	5	1.5	344	6	US-10-967-527-24	Sequence 24, App
611	5	1.5	298	6	US-10-499-715-6	Sequence 6, App	684	5	1.5	344	6	US-11-082-389-288	Sequence 288, App
612	5	1.5	298	6	US-10-793-626-1298	Sequence 1298, App	685	5	1.5	344	6	US-11-000-463-317	Sequence 317, App
613	5	1.5	298	7	US-11-138-949-9	Sequence 9, App	686	5	1.5	345	6	US-10-995-561-971	Sequence 971, App
614	5	1.5	299	7	US-11-112-882-10	Sequence 30, App	687	5	1.5	346	6	US-10-467-657-5946	Sequence 5946, App
615	5	1.5	301	7	US-11-074-176-362	Sequence 362, App	688	5	1.5	347	6	US-10-793-626-462	Sequence 462, App
616	5	1.5	301	7	US-11-000-463-380	Sequence 380, App	689	5	1.5	347	6	US-10-793-626-1268	Sequence 1268, App
617	5	1.5	301	7	US-11-000-463-752	Sequence 752, App	690	5	1.5	347	6	US-10-793-626-3326	Sequence 3326, App
618	5	1.5	302	6	US-10-878-556-61	Sequence 61, App	691	5	1.5	347	6	US-10-467-657-2014	Sequence 2014, App
619	5	1.5	303	7	US-11-102-240-166	Sequence 166, App	692	5	1.5	347	7	US-11-066-648-2	Sequence 2, App
620	5	1.5	304	7	US-11-000-463-315	Sequence 315, App	693	5	1.5	347	7	US-11-066-648-12	Sequence 12, App
							694	5	1.5	347	7	US-11-066-648-14	Sequence 14, App



695	5	1.5	348	6	US-10-674-767-4	Sequence 4, Appli	771	5	1.5	392	6	US-10-793-626-194	Sequence 194, App
696	5	1.5	348	6	US-10-793-626-2866	Sequence 2866, Ap	772	5	1.5	392	6	US-10-467-657-5724	Sequence 5724, Ap
698	5	1.5	349	6	US-11-028-922A-2	Sequence 2, Appl1	773	5	1.5	393	1	US-09-940-308-7	Sequence 7, Appl1
699	5	1.5	350	6	US-10-467-657-1972	Sequence 1972, Ap	774	5	1.5	393	7	US-11-100-352-3	Sequence 3, Appl1
700	5	1.5	350	6	US-10-467-657-3256	Sequence 3256, Ap	775	5	1.5	393	7	US-11-196-475-114	Sequence 114, Appl
701	5	1.5	350	6	US-10-467-657-3588	Sequence 3588, Ap	776	5	1.5	396	7	US-11-061-869-11	Sequence 11, Appl
702	5	1.5	351	6	US-10-793-626-338	Sequence 338, App	777	5	1.5	396	7	US-11-061-869-17	Sequence 17, Appl
703	5	1.5	351	6	US-10-467-657-5088	Sequence 5088, Ap	778	5	1.5	399	7	US-11-077-386-18	Sequence 18, Appl
704	5	1.5	351	6	US-10-467-657-5272	Sequence 5272, Ap	779	5	1.5	400	7	US-11-117-169-2	Sequence 2, Appl1
705	5	1.5	351	6	US-10-467-657-8320	Sequence 8320, Ap	780	5	1.5	400	7	US-11-117-169-4	Sequence 4, Appl1
706	5	1.5	351	7	US-11-108-528-52	Sequence 52, Appl	781	5	1.5	401	7	US-11-134-795-28	Sequence 28, Appl
707	5	1.5	352	7	US-11-055-822-666	Sequence 666, App	782	5	1.5	402	6	US-10-821-234-1581	Sequence 1581, Ap
708	5	1.5	354	6	US-10-467-657-3080	Sequence 3080, Ap	783	5	1.5	402	6	US-10-995-561-719	Sequence 719, App
709	5	1.5	354	6	US-10-995-561-717	Sequence 717, App	784	5	1.5	403	6	US-10-485-517-165	Sequence 165, App
710	5	1.5	355	6	US-10-793-626-3172	Sequence 3172, Ap	785	5	1.5	403	6	US-10-858-730-27	Sequence 27, Appl
711	5	1.5	355	6	US-10-967-527A-22	Sequence 22, Appl	786	5	1.5	403	6	US-10-858-730-28	Sequence 28, Appl
712	5	1.5	359	7	US-11-080-091-1	Sequence 1, Appli	787	5	1.5	403	6	US-10-523-477-11	Sequence 11, Appl
713	5	1.5	359	7	US-11-116-939-15	Sequence 15, Appl	788	5	1.5	403	6	US-10-770-726-83	Sequence 83, Appl
714	5	1.5	359	7	US-11-129-143-71	Sequence 71, Appl	789	5	1.5	403	6	US-10-770-726-85	Sequence 85, Appl
715	5	1.5	360	7	US-11-084-408-3	Sequence 3, Appl1	790	5	1.5	403	7	US-11-109-156-12	Sequence 12, Appl
716	5	1.5	361	6	US-10-995-561-701	Sequence 54, Appl	791	5	1.5	403	7	US-11-055-822-776	Sequence 776, App
717	5	1.5	361	7	US-11-012-762-54	Sequence 54, Appl	792	5	1.5	407	6	US-10-793-626-886	Sequence 886, App
718	5	1.5	362	6	US-10-858-730-123	Sequence 123, App	793	5	1.5	407	6	US-10-613-744-14	Sequence 14, Appl
720	5	1.5	364	6	US-10-984-376-5	Sequence 5, Appli	794	5	1.5	407	6	US-10-995-561-811	Sequence 811, App
721	5	1.5	364	6	US-10-984-376-6	Sequence 6, Appl1	795	5	1.5	409	6	US-10-627-633-4	Sequence 4, Appl1
722	5	1.5	364	6	US-10-995-561-699	Sequence 699, App	796	5	1.5	409	6	US-10-467-657-342	Sequence 342, App
723	5	1.5	364	7	US-11-091-334-2	Sequence 2, Appl1	797	5	1.5	410	6	US-10-793-626-3258	Sequence 3258, Ap
724	5	1.5	365	6	US-10-995-561-545	Sequence 545, App	798	5	1.5	410	6	US-10-467-657-4864	Sequence 4864, Ap
725	5	1.5	366	6	US-10-432-483-24	Sequence 24, Appl	799	5	1.5	410	7	US-11-055-822-6	Sequence 6, Appl1
726	5	1.5	366	7	US-11-000-453-410	Sequence 410, App	800	5	1.5	410	7	US-11-055-822-306	Sequence 306, App
727	5	1.5	366	7	US-11-000-463-457	Sequence 457, App	801	5	1.5	410	7	US-11-055-822-332	Sequence 332, App
728	5	1.5	366	7	US-11-000-463-882	Sequence 882, App	802	5	1.5	410	7	US-11-055-822-520	Sequence 520, App
729	5	1.5	367	6	US-10-821-234-1058	Sequence 1058, Ap	803	5	1.5	411	6	US-10-793-626-3236	Sequence 3236, Ap
730	5	1.5	367	6	US-10-858-730-205	Sequence 205, App	804	5	1.5	411	6	US-10-467-657-4076	Sequence 4076, Ap
731	5	1.5	368	6	US-10-793-626-742	Sequence 742, App	805	5	1.5	411	7	US-11-061-869-12	Sequence 12, Appl
732	5	1.5	368	6	US-10-467-657-4756	Sequence 4756, Ap	806	5	1.5	414	6	US-10-821-234-1170	Sequence 1170, Ap
733	5	1.5	369	6	US-10-793-626-1390	Sequence 1390, Ap	807	5	1.5	414	6	US-10-467-657-4316	Sequence 4316, Ap
734	5	1.5	369	6	US-10-793-626-1610	Sequence 1610, Ap	808	5	1.5	414	6	US-11-102-240-102	Sequence 102, Appl
735	5	1.5	370	7	US-11-129-143-58	Sequence 8, Appl	809	5	1.5	415	6	US-10-627-633-2	Sequence 2, Appl1
736	5	1.5	371	6	US-10-467-657-1166	Sequence 1166, Ap	810	5	1.5	415	6	US-10-821-234-936	Sequence 936, App
737	5	1.5	374	6	US-10-467-657-3088	Sequence 3088, Ap	811	5	1.5	416	7	US-11-061-869-18	Sequence 18, Appl
738	5	1.5	374	7	US-11-051-267-8	Sequence 8, Appl1	812	5	1.5	417	6	US-10-821-234-1536	Sequence 1536, Ap
739	5	1.5	375	6	US-11-051-267-20	Sequence 20, Appl	813	5	1.5	418	6	US-10-878-556A-53	Sequence 53, Appl
740	5	1.5	375	6	US-10-793-626-1840	Sequence 1840, Ap	814	5	1.5	418	6	US-10-995-561-753	Sequence 753, App
741	5	1.5	375	7	US-11-051-267-2	Sequence 2, Appl1	815	5	1.5	418	6	US-10-995-561-754	Sequence 754, App
742	5	1.5	375	7	US-11-051-267-10	Sequence 10, Appl	816	5	1.5	418	6	US-10-995-561-755	Sequence 755, App
743	5	1.5	375	7	US-11-051-267-12	Sequence 12, Appl	817	5	1.5	418	6	US-10-995-561-756	Sequence 756, App
744	5	1.5	375	7	US-11-051-267-14	Sequence 14, Appl	818	5	1.5	418	6	US-10-995-561-757	Sequence 757, App
745	5	1.5	375	7	US-11-051-267-16	Sequence 16, Appl	819	5	1.5	418	6	US-10-995-561-758	Sequence 758, App
746	5	1.5	375	7	US-11-051-267-18	Sequence 18, Appl	820	5	1.5	418	6	US-10-995-561-759	Sequence 759, App
747	5	1.5	376	6	US-10-793-626-490	Sequence 490, App	821	5	1.5	418	7	US-11-074-176-328	Sequence 328, App
748	5	1.5	376	6	US-10-793-626-2260	Sequence 2260, Ap	822	5	1.5	419	6	US-10-821-234-1556	Sequence 1556, Ap
749	5	1.5	376	7	US-11-051-267-4	Sequence 4, Appl1	823	5	1.5	419	6	US-10-821-234-1564	Sequence 1664, Ap
750	5	1.5	376	7	US-11-051-267-6	Sequence 6, Appl1	824	5	1.5	422	7	US-11-055-822-626	Sequence 626, App
751	5	1.5	377	6	US-10-467-657-7508	Sequence 7508, Ap	825	5	1.5	424	7	US-11-137-850-7	Sequence 7, Appl1
752	5	1.5	377	6	US-10-467-657-8228	Sequence 8228, Ap	826	5	1.5	424	7	US-11-137-850-8	Sequence 8, Appl1
753	5	1.5	379	7	US-11-055-822-446	Sequence 446, App	830	5	1.5	426	6	US-10-467-657-2120	Sequence 9, Appl1
754	5	1.5	378	7	US-11-129-143-49	Sequence 49, Appl	831	5	1.5	427	7	US-11-182-946-5	Sequence 5, Appl1
755	5	1.5	378	6	US-10-467-657-734	Sequence 734, App	832	5	1.5	427	7	US-11-112-882-1	Sequence 1, Appl1
756	5	1.5	380	7	US-11-196-475-118	Sequence 118, App	833	5	1.5	428	7	US-11-029-003-24	Sequence 24, Appl
757	5	1.5	380	7	US-11-116-939-2	Sequence 2, Appli	834	5	1.5	430	6	US-10-467-657-1622	Sequence 1622, Ap
762	5	1.5	381	6	US-10-510-386-168	Sequence 168, App	835	5	1.5	430	6	US-10-992-577-8	Sequence 8, Appl1
763	5	1.5	381	6	US-10-821-234-3342	Sequence 3342, Ap	836	5	1.5	430	6	US-11-194-246-438	Sequence 438, App
764	5	1.5	383	6	US-10-467-657-3226	Sequence 3226, Ap	837	5	1.5	431	6	US-10-821-234-1065	Sequence 1065, Ap
765	5	1.5	384	6	US-10-467-657-508	Sequence 508, App	838	5	1.5	431	7	US-11-069-642-1	Sequence 1, Appl1
766	5	1.5	387	7	US-11-055-822-112	Sequence 112, App	839	5	1.5	432	6	US-10-793-626-2942	Sequence 2942, Ap
767	5	1.5	387	7	US-11-055-822-472	Sequence 472, App	840	5	1.5	432	6	US-10-992-577-2	Sequence 2, Appl1
768	5	1.5	389	7	US-11-188-743-33	Sequence 33, Appl	841	5	1.5	433	7	US-11-196-475-180	Sequence 180, App
769	5	1.5	391	6	US-10-878-556A-86	Sequence 86, Appl	842	5	1.5	434	6	US-10-821-234-1680	Sequence 1680, Ap
770	5	1.5	392	6	US-10-392-234A-50	Sequence 50, Appl	843	5	1.5	434	7	US-11-055-822-794	Sequence 794, App



844	5	1.5	434	7	US-11-196-475-164	Sequence 164, App	921	5	1.5	466	7	US-11-196-475-110	Sequence 110, App
845	5	1.5	435	6	US-10-327-386-19	Sequence 19, App1	922	5	1.5	467	7	US-11-000-463-452	Sequence 452, App
847	5	1.5	437	6	US-10-521-536-2	Sequence 2, App1	923	5	1.5	467	7	US-11-000-463-924	Sequence 924, App
848	5	1.5	437	6	US-10-821-234-1392	Sequence 18, App	924	5	1.5	467	7	US-11-000-463-925	Sequence 925, App
849	5	1.5	437	6	US-10-525-710-18	Sequence 92, App1	925	5	1.5	468	6	US-10-763-712A-3	Sequence 3, App1
850	5	1.5	437	7	US-11-069-642-92	Sequence 2, App1	926	5	1.5	470	6	US-10-485-517-119	Sequence 119, App
851	5	1.5	437	7	US-11-199-124-7	Sequence 508, App	927	5	1.5	470	7	US-11-008-727-20	Sequence 20, App1
852	5	1.5	438	6	US-10-793-626-508	Sequence 49, App1	928	5	1.5	472	6	US-10-467-657-2268	Sequence 2268, App
853	5	1.5	438	7	US-11-069-642-47	Sequence 47, App1	929	5	1.5	473	7	US-11-075-185-12	Sequence 12, App
854	5	1.5	438	7	US-11-069-642-49	Sequence 51, App1	930	5	1.5	474	6	US-10-793-626-946	Sequence 946, App
855	5	1.5	438	7	US-11-069-642-51	Sequence 53, App1	931	5	1.5	475	7	US-11-061-869-15	Sequence 15, App1
856	5	1.5	438	7	US-11-069-642-53	Sequence 55, App1	932	5	1.5	477	6	US-10-793-626-1250	Sequence 3250, App
857	5	1.5	438	7	US-11-069-642-55	Sequence 57, App1	933	5	1.5	479	7	US-11-147-047-44	Sequence 44, App1
858	5	1.5	438	7	US-11-069-642-57	Sequence 59, App1	934	5	1.5	479	7	US-11-024-251-33	Sequence 33, App1
859	5	1.5	438	7	US-11-069-642-59	Sequence 61, App1	935	5	1.5	479	7	US-11-194-246-110	Sequence 310, App
860	5	1.5	438	7	US-11-069-642-61	Sequence 63, App1	936	5	1.5	480	6	US-10-510-386-12	Sequence 12, App1
861	5	1.5	438	7	US-11-069-642-63	Sequence 31, App1	937	5	1.5	480	6	US-10-336-263A-8	Sequence 8, App1
862	5	1.5	438	7	US-11-090-439-31	Sequence 168, App	938	5	1.5	480	6	US-10-821-234-886	Sequence 886, App
863	5	1.5	438	7	US-11-196-475-168	Sequence 10, App1	939	5	1.5	480	7	US-11-080-991-76	Sequence 76, App1
864	5	1.5	438	7	US-11-199-124-10	Sequence 3034, App	940	5	1.5	481	7	US-11-116-939-14	Sequence 14, App1
865	5	1.5	439	6	US-10-467-657-3034	Sequence 80, App1	941	5	1.5	482	6	US-10-878-556A-139	Sequence 139, App1
866	5	1.5	439	7	US-11-082-389-80	Sequence 178, App	942	5	1.5	482	7	US-11-055-822-20	Sequence 20, App1
867	5	1.5	440	7	US-11-196-475-178	Sequence 120, App	943	5	1.5	485	6	US-10-204-029-7	Sequence 326, App
868	5	1.5	441	7	US-11-196-475-120	Sequence 1594, App	944	5	1.5	485	6	US-10-467-657-326	Sequence 326, App
869	5	1.5	442	6	US-10-821-234-1594	Sequence 158, App	945	5	1.5	485	6	US-10-467-657-4512	Sequence 4512, App
870	5	1.5	443	6	US-10-793-626-1594	Sequence 362, App	946	5	1.5	485	7	US-11-055-822-18	Sequence 18, App1
871	5	1.5	444	6	US-10-467-657-362	Sequence 154, App	947	5	1.5	486	7	US-11-000-463-373	Sequence 273, App
872	5	1.5	445	7	US-11-102-240-32	Sequence 32, App1	948	5	1.5	487	7	US-11-113-424-56	Sequence 56, App1
873	5	1.5	445	7	US-11-115-564-2	Sequence 150, App	949	5	1.5	487	7	US-11-113-424-57	Sequence 57, App1
874	5	1.5	446	7	US-11-196-475-150	Sequence 154, App	950	5	1.5	488	6	US-10-984-376-4	Sequence 4, App1
875	5	1.5	446	7	US-11-196-475-154	Sequence 158, App	951	5	1.5	488	6	US-10-984-376-4	Sequence 4, App1
876	5	1.5	446	7	US-11-196-475-158	Sequence 379, App	952	5	1.5	488	6	US-10-995-561-860	Sequence 860, App
877	5	1.5	447	6	US-10-884-730-379	Sequence 379, App	953	5	1.5	491	6	US-10-793-626-1798	Sequence 1798, App
878	5	1.5	447	7	US-11-055-822-978	Sequence 162, App	954	5	1.5	491	7	US-11-098-662-14	Sequence 14, App1
879	5	1.5	447	7	US-11-196-475-162	Sequence 24, App1	955	5	1.5	491	7	US-11-165-141-2	Sequence 2, App1
880	5	1.5	448	7	US-11-112-882-24	Sequence 26, App1	956	5	1.5	492	6	US-10-467-657-4326	Sequence 4326, App
881	5	1.5	448	7	US-10-858-730-26	Sequence 4, App1	957	5	1.5	492	6	US-10-467-657-7112	Sequence 7112, App
882	5	1.5	449	6	US-10-525-710-4	Sequence 20, App1	958	5	1.5	494	6	US-10-467-657-376	Sequence 376, App
883	5	1.5	450	6	US-10-995-561-815	Sequence 148, App	959	5	1.5	496	7	US-11-067-121-3	Sequence 3, App1
884	5	1.5	450	7	US-11-077-386-20	Sequence 146, App	960	5	1.5	496	7	US-11-067-121-12	Sequence 12, App1
885	5	1.5	450	7	US-11-196-475-148	Sequence 310, App	961	5	1.5	496	7	US-11-102-240-158	Sequence 158, App
886	5	1.5	450	7	US-11-055-822-304	Sequence 330, App	962	5	1.5	496	7	US-11-186-284-103	Sequence 103, App
887	5	1.5	450	7	US-11-055-822-310	Sequence 330, App	963	5	1.5	499	6	US-10-508-263-94	Sequence 94, App1
888	5	1.5	452	6	US-10-467-657-1312	Sequence 146, App	964	5	1.5	500	6	US-10-467-657-38	Sequence 38, App1
889	5	1.5	453	7	US-11-196-475-146	Sequence 150, App	965	5	1.5	502	6	US-10-689-742-148	Sequence 148, App
890	5	1.5	453	7	US-11-196-475-152	Sequence 35, App1	966	5	1.5	502	6	US-10-821-234-1554	Sequence 1554, App
891	5	1.5	453	7	US-11-089-551A-35	Sequence 156, App	967	5	1.5	502	6	US-11-102-240-158	Sequence 158, App
892	5	1.5	454	7	US-11-196-475-116	Sequence 116, App	968	5	1.5	504	7	US-11-152-747-4	Sequence 4, App1
893	5	1.5	454	7	US-11-196-475-160	Sequence 5786, App	969	5	1.5	505	6	US-10-485-517-144	Sequence 144, App
894	5	1.5	456	6	US-10-467-657-5786	Sequence 304, App	970	5	1.5	506	6	US-11-063-343-38	Sequence 38, App1
895	5	1.5	456	7	US-11-055-822-304	Sequence 330, App	971	5	1.5	510	7	US-11-194-246-442	Sequence 442, App
896	5	1.5	456	7	US-11-055-822-310	Sequence 330, App	972	5	1.5	510	7	US-11-152-747-4	Sequence 4, App1
897	5	1.5	456	7	US-10-467-657-4348	Sequence 4348, App	973	5	1.5	511	7	US-11-032-236-6	Sequence 6, App1
898	5	1.5	462	6	US-10-467-657-7636	Sequence 186, App	974	5	1.5	513	6	US-10-821-234-1112	Sequence 1112, App
899	5	1.5	463	6	US-10-510-386-186	Sequence 4228, App	975	5	1.5	513	6	US-11-102-240-124	Sequence 124, App
900	5	1.5	463	6	US-10-467-657-4228	Sequence 46, App1	976	5	1.5	513	7	US-11-000-463-158	Sequence 158, App
901	5	1.5	464	6	US-10-763-712A-46	Sequence 1676, App	977	5	1.5	513	7	US-10-467-657-1124	Sequence 1124, App
902	5	1.5	465	6	US-10-967-648A-6	Sequence 1550, App	978	5	1.5	518	6	US-10-821-234-1546	Sequence 1546, App
903	5	1.5	465	6	US-10-821-234-1550	Sequence 14, App1	979	5	1.5	518	6	US-10-467-657-1124	Sequence 1124, App
904	5	1.5	465	6	US-10-821-234-1550	Sequence 104, App	980	5	1.5	518	6	US-10-467-657-1124	Sequence 1124, App
905	5	1.5	466	7	US-11-102-240-104	Sequence 107, App	981	5	1.5	518	6	US-10-467-657-1124	Sequence 1124, App
906	5	1.5	466	7	US-11-196-475-107		982	5	1.5	518	6	US-10-467-657-1124	Sequence 1124, App
907	5	1.5	466	7			983	5	1.5	518	6	US-10-467-657-1124	Sequence 1124, App
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918	5	1.5	466	7			994	5	1.5	518	6	US-10-467-657-1124	Sequence 1124, App
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920	5	1.5	466	7			996	5	1.5	518	6	US-10-467-657-1124	Sequence 1124, App



997	5	1.5	529	7	US-11-113-424-82	Sequence 82, Appl	1074	5	1.5	628	7	US-11-147-047-45	Sequence 45, Appl
998	5	1.5	530	6	US-10-858-730-232	Sequence 22, App	1075	5	1.5	633	7	US-11-119-683-3	Sequence 3, Appl1
999	5	1.5	530	6	US-10-980-388-52	Sequence 62, Appl	1076	5	1.5	634	7	US-11-137-683-3	Sequence 63, Appl1
1000	5	1.5	531	6	US-10-878-556A-70	Sequence 70, Appl	1077	5	1.5	638	6	US-10-793-626-1468	Sequence 1468, Ap
1001	5	1.5	532	6	US-10-821-234-918	Sequence 918, App	1079	5	1.5	641	6	US-10-821-234-1519	Sequence 1519, Ap
1002	5	1.5	533	6	US-10-467-657-8	Sequence 8, Appl1	1080	5	1.5	641	6	US-10-491-096-189	Sequence 189, App
1003	5	1.5	533	6	US-10-467-657-8	Sequence 2668, Ap	1081	5	1.5	643	7	US-11-074-176-318	Sequence 318, App
1004	5	1.5	534	6	US-10-858-730-56	Sequence 66, Appl	1082	5	1.5	644	6	US-10-467-657-5958	Sequence 5958, Ap
1005	5	1.5	534	7	US-11-082-389-348	Sequence 348, App	1083	5	1.5	645	6	US-10-510-386-32	Sequence 32, Appl
1006	5	1.5	534	7	US-11-075-185-17	Sequence 17, Appl	1084	5	1.5	645	6	US-10-821-234-1409	Sequence 1409, Ap
1007	5	1.5	539	6	US-10-467-657-7736	Sequence 7736, Ap	1085	5	1.5	646	6	US-10-491-096-190	Sequence 190, App
1008	5	1.5	541	7	US-11-112-882-34	Sequence 34, Appl	1086	5	1.5	647	7	US-11-080-991-32	Sequence 32, Appl
1009	5	1.5	544	6	US-10-467-657-468	Sequence 468, App	1087	5	1.5	648	6	US-10-501-039-6	Sequence 6, Appl1
1010	5	1.5	546	6	US-10-821-234-902	Sequence 902, App	1088	5	1.5	652	6	US-10-821-234-1016	Sequence 1016, Ap
1011	5	1.5	547	6	US-10-770-726-87	Sequence 87, Appl	1089	5	1.5	654	6	US-10-770-726-82	Sequence 82, Appl
1012	5	1.5	548	6	US-10-995-561-810	Sequence 810, App	1090	5	1.5	654	7	US-11-110-082-24	Sequence 24, Appl
1013	5	1.5	549	7	US-11-194-246-431	Sequence 431, App	1091	5	1.5	656	6	US-10-995-651-871	Sequence 871, App
1014	5	1.5	550	7	US-11-184-380-14	Sequence 14, Appl	1092	5	1.5	657	7	US-11-109-156-27	Sequence 27, Appl
1015	5	1.5	551	7	US-11-000-463-346	Sequence 346, App	1093	5	1.5	658	6	US-10-467-657-4782	Sequence 4782, Ap
1016	5	1.5	554	6	US-10-793-626-1414	Sequence 1414, App	1094	5	1.5	662	7	US-11-090-439-9	Sequence 9, Appl1
1017	5	1.5	554	6	US-10-763-712A-33	Sequence 33, Appl	1095	5	1.5	667	6	US-10-793-626-198	Sequence 198, App
1018	5	1.5	554	7	US-11-055-822-998	Sequence 998, App	1096	5	1.5	667	7	US-11-074-176-64	Sequence 64, Appl
1020	5	1.5	555	6	US-10-763-712A-119	Sequence 119, App	1097	5	1.5	668	6	US-10-467-657-4238	Sequence 4238, Ap
1021	5	1.5	562	6	US-10-467-657-4346	Sequence 4346, Ap	1098	5	1.5	668	7	US-11-113-424-12	Sequence 12, Appl
1022	5	1.5	562	6	US-10-508-263-24	Sequence 24, Appl	1099	5	1.5	669	7	US-11-076-187-3	Sequence 3, Appl1
1023	5	1.5	564	7	US-10-485-517-298	Sequence 298, App	1100	5	1.5	669	7	US-11-119-683-2	Sequence 2, Appl1
1024	5	1.5	564	7	US-11-082-389-78	Sequence 78, Appl	1101	5	1.5	670	6	US-10-821-234-879	Sequence 879, App
1026	5	1.5	567	6	US-10-467-657-4328	Sequence 4328, App	1102	5	1.5	672	6	US-10-467-657-5126	Sequence 5126, Ap
1027	5	1.5	567	6	US-10-995-561-813	Sequence 813, App	1103	5	1.5	673	7	US-11-102-240-16	Sequence 16, Appl
1028	5	1.5	569	6	US-10-821-234-664	Sequence 864, App	1104	5	1.5	675	6	US-10-467-657-3802	Sequence 3802, Ap
1029	5	1.5	573	7	US-11-196-475-112	Sequence 112, App	1105	5	1.5	677	6	US-10-982-545-12	Sequence 12, Appl
1030	5	1.5	574	6	US-10-507-275-7	Sequence 7, Appl1	1106	5	1.5	678	7	US-11-102-240-34	Sequence 34, Appl
1031	5	1.5	574	6	US-10-763-712A-1	Sequence 1, Appl1	1107	5	1.5	679	6	US-10-995-561-872	Sequence 872, App
1032	5	1.5	574	6	US-10-763-712A-102	Sequence 102, Appl	1108	5	1.5	687	6	US-11-099-691-9	Sequence 9, Appl1
1033	5	1.5	574	6	US-10-770-726-50	Sequence 50, Appl	1109	5	1.5	687	6	US-10-485-517-274	Sequence 274, App
1034	5	1.5	576	6	US-11-137-465-64	Sequence 64, Appl	1110	5	1.5	687	7	US-11-117-169-6	Sequence 6, Appl1
1035	5	1.5	580	6	US-10-995-561-987	Sequence 987, App	1111	5	1.5	688	7	US-11-113-424-48	Sequence 48, Appl
1036	5	1.5	582	7	US-11-074-176-110	Sequence 110, App	1112	5	1.5	689	7	US-11-113-424-46	Sequence 46, Appl
1037	5	1.5	583	6	US-10-793-626-1358	Sequence 1358, App	1113	5	1.5	689	7	US-11-113-424-47	Sequence 47, Appl
1038	5	1.5	585	6	US-10-510-386-20	Sequence 20, Appl	1114	5	1.5	692	7	US-11-038-284-33	Sequence 33, Appl
1039	5	1.5	585	7	US-11-012-762-6	Sequence 6, Appl1	1115	5	1.5	692	7	US-11-045-802-26	Sequence 26, Appl
1040	5	1.5	585	7	US-11-074-176-190	Sequence 190, App	1116	5	1.5	697	7	US-11-074-176-62	Sequence 62, Appl
1041	5	1.5	588	6	US-10-650-326B-7	Sequence 7, Appl1	1117	5	1.5	703	7	US-11-069-642-113	Sequence 113, App
1042	5	1.5	588	6	US-11-196-475-122	Sequence 122, App	1118	5	1.5	706	6	US-10-485-517-146	Sequence 146, App
1043	5	1.5	589	7	US-11-074-176-196	Sequence 196, App	1119	5	1.5	708	7	US-11-196-475-76	Sequence 76, Appl
1044	5	1.5	590	1	US-09-940-308-2	Sequence 2, Appl1	1120	5	1.5	709	6	US-10-821-234-1138	Sequence 1138, Ap
1045	5	1.5	594	6	US-10-510-386-38	Sequence 38, Appl	1121	5	1.5	711	6	US-11-074-176-158	Sequence 158, App
1046	5	1.5	594	6	US-10-467-657-3952	Sequence 3952, Ap	1122	5	1.5	711	7	US-10-821-234-1017	Sequence 1017, Ap
1047	5	1.5	594	7	US-11-012-762-4	Sequence 4, Appl1	1123	5	1.5	711	7	US-11-087-100-18	Sequence 18, Appl
1048	5	1.5	599	6	US-10-995-561-812	Sequence 812, App	1124	5	1.5	711	7	US-11-087-084-18	Sequence 18, Appl
1049	5	1.5	600	6	US-10-606-302-3	Sequence 3, Appl1	1125	5	1.5	711	7	US-11-087-085-18	Sequence 18, Appl
1050	5	1.5	602	7	US-11-055-822-74	Sequence 74, Appl	1126	5	1.5	721	6	US-11-060-920-5	Sequence 5, Appl1
1051	5	1.5	604	6	US-10-995-561-839	Sequence 839, App	1128	5	1.5	724	6	US-10-793-626-968	Sequence 968, Appl
1054	5	1.5	607	7	US-11-167-856-18	Sequence 18, App	1129	5	1.5	727	6	US-10-793-626-2862	Sequence 2862, Ap
1055	5	1.5	607	7	US-11-176-863-2	Sequence 2, Appl1	1130	5	1.5	727	6	US-10-995-561-864	Sequence 864, App
1056	5	1.5	609	7	US-11-058-555-2	Sequence 2, Appl1	1131	5	1.5	727	6	US-11-117-169-8	Sequence 8, Appl1
1057	5	1.5	609	7	US-11-062-225-3	Sequence 3, Appl1	1132	5	1.5	728	6	US-10-467-657-1742	Sequence 1442, Ap
1058	5	1.5	609	7	US-11-062-225-4	Sequence 4, Appl1	1133	5	1.5	728	6	US-10-467-657-8376	Sequence 8376, Ap
1059	5	1.5	609	7	US-11-062-225-5	Sequence 5, Appl1	1134	5	1.5	730	7	US-11-082-389-358	Sequence 358, App
1060	5	1.5	609	7	US-11-062-225-6	Sequence 6, Appl1	1135	5	1.5	734	6	US-10-652-893-2	Sequence 2, Appl1
1061	5	1.5	609	7	US-11-062-225-7	Sequence 7, Appl1	1136	5	1.5	734	6	US-10-995-561-770	Sequence 770, App
1063	5	1.5	609	7	US-11-062-225-8	Sequence 8, Appl1	1137	5	1.5	734	6	US-11-137-465-65	Sequence 65, Appl
1064	5	1.5	610	6	US-10-606-302-1	Sequence 1, Appl1	1138	5	1.5	736	6	US-10-467-657-4780	Sequence 4780, Ap
1065	5	1.5	610	7	US-11-184-380-3	Sequence 3, Appl1	1139	5	1.5	737	6	US-10-878-556A-25	Sequence 25, Appl
1066	5	1.5	614	6	US-10-821-224-1041	Sequence 1041, Ap	1140	5	1.5	737	7	US-11-128-420-9	Sequence 9, Appl1
1067	5	1.5	614	6	US-11-155-492-107	Sequence 107, App	1141	5	1.5	743	6	US-10-467-657-4082	Sequence 4082, Ap
1068	5	1.5	616	7	US-11-083-800-4	Sequence 4, Appl1	1142	5	1.5	746	6	US-10-793-626-652	Sequence 652, App
1069	5	1.5	617	7	US-11-143-980-35	Sequence 35, Appl	1144	5	1.5	747	6	US-10-995-561-840	Sequence 840, App
1070	5	1.5	620	6	US-10-467-657-5892	Sequence 5892, Ap	1145	5	1.5	747	7	US-11-018-018-1	Sequence 1, Appl1
1071	5	1.5	622	7	US-11-199-124-12	Sequence 12, Appl	1146	5	1.5	747	7	US-11-047-757-1	Sequence 1, Appl1
1072	5	1.5	625	7	US-11-021-441-37	Sequence 37, Appl	1147	5	1.5	750	6	US-10-689-742-86	Sequence 86, Appl
1073	5	1.5	626	6	US-10-467-657-1196	Sequence 1196, Ap	1148	5	1.5	753	6	US-10-485-517-173	Sequence 173, App
			626	7	US-11-010-748A-1	Sequence 1, Appl1	1149	5	1.5	753	7	US-11-137-465-51	Sequence 51, Appl



1150	5	1.5	757	7	US-11-110-082-35	Sequence 35, Appl	1225	5	1.5	919	7	US-11-074-176-284	Sequence 284, App
1151	5	1.5	758	6	US-10-467-962B-12	Sequence 12, Appl	1226	5	1.5	932	7	US-11-057-058-59	Sequence 59, Appl
1152	5	1.5	761	7	US-11-110-082-34	Sequence 34, Appl	1227	5	1.5	932	7	US-11-071-581-1	Sequence 1, Appl
1153	5	1.5	769	6	US-10-467-657-3280	Sequence 3280, Ap	1228	5	1.5	934	6	US-10-858-730-8	Sequence 8, Appl
1154	5	1.5	773	6	US-10-821-234-1134	Sequence 1134, Ap	1229	5	1.5	934	6	US-11-188-743-19	Sequence 19, Appl
1155	5	1.5	773	6	US-10-995-561-852	Sequence 852, App	1230	5	1.5	943	6	US-10-467-657-5508	Sequence 5508, Ap
1156	5	1.5	774	7	US-11-000-463-459	Sequence 459, App	1231	5	1.5	944	6	US-10-793-626-3324	Sequence 3324, Ap
1157	5	1.5	774	7	US-11-077-886-34	Sequence 34, Appl	1232	5	1.5	948	6	US-10-485-517-131	Sequence 131, App
1158	5	1.5	777	6	US-10-821-234-1658	Sequence 1658, Ap	1233	5	1.5	948	6	US-10-523-477-14	Sequence 14, Appl
1159	5	1.5	779	7	US-11-128-420-12	Sequence 12, Appl	1234	5	1.5	950	6	US-10-467-657-854	Sequence 854, App
1160	5	1.5	781	7	US-11-194-246-344	Sequence 344, App	1235	5	1.5	952	6	US-11-174-166-18	Sequence 18, Appl
1161	5	1.5	782	6	US-10-793-626-2352	Sequence 2352, Ap	1236	5	1.5	963	7	US-11-174-166-20	Sequence 20, Appl
1162	5	1.5	782	6	US-10-821-234-1592	Sequence 1592, Ap	1237	5	1.5	977	7	US-11-093-274-39	Sequence 39, Appl
1163	5	1.5	782	6	US-10-972-053-2	Sequence 2, Appl	1238	5	1.5	966	6	US-10-821-334-1310	Sequence 1310, Ap
1164	5	1.5	782	6	US-10-972-053-8	Sequence 8, Appl	1239	5	1.5	1005	7	US-11-113-424-63	Sequence 63, Appl
1165	5	1.5	782	6	US-10-995-561-861	Sequence 861, App	1240	5	1.5	1008	7	US-11-055-822-312	Sequence 312, App
1166	5	1.5	783	7	US-11-082-389-354	Sequence 354, App	1241	5	1.5	1015	6	US-10-957-569-51	Sequence 51, Appl
1167	5	1.5	784	6	US-10-972-053-10	Sequence 10, Appl	1242	5	1.5	1022	7	US-11-186-284-163	Sequence 163, App
1169	5	1.5	790	7	US-11-080-991-82	Sequence 82, Appl	1243	5	1.5	1029	6	US-10-821-234-908	Sequence 908, App
1170	5	1.5	791	6	US-10-972-053-4	Sequence 4, Appl	1246	5	1.5	1031	6	US-10-857-780-22	Sequence 22, Appl
1171	5	1.5	791	6	US-10-467-657-5014	Sequence 5014, Ap	1247	5	1.5	1044	7	US-11-110-204-2	Sequence 2, Appl
1172	5	1.5	792	6	US-10-972-053-12	Sequence 12, Appl	1248	5	1.5	1045	7	US-11-055-822-100	Sequence 100, App
1173	5	1.5	792	6	US-10-467-657-6026	Sequence 6026, Ap	1249	5	1.5	1045	7	US-11-113-424-54	Sequence 54, Appl
1174	5	1.5	792	6	US-10-467-657-7528	Sequence 7528, Ap	1250	5	1.5	1047	6	US-10-510-386-200	Sequence 200, App
1175	5	1.5	797	6	US-10-995-561-802	Sequence 802, App	1251	5	1.5	1048	6	US-10-392-234A-14	Sequence 14, Appl
1176	5	1.5	805	6	US-10-518-599-2	Sequence 2, Appl	1252	5	1.5	1048	6	US-10-392-234A-18	Sequence 18, Appl
1177	5	1.5	805	6	US-10-518-599-4	Sequence 4, Appl	1253	5	1.5	1048	6	US-10-392-234A-20	Sequence 20, Appl
1178	5	1.5	805	6	US-10-518-599-24	Sequence 24, Appl	1254	5	1.5	1049	7	US-10-392-234A-12	Sequence 12, Appl
1179	5	1.5	806	6	US-10-467-657-8246	Sequence 8246, Ap	1255	5	1.5	1049	7	US-11-137-465-42	Sequence 42, Appl
1180	5	1.5	808	7	US-10-878-556A-80	Sequence 80, Appl	1256	5	1.5	1052	6	US-10-467-657-3992	Sequence 3992, Ap
1181	5	1.5	808	7	US-11-110-082-58	Sequence 38, Appl	1257	5	1.5	1059	7	US-10-467-657-3992	Sequence 5, Appl
1182	5	1.5	814	6	US-10-878-556A-161	Sequence 161, App	1258	5	1.5	1062	7	US-11-137-465-43	Sequence 43, Appl
1183	5	1.5	816	7	US-11-090-439-48	Sequence 48, Appl	1259	5	1.5	1068	6	US-10-467-657-2904	Sequence 2904, Ap
1184	5	1.5	817	7	US-11-012-762-2	Sequence 2, Appl	1260	5	1.5	1073	6	US-10-467-657-5230	Sequence 5230, Ap
1185	5	1.5	826	6	US-10-878-556A-68	Sequence 68, Appl	1261	5	1.5	1075	7	US-11-089-551A-23	Sequence 23, Appl
1186	5	1.5	828	6	US-10-501-039-2	Sequence 2, Appl	1262	5	1.5	1084	7	US-11-062	Sequence 8, Appl
1187	5	1.5	833	7	US-10-667-295-102	Sequence 102, App	1263	5	1.5	1094	6	US-10-821-234-1097	Sequence 1097, Ap
1188	5	1.5	833	7	US-11-076-187-5	Sequence 5, Appl	1264	5	1.5	1114	6	US-10-857-780-27	Sequence 27, Appl
1190	5	1.5	839	6	US-10-667-295-101	Sequence 101, App	1265	5	1.5	1116	6	US-10-485-517-238	Sequence 238, App
1191	5	1.5	839	7	US-11-076-431-2	Sequence 2, Appl	1266	5	1.5	1117	6	US-10-485-517-206	Sequence 206, App
1192	5	1.5	839	7	US-11-076-431-4	Sequence 4, Appl	1267	5	1.5	1122	6	US-10-821-334-1657	Sequence 1657, Ap
1193	5	1.5	839	7	US-11-076-431-6	Sequence 6, Appl	1268	5	1.5	1124	6	US-10-858-730-12	Sequence 12, Appl
1194	5	1.5	839	7	US-11-076-431-8	Sequence 8, Appl	1269	5	1.5	1126	7	US-11-075-185-3	Sequence 3, Appl
1195	5	1.5	840	6	US-10-645-441-1	Sequence 1, Appl	1270	5	1.5	1127	6	US-10-858-730-13	Sequence 13, Appl
1196	5	1.5	840	7	US-11-108-172-1102	Sequence 1102, Ap	1271	5	1.5	1133	6	US-10-821-334-1219	Sequence 1219, Ap
1197	5	1.5	841	6	US-10-624-932-6	Sequence 6, Appl	1272	5	1.5	1137	6	US-10-499-715-4	Sequence 4, Appl
1198	5	1.5	841	6	US-10-624-932-8	Sequence 8, Appl	1273	5	1.5	1141	6	US-10-995-561-1009	Sequence 1009, Ap
1199	5	1.5	842	6	US-10-645-441-2	Sequence 2, Appl	1274	5	1.5	1141	6	US-10-995-561-1010	Sequence 1010, Ap
1200	5	1.5	842	6	US-11-038-284-38	Sequence 38, Appl	1275	5	1.5	1142	7	US-11-044-051-73	Sequence 73, Appl
1201	5	1.5	845	7	US-11-147-047-46	Sequence 46, Appl	1276	5	1.5	1144	6	US-10-467-657-1820	Sequence 1820, App
1202	5	1.5	847	6	US-10-995-561-863	Sequence 863, App	1277	5	1.5	1152	7	US-11-055-822-308	Sequence 308, App
1203	5	1.5	847	6	US-10-995-561-865	Sequence 865, App	1278	5	1.5	1158	7	US-11-075-646-6	Sequence 6, Appl
1204	5	1.5	847	7	US-11-038-284-42	Sequence 42, App	1279	5	1.5	1163	7	US-11-044-899-2	Sequence 2, Appl
1205	5	1.5	852	6	US-10-467-657-5004	Sequence 5004, Ap	1280	5	1.5	1163	7	US-11-044-899-30	Sequence 30, Appl
1206	5	1.5	852	6	US-10-645-441-15	Sequence 15, Appl	1281	5	1.5	1167	6	US-10-942-072-6	Sequence 6, Appl
1207	5	1.5	853	6	US-10-420-192-6	Sequence 6, Appl	1282	5	1.5	1168	6	US-10-942-072-13	Sequence 13, Appl
1208	5	1.5	858	6	US-10-645-441-18	Sequence 18, Appl	1283	5	1.5	1170	6	US-10-942-072-11	Sequence 11, Appl
1209	5	1.5	858	6	US-10-645-441-20	Sequence 20, Appl	1284	5	1.5	1170	6	US-10-831-997-22	Sequence 22, Appl
1210	5	1.5	858	6	US-10-645-441-23	Sequence 23, Appl	1285	5	1.5	1170	6	US-10-995-561-594	Sequence 594, App
1211	5	1.5	858	6	US-10-645-441-25	Sequence 25, Appl	1286	5	1.5	1170	6	US-10-995-561-595	Sequence 595, App
1212	5	1.5	858	6	US-10-878-556A-113	Sequence 113, App	1287	5	1.5	1170	6	US-10-995-561-596	Sequence 596, App
1213	5	1.5	858	6	US-10-995-561-854	Sequence 854, App	1288	5	1.5	1170	7	US-11-046-456-28	Sequence 28, Appl
1214	5	1.5	862	7	US-11-128-420-11	Sequence 11, Appl	1289	5	1.5	1170	7	US-11-046-644-28	Sequence 28, Appl
1215	5	1.5	873	7	US-11-038-284-35	Sequence 35, Appl	1290	5	1.5	1178	6	US-10-995-561-851	Sequence 851, App
1216	5	1.5	874	6	US-10-510-386-28	Sequence 28, Appl	1291	5	1.5	1178	6	US-11-044-899-29	Sequence 29, Appl
1217	5	1.5	877	6	US-10-821-234-960	Sequence 960, App	1292	5	1.5	1179	7	US-11-097-125-1	Sequence 1, Appl
1218	5	1.5	885	6	US-10-467-657-2302	Sequence 2302, Ap	1293	5	1.5	1189	7	US-11-074-176-134	Sequence 134, App
1219	5	1.5	889	7	US-11-038-284-15	Sequence 15, Appl	1294	5	1.5	1189	6	US-10-667-295-259	Sequence 259, App
1220	5	1.5	892	6	US-10-507-275-3	Sequence 3, Appl	1295	5	1.5	1196	6	US-10-667-295-100	Sequence 100, App
1221	5	1.5	898	7	US-11-099-691-7	Sequence 7, Appl	1296	5	1.5	1196	6	US-10-995-561-921	Sequence 921, App
1222	5	1.5	914	7	US-11-108-172-1066	Sequence 1066, Ap	1298	5	1.5	1211	7	US-11-186-284-4	Sequence 4, Appl
1223	5	1.5	914	7	US-11-148-108-41	Sequence 41, Appl	1299	5	1.5	1218	7	US-11-078-735-20	Sequence 20, Appl
1224	5	1.5	919	6	US-10-821-234-1144	Sequence 1144, Ap	1300	5	1.5	1234	6	US-10-667-295-260	Sequence 260, App



1301	5	1.5	1234	6	US-10-995-561-870	Sequence 870, Appl	1374	5	1.5	3704	6	US-10-513-786-1	Sequence 1, Appl1
1302	5	1.5	1250	7	US-11-137-465-62	Sequence 62, Appl	1375	5	1.5	3803	6	US-10-995-561-773	Sequence 773, Appl
1303	5	1.5	1263	7	US-11-076-163-3	Sequence 3, Appl1	1376	5	1.5	3960	6	US-10-995-561-771	Sequence 771, Appl
1304	5	1.5	1271	6	US-10-770-726-46	Sequence 46, Appl	1377	5	1.5	4128	6	US-10-770-726-77	Sequence 77, Appl
1305	5	1.5	1279	6	US-10-793-626-3188	Sequence 3188, Ap	1378	5	1.5	4346	6	US-10-995-561-671	Sequence 671, Appl
1306	5	1.5	1299	6	US-10-821-234-1145	Sequence 1145, Ap	1379	5	1.5	4347	6	US-10-995-561-670	Sequence 670, Appl
1307	5	1.5	1342	6	US-10-770-726-63	Sequence 63, Appl	1380	5	1.5	4374	7	US-11-128-572-2	Sequence 2, Appl1
1308	5	1.5	1342	7	US-11-113-202-12	Sequence 12, Appl	1381	5	1.5	4384	6	US-10-821-234-1120	Sequence 1120, Ap
1309	5	1.5	1342	7	US-11-113-202-14	Sequence 14, Appl	1382	5	1.5	4419	6	US-10-821-234-1135	Sequence 1155, Ap
1310	5	1.5	1346	7	US-11-060-005-2	Sequence 2, Appl1	1383	5	1.5	5335	6	US-10-995-561-777	Sequence 777, Appl
1311	5	1.5	1365	6	US-11-188-743-22	Sequence 22, Appl	1384	5	1.5	5405	7	US-11-108-172-1116	Sequence 1116, Ap
1312	5	1.5	1365	6	US-10-995-561-867	Sequence 867, App	1385	5	1.5	5415	6	US-10-995-561-779	Sequence 779, App
1313	5	1.5	1366	6	US-10-995-561-868	Sequence 868, App	1386	5	1.5	5464	6	US-10-995-561-775	Sequence 775, App
1314	5	1.5	1375	6	US-10-995-561-809	Sequence 809, App	1387	5	1.2	5935	4	US-10-995-561-776	Sequence 776, App
1315	5	1.5	1377	6	US-10-821-234-1070	Sequence 1070, Ap	1388	5	1.2		7	US-11-016-503-35	Sequence 35, Appl
1316	5	1.5	1381	6	US-10-467-657-178	Sequence 178, App	1389	4	1.2	5	6	US-10-467-657-6796	Sequence 6796, Ap
1317	5	1.5	1402	6	US-10-467-657-1726	Sequence 3726, Ap	1390	4	1.2	5	7	US-11-178-373-14	Sequence 14, Appl
1318	5	1.5	1404	6	US-10-995-561-526	Sequence 526, Appl	1391	4	1.2	5	7	US-11-127-601-16	Sequence 16, Appl
1319	5	1.5	1411	6	US-10-995-561-869	Sequence 869, App	1392	4	1.2	5	7	US-11-062-186-72	Sequence 72, Appl
1320	5	1.5	1411	6	US-10-995-561-869	Sequence 869, App	1393	4	1.2	6	7	US-11-009-939-23	Sequence 23, Appl
1321	5	1.5	1420	7	US-11-074-550-110	Sequence 110, App	1394	4	1.2	6	7	US-11-167-710-10	Sequence 10, Appl
1322	5	1.5	1437	7	US-11-074-176-96	Sequence 96, Appl	1395	4	1.2	6	7	US-10-509-170-4	Sequence 4, Appl1
1323	5	1.5	1458	7	US-11-096-274-2	Sequence 2, Appl1	1396	4	1.2	7	6	US-10-981-873-35	Sequence 35, Appl
1324	5	1.5	1463	6	US-10-971-982-3	Sequence 3, Appl1	1397	4	1.2	7	6	US-10-467-657-8713	Sequence 8713, Ap
1325	5	1.5	1510	7	US-11-055-822-72	Sequence 72, Appl	1398	4	1.2	7	6	US-10-467-657-8863	Sequence 8863, Ap
1326	5	1.5	1581	7	US-11-090-439-24	Sequence 24, Appl	1399	4	1.2	7	6	US-10-925-366A-35	Sequence 35, Appl
1327	5	1.5	1581	7	US-11-090-439-26	Sequence 26, Appl	1400	4	1.2	7	6	US-10-925-366A-50	Sequence 50, Appl
1328	5	1.5	1588	6	US-10-995-561-527	Sequence 527, App	1401	4	1.2	7	6	US-10-925-366A-65	Sequence 65, Appl
1329	5	1.5	1596	7	US-11-060-005-4	Sequence 4, Appl1	1402	4	1.2	7	6	US-10-925-366A-68	Sequence 68, Appl
1330	5	1.5	1614	7	US-11-108-528-82	Sequence 82, Appl	1403	4	1.2	7	7	US-11-036-706-89	Sequence 89, Appl
1331	5	1.5	1615	7	US-11-108-528-80	Sequence 80, Appl	1404	4	1.2	7	7	US-11-033-365-25	Sequence 25, Appl
1332	5	1.5	1618	6	US-10-984-645-2	Sequence 2, Appl1	1405	4	1.2	7	7	US-11-101-287-89	Sequence 89, Appl
1333	5	1.5	1637	6	US-10-821-234-1204	Sequence 1204, Ap	1406	4	1.2	7	7	US-11-115-922-89	Sequence 89, Appl
1334	5	1.5	1734	7	US-11-192-967-6	Sequence 6, Appl1	1407	4	1.2	7	7	US-11-115-922-160	Sequence 160, App
1335	5	1.5	1804	6	US-10-513-786-2	Sequence 2, Appl1	1408	4	1.2	7	7	US-11-135-414-3	Sequence 3, Appl1
1336	5	1.5	1857	7	US-11-057-058-60	Sequence 60, Appl	1409	4	1.2	8	6	US-11-055-163-23	Sequence 8559, Ap
1337	5	1.5	1857	7	US-11-057-058-60	Sequence 60, Appl	1410	4	1.2	8	6	US-10-467-657-8959	Sequence 8559, Ap
1338	5	1.5	1874	6	US-10-821-234-1182	Sequence 61, Appl	1411	4	1.2	8	7	US-11-011-666-6	Sequence 6, Appl
1339	5	1.5	1889	7	US-11-102-476-46	Sequence 46, Appl	1412	4	1.2	8	7	US-11-054-515-1157	Sequence 3157, Appl
1340	5	1.5	1892	7	US-11-075-185-6	Sequence 46, Appl1	1413	4	1.2	8	7	US-11-045-024-1116	Sequence 116, App
1341	5	1.5	1933	6	US-10-523-912-2	Sequence 2, Appl1	1414	4	1.2	8	7	US-11-045-024-1104	Sequence 1104, Ap
1342	5	1.5	2080	6	US-10-821-234-1640	Sequence 1640, Ap	1415	4	1.2	8	7	US-11-045-024-1105	Sequence 1105, Ap
1343	5	1.5	2102	6	US-10-995-561-990	Sequence 990, App	1416	4	1.2	8	7	US-11-045-024-1584	Sequence 1584, Ap
1344	5	1.5	2108	6	US-10-995-561-989	Sequence 989, App	1417	4	1.2	8	7	US-11-045-024-1614	Sequence 1614, Ap
1345	5	1.5	2157	6	US-10-995-561-991	Sequence 991, App	1418	4	1.2	8	7	US-11-045-024-1657	Sequence 1657, Ap
1346	5	1.5	2157	6	US-10-995-561-991	Sequence 991, App	1419	4	1.2	8	7	US-11-045-024-1937	Sequence 2937, Ap
1347	5	1.5	2197	7	US-11-075-185-8	Sequence 8, Appl1	1420	4	1.2	8	7	US-11-045-024-1016	Sequence 4016, Ap
1348	5	1.5	2280	7	US-11-022-562-211	Sequence 211, App	1421	4	1.2	8	7	US-11-045-024-1359	Sequence 4359, Ap
1349	5	1.5	2333	7	US-11-096-281-13	Sequence 13, Appl	1422	4	1.2	8	7	US-11-045-024-5291	Sequence 5291, Ap
1350	5	1.5	2339	7	US-11-096-281-11	Sequence 11, Appl	1423	4	1.2	8	7	US-11-045-024-5463	Sequence 5463, Ap
1351	5	1.5	2376	7	US-11-096-051-4	Sequence 4, Appl1	1424	4	1.2	8	7	US-11-045-024-5464	Sequence 5464, Ap
1352	5	1.5	2491	6	US-10-995-561-769	Sequence 769, App	1425	4	1.2	8	7	US-11-045-024-5471	Sequence 5471, Ap
1353	5	1.5	2515	7	US-11-113-424-53	Sequence 53, Appl	1426	4	1.2	8	7	US-11-045-024-5625	Sequence 5625, Ap
1354	5	1.5	2516	6	US-10-647-956A-2	Sequence 2, Appl1	1427	4	1.2	8	7	US-11-045-024-5761	Sequence 5761, Ap
1355	5	1.5	2715	7	US-11-096-051-2	Sequence 2, Appl1	1428	4	1.2	8	7	US-11-045-024-5979	Sequence 5979, Ap
1356	5	1.5	2715	7	US-11-113-424-51	Sequence 51, Appl	1429	4	1.2	8	7	US-11-045-024-7316	Sequence 7316, Ap
1357	5	1.5	2725	7	US-11-096-051-10	Sequence 10, Appl	1430	4	1.2	8	7	US-11-045-024-7517	Sequence 7517, Ap
1358	5	1.5	2725	7	US-11-096-051-8	Sequence 8, Appl1	1431	4	1.2	8	7	US-11-045-024-9035	Sequence 9035, Ap
1359	5	1.5	2725	7	US-11-113-424-52	Sequence 52, Appl	1432	4	1.2	8	7	US-11-045-024-9149	Sequence 9149, Ap
1360	5	1.5	2763	7	US-11-113-424-14	Sequence 14, Appl	1433	4	1.2	8	7	US-11-045-024-9188	Sequence 9188, Ap
1361	5	1.5	2828	7	US-11-080-991-54	Sequence 54, Appl	1434	4	1.2	8	7	US-11-045-024-11343	Sequence 11343, A
1362	5	1.5	2828	7	US-11-186-284-49	Sequence 49, Appl	1435	4	1.2	8	7	US-11-045-024-9204	Sequence 9204, Ap
1363	5	1.5	2897	6	US-10-499-715-2	Sequence 2, Appl1	1436	4	1.2	8	7	US-11-045-024-9284	Sequence 9284, Ap
1364	5	1.5	2910	7	US-11-087-100-2	Sequence 2, Appl1	1437	4	1.2	8	7	US-11-045-024-10113	Sequence 10113, A
1365	5	1.5	2910	7	US-11-087-084-2	Sequence 2, Appl1	1438	4	1.2	8	7	US-11-045-024-10266	Sequence 10266, A
1366	5	1.5	2910	7	US-11-087-085-2	Sequence 2, Appl1	1439	4	1.2	8	7	US-11-045-024-10286	Sequence 10286, A
1367	5	1.5	3011	6	US-10-985-205-3	Sequence 3, Appl1	1440	4	1.2	8	7	US-11-045-024-11331	Sequence 11331, A
1368	5	1.5	3056	7	US-11-109-156-20	Sequence 20, Appl	1441	4	1.2	8	7	US-11-045-024-11351	Sequence 11351, A
1369	5	1.5	3073	7	US-11-143-980-50	Sequence 50, Appl	1442	4	1.2	8	7	US-11-045-024-12002	Sequence 12002, A
1370	5	1.5	3144	7	US-11-055-035-1	Sequence 1, Appl1	1443	4	1.2	9	6	US-11-045-024-12116	Sequence 12116, A
1371	5	1.5	3588	6	US-10-995-561-672	Sequence 672, App	1444	4	1.2	9	6	US-10-984-376-15	Sequence 15, Appl
1372	5	1.5	3623	6	US-10-995-561-593	Sequence 593, Appl	1445	4	1.2	9	6	US-10-981-873-22	Sequence 22, Appl
1373	5	1.5	3655	7	US-11-075-185-5	Sequence 5, Appl1	1446	4	1.2	9	6	US-10-952-535A-44	Sequence 44, Appl



1447	4	1.2	9	6	US-10-623-155-226	Sequence 226, App
1448	4	1.2	9	6	US-10-481-096-66	Sequence 66, App1
1449	4	1.2	9	6	US-10-481-096-68	Sequence 68, App1
1450	4	1.2	9	6	US-10-491-096-100	Sequence 100, App
1451	4	1.2	9	6	US-10-491-096-165	Sequence 165, App
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1494	4	1.2	9	7	US-11-010-748A-734	Sequence 734, App
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1497	4	1.2	9	7	US-11-010-748A-740	Sequence 740, App
1498	4	1.2	9	7	US-11-010-748A-742	Sequence 742, App
1499	4	1.2	9	7	US-11-010-748A-743	Sequence 743, App
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Job time : 15 secs



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## OM protein - protein search, using sw model

Run on: December 16, 2005, 11:35:44 ; Search time 164 Seconds  
(without alignments)  
853.493 Million cell updates/sec

Perfect score: 335  
Sequence: 1 MAGSPCTLTLYILMQLTGS.....PHSLTMPDTRRLPAYENV1 335

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

## Database :

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5: /cgn2\_6/ptodaca/1/pubpaa/US10B\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	335	100.0	335	3	US-09-732-524-2
8	335	100.0	335	3	US-09-745-605-4
29	335	100.0	335	3	US-09-997-428-253
540	335	100.0	335	4	US-10-021-741A-2
565	335	100.0	335	4	US-10-174-587-192
629	335	100.0	335	4	US-10-063-742-46
739	335	100.0	335	4	US-10-262-839-110
745	335	100.0	335	5	US-10-842-011-2
746	335	100.0	335	5	US-10-972-317-46
748	335	100.0	335	5	US-10-950-374-253
751	312	93.1	312	3	US-09-732-524-4
752	234	69.9	335	4	US-10-104-943-5
753	234	69.9	335	4	US-10-436-523-60
754	234	69.9	335	4	US-10-408-765A-1405
755	217	64.8	348	4	US-10-262-839-112
761	110	32.8	110	4	US-10-143-050-125
762	110	32.8	110	5	US-10-960-251-125
763	92	27.5	684	5	US-10-450-763-42056
764	91	27.2	91	3	US-09-864-761-41706
765	33	9.9	33	3	US-09-984-245-244
766	33	9.9	33	3	US-09-966-262-244
767	33	9.9	33	3	US-09-983-966-244
768	33	9.9	33	4	US-10-059-395-244

769	33	9.9	33	4	US-10-143-090-244	Sequence 244, App
770	33	9.9	33	5	US-10-960-251-244	Sequence 244, App
771	27	8.1	28	3	US-09-984-245-243	Sequence 243, App
772	27	8.1	28	3	US-09-966-262-243	Sequence 243, App
773	27	8.1	28	3	US-09-983-966-243	Sequence 243, App
774	27	8.1	28	4	US-10-059-395-243	Sequence 243, App
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779	8	2.4	130	5	US-10-739-930-9038	Sequence 9038, Ap
780	8	2.4	152	4	US-10-767-701-56655	Sequence 56655, A
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783	8	2.4	200	4	US-10-767-701-36759	Sequence 36759, A
784	8	2.4	224	4	US-10-767-701-45460	Sequence 45460, A
785	8	2.4	289	5	US-10-960-275-8	Sequence 8, Appl1
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1411	8	2.4	1280	4	US-10-262-839-92	Sequence 92, Appl1
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